Examination of the regulatory cascade leading to clavulanic acid production in *Streptomyces clavuligerus*

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ABSTRACT

The soil bacterium *Streptomyces clavuligerus* is important from a pharmacological and commercial standpoint because it is capable of producing many known secondary metabolites, including the potent β-lactamase inhibitor clavulanic acid (CA). This research sought to elucidate unknown aspects of the regulation of CA production in *S. clavuligerus* via an iTRAQ®-based proteomic study comparing the CA producing wild-type strain and two bald mutants, one of which is defective in both CA production and normal development (*ΔbldG*) and one which is defective only in normal development (*ΔbldA*). A total of 33.5% of the entire *S. clavuligerus* proteome was covered, including 10 sigma factors and over 200 regulators and hypothetical regulators. Many of the regulatory elements were differentially expressed among the strains and several are putatively regulated by the pleiotropic regulator BldG. This study represents the most complete proteomic analysis of *S. clavuligerus* to date and the only such analysis of a CA producing and a non-producing strain. The protein expression data can serve as a useful tool to direct future research into additional aspects of CA biosynthesis and secondary metabolism.

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List of Abbreviations and Symbols

The following table includes the various abbreviations and acronyms used throughout the thesis and their significance. Acronyms common throughout the life sciences, such as DNA, are not included in this list.

Abbreviation	Meaning
Apra	Apramycin
APS	Ammonium persulfate
BCA	Bicinchronic acid
BSA	Bovine serum albumin
CA	Clavulanic acid
CDD	Conserved domain database (NCBI)
CID	Collision induced dissociation
DAD	Diode array detector
DMSO	Dimethyl sulfoxide
DTT	Dithiothreitol
ECF	Extracytoplasmic function
EDTA	Ethylenediaminetetraacetic acid
FDR	False discovery rate
HCD	Higher-energy collisional dissociation
HPLC	High performance liquid chromatography
IPTG	Isopropyl-beta-D-thiogalactopyranoside
ISP-4	International *Streptomyces* Project Media #4
iTRAQ®	Isobaric tag for relative and absolute quantitation
LB	Lennox broth
LC-MS/MS	Liquid chromatography-tandem mass spectrometry
MS	Mass spectrometry
MMTS	Methyl methanethiosulfonate
MYM	Maltose-Yeast Extract-Malt Extract
NCBI	National Center for Biotechnology Information
NRPS	Non-ribosomal polyketide synthetase
OD	Optical density
PAG	Polyacrylamide gel
PAGE	Polyacrylamide gel electrophoresis
PBS	Phosphate buffered saline
PCR	Polymerase chain reaction
PKS	Polyketide synthase
SA	Starch asparagine media
SDS	Sodium dodecyl sulfate
TBE	Tris-borate-EDTA
TCEP	Tris(2-carboxyethyl)phosphine hydrochloride
TE	Tris-EDTA
TEAB	Triethylammonium bicarbonate
TEMED	Tetramethylethylenediamine
TSBA	Trypticase soy agar
TSBS	Trypticase soy broth, supplemented with starch
Tsr	Thiostrepton
WT	Wild-type
X-gal	5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside
YT	Yeast extract-tryptone medium

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Chapter 1: Introduction

1.1: The genus *Streptomyces*

The genus *Streptomyces* is defined by a combination of chemical and phenotypic characteristics, namely 16S rRNA gene sequence homologies, the presence of the LL isomer of diaminopimelic acid in the peptidoglycan cross links of the cell wall and colony morphology (Wellington et al. 1992; Williams et al. 1983). This third characteristic is the most unique feature of the genus. The *Streptomyces* lifecycle includes vegetative mycelia (the portion that obtains nutrients from the substrate), aerial hyphae (the portion involved in reproduction and gives *Streptomyces* colonies their characteristic "fuzzy" appearance) and spores (that assist in their dispersal). Furthermore, the *Streptomyces* are capable of producing a wide variety of secondary metabolites or compounds that are not necessary for the growth, development, or the reproduction of the organism. While the function of many of these metabolites in the producing species remains unknown, several of them are important to human society and are used in medicine as antitumor agents, immunosuppressants, and two-thirds of all clinically used antibiotics (Augustine et al. 2005; Goto et al. 1987; Hopwood 1999; Schmitz et al. 1962; Watve et al. 2001).

1.1.1: Growth and physiology

Streptomyces species have growth characteristics that resemble eukaryotic organisms such as fungi. Their complex lifecycle begins when a germination trigger such as favorable environmental conditions causes the germ tube to emerge from the unigenomic spore (Chater and Losick 1996). Germination is thought to be density-

dependent, as higher spore densities inhibits germination (Triger et al. 1991). From here, the cell wall grows primarily at the tips of the mycelia, and after several rounds of DNA replication, new tips branch out as further chromosomal doublings take place. This stage of the *Streptomyces* life cycle leads to multi-cellular mycelia. As the colonies grow, the mycelia become dense and several key changes take place. There is increased production of extracellular proteins, biosynthesis and storage of glycogen in substrate hyphae, initiation of programmed compartmental lysis of substrate hyphae, the onset of secondary metabolism and initiation of aerial hyphae formation (Chakraburtty and Bibb 1997; Kieser et al. 2000; Ochi 1986).

The aerial hyphae extend via tip growth implying that there is a need to diffuse nutrients to the basal part of the colony to support this (Miguelez et al. 1994). Septa form some distance behind the mycelial tips to produce apical and a sub-apical compartments, and the sub-apical compartments cease new cell wall synthesis (Chater and Losick 1996). Under the control of several regulatory genes, the multigenomic tips undergo synchronous cellular division, which results in the formation of unigenomic, cylindrical pre-spore compartments that will eventually become a chain of spores (Flardh and Buttner 2009). Glycogen deposits form in these compartments using enzymes that are distinct from those involved in substrate hyphae glycogen synthesis (Bruton et al. 1995). These glycogen deposits are used as the compartments begin to develop grey-pigmented walls in the mature spores (Wildermuth and Hopwood 1970).

As soil colonizers, the ability to grow into a hyphal mass and to sporulate allows members of this genus to spread and to be incredibly persistent, leading to the ubiquity of the *Streptomyces* in nature. In addition to being soil colonizers, many *Streptomyces* are also able to successfully colonize the rhizophere, particularly in dryer climates (Watson and Williams 1974). This may be in part because they are non-motile and are able to form hyphae, providing an advantage over Gram-negative soil bacteria that are typically motile and are more common in more aqueous environments (Juhnke et al. 1987).

1.1.2: *Streptomyces clavuligerus*

Streptomyces clavuligerus was first isolated from a South American soil sample (Higgens and Kastner 1971). The species is important from a pharmacological and commercial standpoint because it is capable of producing many known secondary metabolites. These include several antibiotics such as cephamycin C, penicillin N, and holomycin, the β-lactamase inhibitor clavulanic acid (CA), as well as the immunosuppressant FK506 (Figure 1.1.2.1) (Li and Walsh 2010; Mo et al. 2009; Reading and Cole 1977). The *S. clavuligerus* genome sequence has revealed that it contains a large number of putative secondary metabolite gene clusters (48 in total) (Song et al. 2010). *S. clavuligerus* also contains the largest plasmid sequenced to date (pSCL4), which is 1.8 Mbp in size and contains 25 of the 48 putative secondary metabolite encoding gene clusters in this organism (Medema et al. 2010). Additionally, *S. clavuligerus* is unique from other *Streptomyces* species in that it is incapable of utilizing glucose and possesses all of the enzymes of the urea cycle, though it is at this time uncertain if the cycle is functional (Garcia-Dominguez et al. 1989).

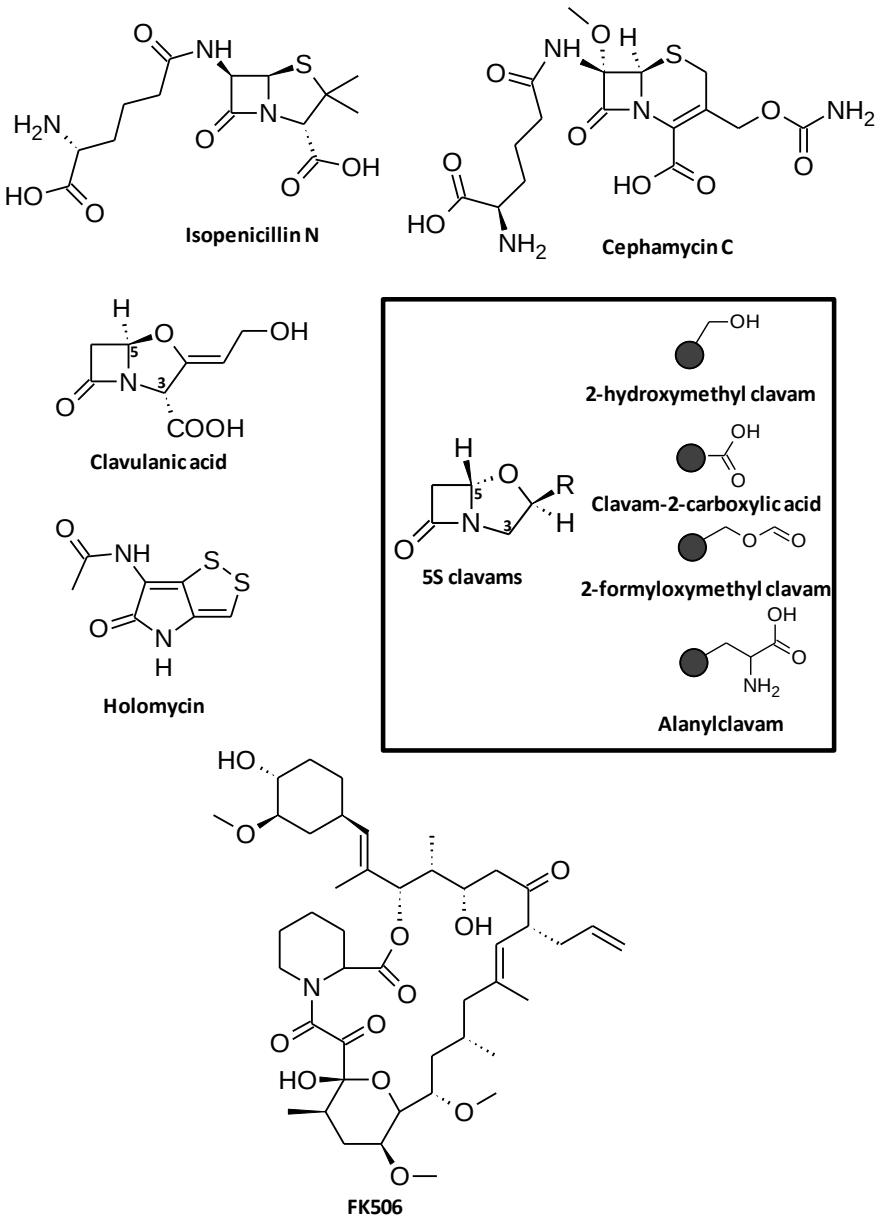

Figure 1.1.2.1: Selected secondary metabolites produced by *S. clavuligerus*. The β-lactam antibiotics isopenicillin N and cephamycin C, the β-lactamase inhibitor clavulanic acid and the related 5*S* clavams, the pyrrothine antibiotic holomycin and the immunosuppressant FK506 are shown. The core structure present in the 5*S* clavams is shown and the respective side groups (designated by R) present in the different members are shown in the box. The grey spheres attached to the side groups in the box represent the 5*S* clavam core. The positions of the carbon atoms with different stereochemistry in clavulanic acid and the 5*S* clavams are indicated by numbers.

1.2: Clavulanic acid biosynthesis

The ability of *S. clavuligerus* to produce CA was discovered in 1976 (Reading and Cole 1977). The annual market value of CA production by *S. clavuligerus* is estimated at over 1 billion dollars (Saudagar et al. 2008). CA is a clavam metabolite (β-lactam containing an oxazolidine ring) similar in structure to penicillin (a β-lactam containing an thiazolidine ring) (Reading and Cole 1977). The β-lactam ring is a four-membered cyclic amide in which a nitrogen atom is attached to the β-carbon relative to the carbonyl (Neu 1985). The β-lactam antibiotics bind to and inhibit transpeptidases involved in the formation of the peptide cross links present in the cell walls of bacteria (Tipper and Strominger 1965). This causes weakening of the cell wall leading to lysis due to the internal turgor pressure of the cell. Therefore, members of the β-lactam family of antibiotics are used to treat a wide variety of Gram-positive and some Gram-negative bacterial infections (Fleming 1929).

While β-lactams can be very helpful in treating bacterial infections, improper use of these and other antibiotics has led to the emergence of antibiotic resistant strains of bacteria. One mode of resistance to the β-lactams is the presence of genes encoding β-lactamase enzymes, produced by both Gram-negative and Gram-positive bacteria, which cleave the β-lactam ring of the antibiotic and inactivate it (Abraham and Chain 1940; Vu and Nikaido 1985). While not a particularly effective antibiotic on its own, CA is a potent β-lactamase inhibitor. Therefore, CA can restore the activity of other β-lactam antibiotics against β-lactamase-producing bacteria when given in combination. CA has 3*R*,5*R* stereochemistry as opposed to the 3*S*,5*S* stereochemistry of the other clavams, which are

commonly referred to as the 5*S* clavams (Figure 1.1.2.1) (Baldwin and Schofield 1992). It inhibits group 2, or β-lactamases of classes A and D, which include the penicillinases, cephalosporinases and broad spectrum β-lactamases, by acting as a suicide inhibitor (Bush et al. 1995; Shahid et al. 2009). It binds irreversibly to the active site serine hydroxyl group of the β-lactamase producing a stable acylated intermediate, which results in the inactivation of the enzyme (Liras and Rodriguez-Garcia 2000). CA is currently used in combination with other β-lactams such as amoxicillin or ticarcillin in commercial preparations such as Augmentin^{TM} and Timentin^{TM}, respectively.

1.2.1: *S. clavuligerus* produces CA and the 5*S* clavams

While there are a few other species capable of producing CA, *S. clavuligerus* is unique in that it is also capable of producing the 5*S* clavams (Figure 1.1.2.1) (Brown et al. 1979; Jensen 2012). While CA and the 5*S* clavams share a biosynthetic pathway, early studies made it clear that CA biosynthesis is quite different from that of the 5*S* clavams (Romero et al. 1986). Based on the results of decades of work into the biosynthetic pathways leading to CA and the 5*S* clavams, it is proposed that the two share several "early steps" in their biosynthesis and have divergent "late steps" leading to either CA or 5*S* clavam production (Figure 1.2.1.1) (Jensen 2012; MacKenzie et al. 2007; Romero et al. 1986).

1.2.2: Organization of genes involved in CA biosynthesis

It has been determined that the genes required for producing CA and the 5*S* clavams are distributed amongst three unlinked gene clusters known as the clavulanic acid gene cluster, the clavam gene cluster and the paralogue gene cluster (Figure 1.2.3.1)

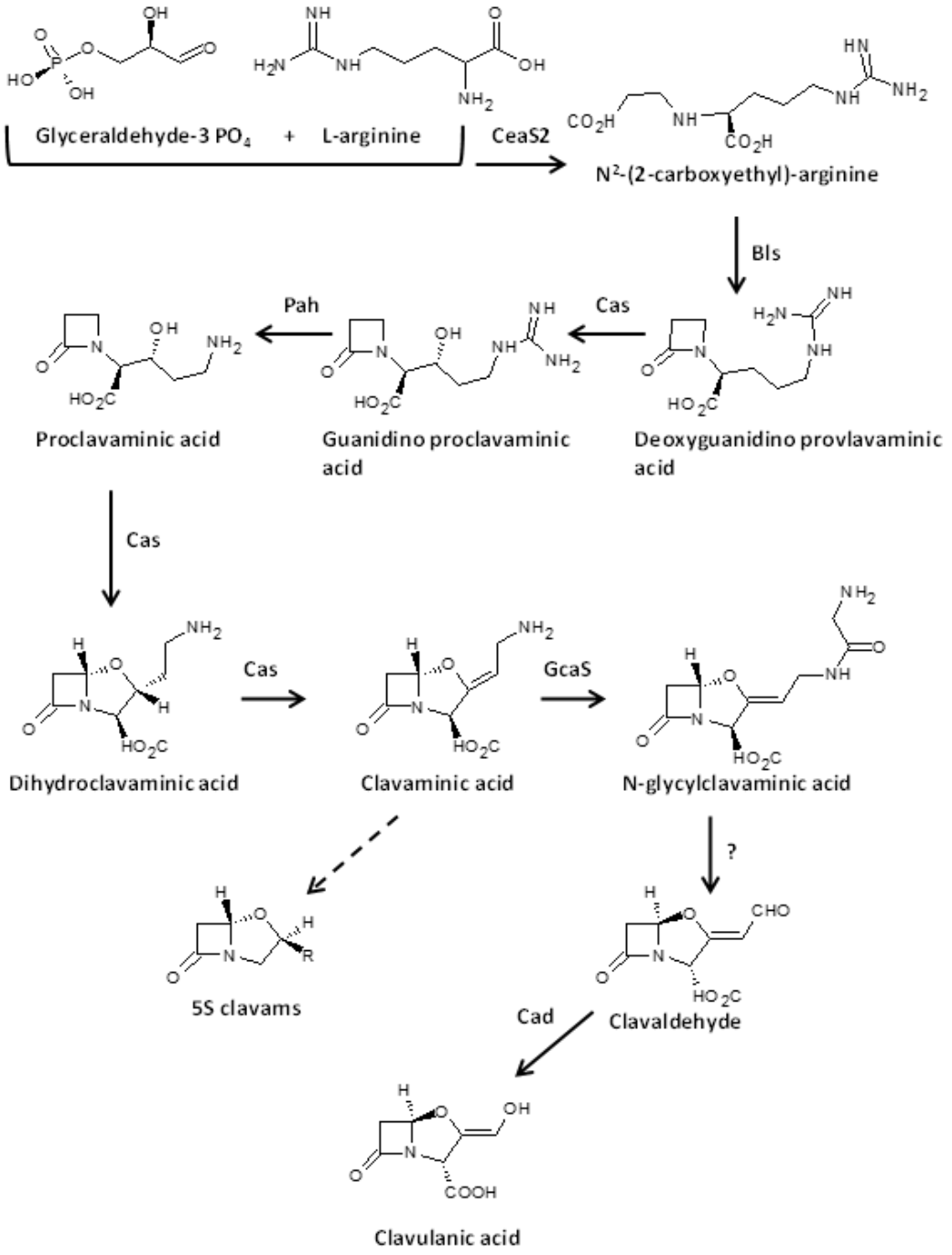

Figure 1.2.1.1: The currently proposed biosynthetic pathway leading to clavulanic acid and 5*S* clavam production in *S. clavuligerus*. Identities of the intermediates are shown and enzymes involved are also indicated above the solid arrows. Unknown enzymes are indicated with a question mark. The dotted arrow represents unknown multiple reactions leading to the respective metabolite. Please see sections 1.2.3 and 1.2.4 for more details.

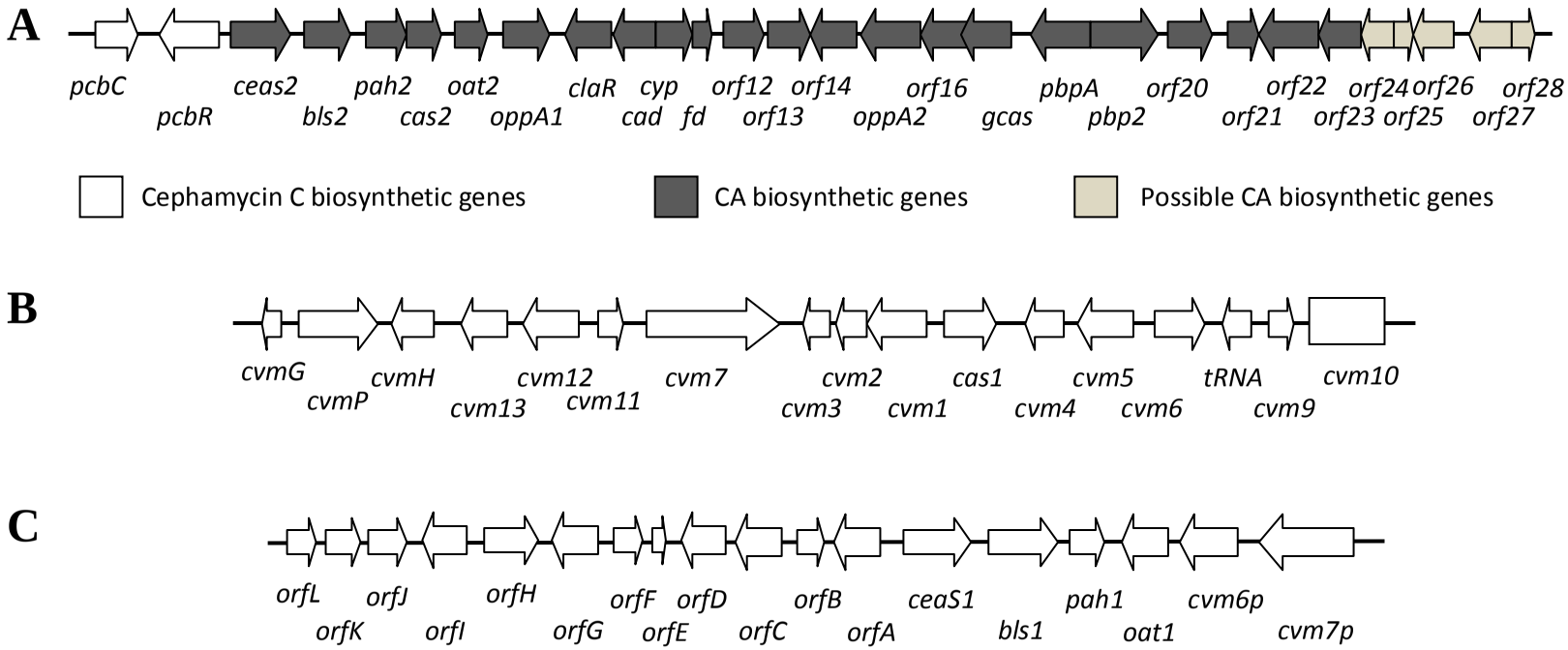

Figure 1.2.3.1: The three unlinked gene clusters for clavulanic acid (CA) and 5*S* clavam biosynthesis in *S. clavuligerus*. The arrows represent each gene with the arrowheads indicating their orientation and the solid line represents the *S. clavuligerus* chromosome. The names and designations of the genes as to date are also indicated. **(A)** Clavulanic acid gene cluster. Genes involved in cephamycin C biosynthesis as well as genes putatively involved in CA biosynthesis are indicated (Note: not all the genes involved in cephamycin C are shown). **(B)** Clavam gene cluster. **(C)** Paralogue gene cluster.

(Tahlan et al. 2004b; Ward and Hodgson 1993). The CA gene cluster contains most of the genes required for the early stages of CA and 5*S* clavam biosynthesis and the late stages of CA biosynthesis (Figure 1.2.3.1 A). Deletion of some of the genes involved in the early steps does not result in complete loss of CA production indicating that additional genes outside of the cluster are involved (Aidoo et al. 1994; Elson et al. 1993; Hodgson et al. 1995; Jensen et al. 2004; Jnawali et al. 2008; Li et al. 2000; Mellado et al. 2002; Song et al. 2009). The CA cluster lies adjacent to the gene cluster for cephamycin C biosynthesis, creating a CA-cephamycin C super-cluster (Ward and Hodgson 1993). The clavam cluster (Figure 1.2.3.1 B) was found to contain a second copy of the *cas* gene involved in the biosynthesis of both CA and the 5*S* clavams along with genes involved exclusively in 5*S* clavam production (Mosher et al. 1999; Paradkar and Jensen 1995). The paralogue cluster (Figure 1.2.3.1 C) was later found to contain second copies of most of the early genes from the CA cluster (Tahlan et al. 2004a; Tahlan et al. 2004c). In *S. clavuligerus*, the CA-cephamycin C super-cluster and the clavam gene cluster lie on the chromosome whereas the paralogue cluster is located on the pSCL4 mega-plasmid (Medema et al. 2010).

1.2.3: The "early" steps of CA biosynthesis

Despite the presence of a β-lactam ring in the clavams (CA and 5*S*), a tripeptide precursor is not required for their biosynthesis as compared to other conventional β-lactams such as the penicillins and cephalosporins. Arginine and ornithine were proposed to be the precursors providing the nitrogen atom present in the clavams (Romero et al. 1986), and eventually it was shown that arginine is the more direct precursor (Valentine

et al. 1993). Later, it was determined that glyceraldehyde-3-phosphate (G3P) is also directly incorporated as a starting precursor (Khaleeli et al. 1999). These two precursors are used in a thiamine diphosphate-dependent reaction catalyzed by carboxylethylarginine synthase (CeaS), which is encoded by the *ceaS2* gene (Figure 1.2.3.1) in the first dedicated step of the pathway (Khaleeli et al. 1999). This is an unusual reaction because an electrophilic rather than a nucleophilic intermediate of thiamine diphosphate is involved in the formation of an N-C bond (Merski and Townsend 2007) and the result of the reaction is N^2-(2-carboxyethyl) arginine (Figure 1.2.1.1) (Caines et al. 2004). Deletion of the *ceasS2* gene results in almost complete abolition of both CA and the 5*S* clavams (Jensen et al. 2000).

The second step of the pathway generates the β-lactam ring found in the clavams via a step completely distinct from that used for other conventional β-lactams. In this step, β-lactam synthase (Bls) converts N^2-(2-carboxyethyl)arginine to deoxyguanidinoproclavaminate by adenylation and cyclization in the presence of both ATP and Mg^{2+} (Bachmann et al. 1998). Disruption of *bls2* results in markedly decreased clavam yields (Bachmann et al. 1998). Next, clavaminate synthase (Cas) and proclavaminate amidinohyrdolase (Pah) alternate back and forth to catalyze reactions that form the bicyclic intermediate clavaminic acid (Figure 1.2.1.1) (Baldwin et al. 1991; Elson et al. 1993).

A predicted ornithine acetyltransferase is encoded by the gene *oat2* in the CA cluster (Jensen et al. 2000). It was thought that the resulting OAT2 protein was likely

able to catalyze the transfer of an acetyl group to glutamate from *N*-acetylornithine (Kershaw et al. 2002), which is an essential step in the synthesis of arginine. Therefore, *oat2* was initially thought to be involved in the condensation of arginine and G3P to give 2-carboxyethyl-arginine in the first step of CA biosynthesis. However, deletion of the *oat2* gene did not affect the total *N*-acetylornithine transferase activity and only reduced the amount of CA formed under normal culture conditions (de la Fuente et al. 2004). The *oat2* mutant also produced more CA than the WT strain when supplemented with high levels of arginine, suggesting that OAT2 somehow regulates CA production in response to arginine levels (de la Fuente et al. 2004).

The next gene in the CA cluster is *oppA1*, which encodes a predicted oligopeptide permease-type binding protein. This gene shares significant similarity to *oppA2*, which is found further downstream in the cluster, and it is likely they are both involved in peptide transport (Lorenzana et al. 2004; Mackenzie et al. 2010). Peptide binding assays revealed that recombinant OppA1 and OppA2 bind di-tripeptides containing arginine as well as brandykinins, suggesting that these two proteins may act to import peptides and arginine into the cell (Mackenzie et al. 2010). Mutants in either gene lack the ability to produce CA (Jensen et al. 2004).

1.2.4: The "late" steps of CA biosynthesis

Up until the formation of clavaminic acid (which has 3*S*, 5*S* stereochemistry) the biosynthetic pathways for CA and the 5*S* clavams are shared and it is after this step that the two pathways diverge (Figure 1.2.1.1). The *orf17* gene from the CA cluster encodes

an *N*-glycylclavaminic acid synthetase (Gcas) (Mellado et al. 2002), which was originally thought to be a carboxylase (Figure 1.2.3.1) (Jensen et al. 2004). Gcas was later determined to be a member of the ATP-grasp fold superfamily because it catalyzes the ATP-dependent conversion of CA to *N*-glycylclavaminic acid (Arulanantham et al. 2006). The mechanisms underlying the next steps: conversion of *N*-glycyl-aldehyde to clavaldehyde and the inversion of 3*S*, 5*S* to 3*R*, 5*R* stereochemistry (as in clavaldehyde) are not known, but double epimerization and oxidative deamination reactions are predicted to be involved (Jensen 2012). This unstable intermediate (clavaldehyde) also shows β-lactamase inhibitory activity, supporting the notion that such activity is a function of the 3*R*, 5*R* stereochemistry of the oxazolidine ring (Nicholson et al. 1994). In the final step clavaldehyde is reduced in an NADPH-dependent reaction by clavulanic acid dehydrogenase (Cad) to yield CA (Figure 1.2.1.1) (Fulston et al. 2001).

The ninth gene in the cluster is *cyp*, which encodes a cytochrome P-450 that likely carries out oxidative reactions in cooperation with ferredoxin proteins. This is supported by the presence of a ferredoxin protein encoded by *fd*, which lies adjacent to *cyp* (Jensen et al. 2000; Li et al. 2000). Following *fd* in the gene cluster is *orf12*, which shows similarities to class A β-lactamases. Mutation of *orf12* abolishes CA production in *S. clavuligerus* (Jensen et al. 2004; Li et al. 2000). It was thought that because the reaction that forms the β-lactam ring is in effect a reversal of β-lactamase activity, ORF12 might be involved in ring opening or re-closure of the ring for stereochemical inversion. However, the finding that ORF12 lacks several highly conserved active site residues required for β-lactamase activity does not lend support to this hypothesis (Li et al. 2000).

Further work determined that it does not show β-lactamase or penicillin-binding activity though it does show esterase activity towards 3'-O-acetyl cephalosporins, and it is still suspected to be involved in the epimerization of the oxazolidine ring from 3*S*,5*S* to 3*R*,5*R* (Valegard et al. 2013).

The remaining genes in the cluster (*orf13*-*orf16*) have also been studied via targeted inactivation. The inactivation of *orf13* (predicted to encode a membrane transport protein) results in low production levels of CA and the 5*S* clavams, suggesting that it has a role in transporting the metabolites out of the cell (Jensen et al. 2004). Inactivation of *orf14* results in almost complete abolition of CA production making it likely that the gene encodes a protein involved in biosynthesis despite the fact that it shares similarities with acetyltransferases, which can sometimes be involved in antibiotic resistance (Jensen et al. 2004; Mellado et al. 2002). *orf16* mutants are completely lacking in CA production though they do accumulate several novel clavams, namely *N*-acetylglycylclavaminic acid and *N*-glycylclavaminic acid, both of which are possible intermediates and also accumulate in *oppA2* mutants (Jensen et al. 2004). ORF16 carries a possible sortase recognition sequence, which is required for cell wall protein attachment in Gram-positive organisms (Pallen et al. 2001).

1.3: Regulation of secondary metabolism in *Streptomyces*

A majority of secondary metabolite gene clusters in *Streptomyces* species are regulated in a hierarchical manner. At the first level of control are the pathway-specific transcriptional regulators that lie within or near the secondary metabolite gene clusters. These transcriptional regulators are in turn controlled by pleiotropic or global regulatory

elements that tie the production of the secondary metabolite to morphological development (Bibb 2005; Paradkar 2013).

1.3.1: The pathway specific regulators of CA biosynthesis

While there are many genes and gene products involved in regulating CA production (Figure 1.3.1.1), two regulatory genes are of particular importance. The *claR* gene encodes a LysR-family transcriptional regulatory protein that is essential for CA but not 5*S* clavam biosynthesis (Paradkar et al. 1998). Studies comparing *claR* mutants with the WT strain show that the mutants accumulate clavaminic acid, suggesting that ClaR regulates genes involved in the latter stages of the pathway beyond clavaminic acid (Paradkar et al. 1998). A second gene called *ccaR* encodes a regulatory protein that is a member of the *Streptomyces*-antibiotic regulatory protein (SARP) family. CcaR is required for the biosynthesis of CA and cephamycin C but not for the 5*S* clavams (Alexander and Jensen 1998). Despite *ccaR* being located in the cephamycin C cluster, it acts as a direct positive regulator of *bls2*, *cas2*, *ceaS2* and *pah2*, which are involved in the early steps of CA biosynthesis (Santamarta et al. 2011). It is also responsible for the regulation of several late step genes by indirectly controlling *claR* expression levels (Figure 1.3.1.1) (Paradkar et al. 1998; Perez-Llarena et al. 1997; Santamarta et al. 2002; Song et al. 2010). Other research involving a *ccaR* mutant found that neither CA nor cephamycin C was produced but holomycin was produced at higher levels than in the WT strain (de la Fuente et al. 2002).

Further research involving the manipulation of *ccaR* and *claR* has produced promising results, which are of importance to the commercial production of CA. It has

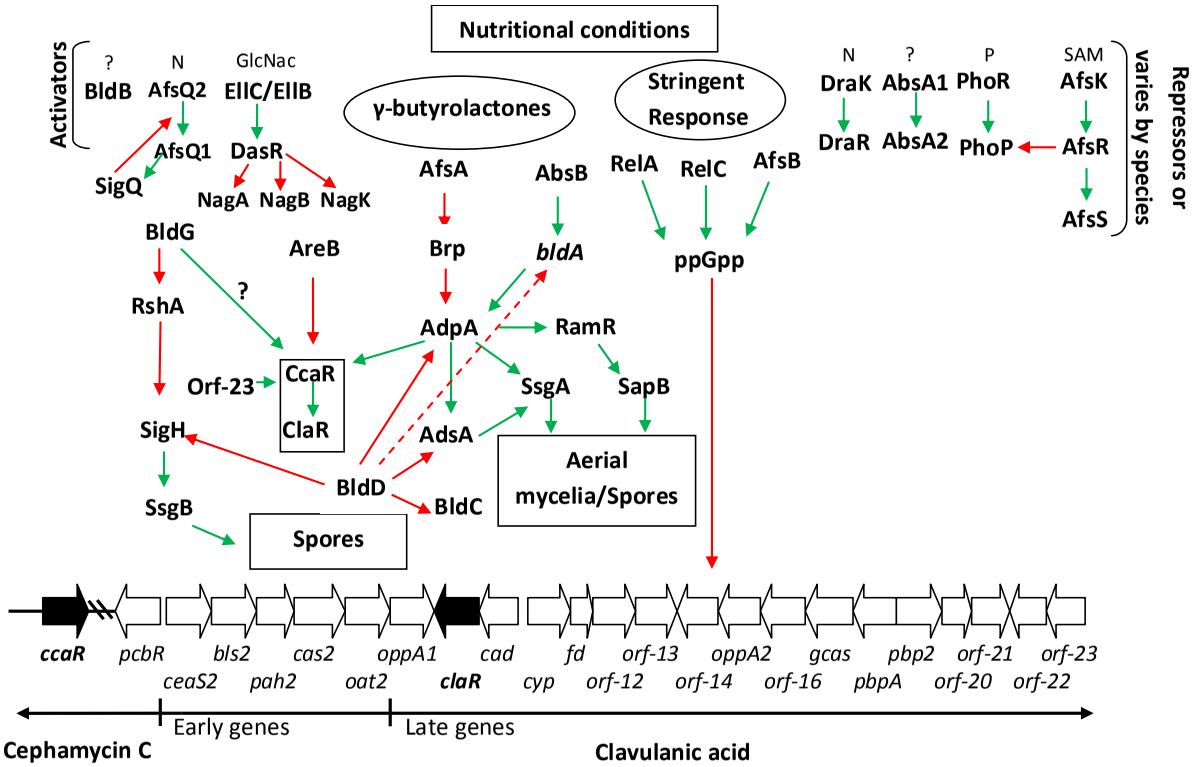

Figure 1.3.1.1: The regulatory cascade leading to clavulanic acid production in *S. clavuligerus* based on published work in *S. clavuligerus* and other *Streptomyces* species. Green arrows indicate positive regulation and red arrows indicate negative regulation. Regulatory elements (activators or repressors) responding to nutritional conditions are shown at the top of the scheme and nutritional signals are indicated if known. Regulatory elements that are part of the γ-butyrolactone-based regulation or the stringent response are depicted under each subheading, respectively. Pleiotropic regulators and pathway specific regulators are also shown and it is indicated if they are involved in mycelia or spore formation. Note that CcaR is the pathway specific regulator of the early genes of the CA gene cluster and ClaR controls expression of the late genes of this cluster, respectively (shown in black box).

been shown that a combined over-expression of *ccaR* and *cas2* (Figure 1.2.3.1) results in an up to 23.8 fold increase in CA production compared to the WT strain (Hung et al. 2007). Earlier research on *claR* showed that its amplification on a multi-copy plasmid improves CA production, however the increased production of this metabolite comes at the expense of reduced cephamycin C production (Perez-Llarena et al. 1997).

1.3.2: The *bld* pleiotropic regulators

The most well known of the pleiotropic *Streptomyces* regulators are encoded by the *bld* ("bald") genes, which are so-called because mutants defective in these genes lack the characteristic fuzzy aerial hyphae and grey-pigmented spores (Bignell et al. 2005; Elliot et al. 1998; Lawlor et al. 1987; Molle et al. 2000; Nguyen et al. 2003; Pope et al. 1998). Some *bld* genes (eg. *bldB* and *bldG*) are required for both differentiation and secondary metabolite biosynthesis (Bignell et al. 2005; Pope et al. 1998), others are only necessary for differentiation (eg. *bldN*/*adsA*) (Bibb et al. 2000), and some like *bldA* display different phenotypes depending on the species being examined (Kwak et al. 1996; Lawlor et al. 1987; Trepanier et al. 2002; White and Bibb 1997). Following is a brief overview of how two different *bld* genes (*bldG* and *bldA*, mutants of which are the focus of the current project) regulate CcaR, the positive regulator of cephamycin C and CA biosynthesis (Figure 1.3.1.1).

The *bldG* gene was the first regulatory gene identified that functions upstream of *ccaR* and *claR* in the CA biosynthesis regulatory cascade (Bignell et al. 2005). The *bldG* gene and a transcriptionally linked open reading frame (*orf3*, also called *apgA*) encode proteins similar to the SpoIIAA/RsbV anti-anti-sigma factors (Benson and Haldenwang

1993; Duncan and Losick 1993) and SpoIIAB/RsbW anti-sigma factors in *Bacillus subtilis*, respectively (Duncan et al. 1996). In this system, the anti-sigma factor (SpoIIAB/RsbW) seizes the cognate sigma factor (the sporulation specific σ^F and the stress response σ^B, respectively), preventing the expression of the target genes. When an activating signal is detected, the anti-anti-sigma factor binds to the anti-sigma factor, freeing the sigma factor to become active and capable of directing transcription (Brown and Hughes 1995). The anti-sigma factor-encoding *orf3*/*apgA* gene is found directly downstream of *bldG* in *S. coelicolor*, *S. clavuligerus*, and other *Streptomyces* species, and in *S. coelicolor* it has been shown that BldG and ApgA interact directly (Bignell et al. 2000; Parashar et al. 2009). A *S. clavuligerus bldG* mutant does not produce CA or cephamycin C because the positive activator CcaR is not expressed, though it is uncertain how BldG exerts its influence on *ccaR* transcription (Bignell et al. 2005). BldG also has a role in regulating SigH, a sigma factor with a dual role in differentiation and the osmotic stress response, by interacting with the SigH anti-sigma factor RshA (Parashar et al. 2009; Sevcikova et al. 2010). BldG also regulates *sigF* in *S. coelicolor* by interacting with the *sigF*-specific anti-sigma factor RfsA (Mingyar et al. 2014).

The *bldA* gene encodes a leucine t-RNA required for translating the TTA codon, which is the rarest codon present in *Streptomyces* genes (Guthrie and Chater 1990). The *Streptomyces* have a high GC content in their DNA (~70%) and therefore they do not use many T or A rich codons. As such, *bldA* is thought to be required for the translation of many of the genes regulating development and secondary metabolite production as these genes contain TTA codons in their 5′ regions (Lawlor et al. 1987). Mutations in *bldA*

result in lack of aerial hyphae formation and secondary metabolite production in *S. coelicolor*, *S. lividans*, and *S. griseus* (Kwak et al. 1996; Lawlor et al. 1987), whereas only differentiation is affected in *S. clavuligerus* (Trepanier et al. 2002). The production of CA in *bldA* mutants of *S. clavuligerus* was surprising as *ccaR* contains a TTA codon. It has been suggested that effective mistranslation of these genes can take place when the TTA codon is followed by a G or an A (as is the case for *ccaR*), whereas TTA codons followed by C or T are thought to be *bldA*-dependent (Trepanier et al. 2002). AdpA (a *bldA*-dependent regulator responsible for the bald phenotype of a *ΔbldA* mutant in *S. coelicolor*), positively regulates *ccaR* gene expression in *S. clavuligerus* and *adpA* mutants produce reduced amounts of CA (Lopez-Garcia et al. 2010; Takano et al. 2003).

1.3.3: The alternative sigma factors

One way in which gene expression is regulated in prokaryotes is through the use of alternate sigma factors that associate with the RNA polymerase core enzyme (Helmann 2002). Sigma factors regulate the promoter sequences recognized by the RNA polymerase holoenzyme and in turn control the initiation of transcription. Many of these alternate sigma factors belong to the extracytoplasmic function (ECF) sigma factor group, which are different from most other known sigma factors (Helmann 2002). Several are known to be involved in stress response and have indirect roles in regulating secondary metabolite biosynthesis in *Streptomyces* species.

Deletion of the cell envelope stress-response sigma factor SigE, which is known to be regulated by SigH under oxidative stress conditions (Raman et al. 2001), results in over-production of the pigmented secondary metabolite actinorhodin in *S. coelicolor*

(Hutchings et al. 2006b). SigL is a positive regulator of secondary metabolite biosynthesis as deletion of the *sigL* gene abolishes production of actinorhodin in *S. coelicolor* (Lee et al. 2005). SigB is involved in osmotic and oxidative responses, which are required for both aerial hyphae development and secondary metabolite biosynthesis in *S. coelicolor* (Cho et al. 2001; Lee et al. 2005). SigF and WhiG are the sporulation specific sigma factors (Homerova et al. 2000; Tan et al. 1998). Further, several of these sigma factor genes are also classified as *bld* genes or are indirectly regulated by *bld* genes as in the case of *sigH* (described in section 1.3.2) and *adsA*. The promoter of *adsA* (also known as *bldN*) shows increased activity during aerial mycelium and spore formation (Bibb et al. 2000) and *adsA* transcripts are not detectable in *bldG* or *bldH* mutant backgrounds in *S. coelicolor* (Bibb et al. 2000). As BldG is an anti-anti-sigma factor, it most likely indirectly regulates *adsA* transcription (Bibb et al. 2000). In *bldD* mutants, *adsA* transcripts are detectable and it is suggested that BldD is a repressor of *adsA* (Elliot et al. 2001). In *S. griseus*, a different mechanism involving the γ-butyrolactone A-factor (described in section 1.3.8) regulates *adsA* (Yamazaki et al. 2000). Neither *S. coelicolor* nor *S. griseus adsA* is required for secondary metabolite biosynthesis (Bibb et al. 2000; Yamazaki et al. 2000). In *S. clavuligerus*, a sigma factor (encoded by *orf21*) positively regulates CA production, as *orf21*-deleted mutants produce less CA than the WT strain and *orf21* over-expression increases CA production (Figure 1.2.3.1 and 1.3.1.1) (Jnawali et al. 2011).

1.3.4: The two-component systems

Another mechanism regulating both secondary metabolite production and differentiation are the two-component sensor kinase-response regulator systems (TCSs). TCSs consist of two proteins, a histidine kinase and a response regulator. Usually the genes encoding the kinase and the response regulator are found next to each other on the chromosome. Each histidine kinase responds to a stimulus by phosphorylating its response regulator partner, allowing the regulator to mediate gene expression (Fabret et al. 1999). The best known *Streptomyces* TCSs are PhoR/PhoP and AbsA1/AbsA2, which negatively regulate secondary metabolite biosynthesis in *S. coelicolor* (Figure 1.3.3.1) (Aceti and Champness 1998; Martin 2004; Ryding et al. 2002).

The biosynthesis of many secondary metabolites including CA is repressed by inorganic phosphate (Lebrihi et al. 1987). It has been proposed that when phosphate levels decrease and growth slows, bacteria increase the production of a variety of secondary metabolites that may function as antagonists to other competing microorganisms (Martin and Demain 1980). The PhoR/PhoP system is the major signal transduction system for phosphate based regulation in the *Streptomyces*. Under inorganic phosphate limitation, deletion of the gene encoding the response regulator (PhoP) results in delayed and reduced secondary metabolite production in *S. coelicolor* (Santos-Beneit et al. 2009), though deletion of the same gene in *S. lividans* (which is closely related to *S. coelicolor*, but does not normally produce any of the secondary metabolites) results in over-production of the same metabolites (Sola-Landa et al. 2003). The effect of PhoR/PhoP is likely indirect as there are no PHO box binding sites for PhoP near any of

the *S. coelicolor* secondary metabolite gene clusters nor near the CA gene cluster in *S. clavuligerus* (Salehghamari et al. 2012; Santos-Beneit et al. 2009). PhoP also acts as a repressor of *afsS* in the AfsK/AfsR/AfsS system described in section 1.3.5 (Horinouchi 2003). The AbsA1/A2 system is a negative regulator of secondary metabolite biosynthesis and responds to an unknown signal (Anderson et al. 1999; McKenzie and Nodwell 2009). Deletion or disruption of either *absA1* or *absA2* results in over-production of secondary metabolites in *S. coelicolor* (Brian et al. 1996).

Two additional TCSs (DraR/DraK and AfsQ1/AfsQ2) regulate secondary metabolite biosynthesis in response to nitrogen (Figure 1.3.3.1). DraR/DraK is a positive regulator of actinorhodin and a negative regulator of undecylprodigiosin (both of which are pigmented secondary metabolites) in *S. coelicolor* (Yu et al. 2012). AfsQ1/AfsQ2 activates expression of secondary metabolites in *S. coelicolor* under conditions of nitrogen excess and AfsQ1 interacts directly with the pathway specific transcriptional regulators of each of the secondary metabolite gene clusters (Shu et al. 2009; Wang et al. 2013). AfsQ1 also activates expression of the putative antagonistic sigma factor SigQ, a media-dependent negative regulator of secondary metabolism (Wang et al. 2013).

Two *S. clavuligerus* genes located downstream of the CA gene cluster (*orf22* and *orf23*) encode a putative TCS (Figure 1.2.3.1) (Jnawali et al. 2008; Song et al. 2009). While deletion of the sensor kinase (*orf22*) had little effect on CA production, deletion of the response regulator (*orf23*) severely reduced CA production and resulted in defective

growth and sporulation. The reduction in CA is due to a reduction in levels of *claR* transcripts (Figure 1.3.1.1) (Jnawali et al. 2008).

1.3.5: The serine/threonine kinases

Though Ser/Thr/Tyr-specific phosphorylation is known best for its role as a regulatory mechanism in eukaryotes, many serine/threonine kinases have been found in complex prokaryotes and some are known to regulate secondary metabolite biosynthesis in the *Streptomyces* (Lee et al. 2002). The AfsK/AfsR system was the first such system shown to have a role in secondary metabolism in *S. coelicolor* (Matsumoto et al. 1994). AfsK is a membrane kinase that autophosphorylates serine and threonine residues. When activated, AfsK phosphorylates the serine and threonine residues of AfsR, a SARP family protein (Lee et al. 2007; Matsumoto et al. 1994; Umeyama et al. 2002). The target of AfsR is the promoter of *afsS* which encodes a sigma factor-like protein located downstream of *afsR* (Lee et al. 2002). AfsR positively regulates the pathway-specific regulators of the actinorhodin and undecylprodigiosin pathways (Horinouchi 2003; Tanaka et al. 2007), and disruption of *afsK*/*afsR*/*afsS* results in reduced production of these metabolites in *S. coelicolor* (Floriano and Bibb 1996; Lee et al. 2002; Lian et al. 2008).

1.3.6: The γ-butyrolactones

A group of diffusible extracellular regulators of secondary metabolism that have been studied in depth are the small autoregulatory signaling molecules called the γ-butyrolactones (Choi et al. 2003). These molecules bind to butyrolactone-binding proteins (BRPs), which in turn bind to regulatory sequences (ARE boxes) located

upstream of target genes that are directly involved in regulating secondary metabolism or differentiation (Kinoshita et al. 1999; Onaka and Horinouchi 1997). The most well-known γ-butyrolactone is A-factor (2-isocaprylyl-3R-hydromethyl-γ-butyrolactone) from *S. griseus*. It is involved in regulating the onset of streptomycin biosynthesis and in morphological differentiation (Kato et al. 2004; Natsume et al. 2004). A BRP encoding gene (*brp* or *scar*) is located on the pSCL4 mega-plasmid and is the only γ-butyrolactone receptor protein in *S. clavuligerus*, and it regulates several regulators encoded on the chromosome (Medema et al. 2010). ARE boxes to which Brp binds have been identified upstream of *ccaR* in *S. clavuligerus*, and both CA and cephamycin C are over-produced in a *brp* mutant (Figure 1.3.1.1) (Kim et al. 2004; Santamarta et al. 2005). Brp may also control *ccaR* expression indirectly through the AdpA pathway as AdpA positively regulates *ccaR*. *adpA* expression is negatively regulated by Brp, and this decreases CA production by preventing the activation of *ccaR* expression by AdpA (Figure 1.3.1.1) (Lopez-Garcia et al. 2010; Paradkar 2013). An IclR-like regulator (AreB) also binds to the same ARE sequence without affecting *ccaR* expression, but CA production is increased in *areB* mutants (Santamarta et al. 2007).

1.3.7: Stringent response

Stringent response is a system used for sensing nutritional starvation and adapting to changing environmental conditions. Under amino-acid starvation conditions, uncharged tRNAs in the A-site of the ribosome activate RelA, which causes an increase in the levels of the highly phosphorylated guanosine nucleotide ppGpp and an associated decrease in guanosine-5'-triphosphate (GTP) (Chakraburtty and Bibb 1997). This burst of

ppGpp is believed to have a role in triggering secondary metabolite production in *Streptomyces* species as production takes place during stationary phase in most species (Ochi 1986). *S. clavuligerus* produces secondary metabolites during exponential phase when ppGpp levels are low and stops production in stationary phase (Sanchez and Brana 1996). In addition, *relA* mutants (which lack ppGpp synthetase activity) are blocked in secondary metabolite production (Figure 1.3.1.1) (Gomez-Escribano et al. 2008). This makes *S. clavuligerus* the first *Streptomyces* species in which ppGpp negatively regulates secondary metabolism (Gomez-Escribano et al. 2008).

1.4: Proteomics studies to elucidate aspects of secondary metabolism

After the isolation of a secondary metabolite via traditional bioassay-guided strategies, the principle challenge is to reveal the specific mechanisms and inner workings of the cell that are responsible for the formation of the metabolite. In order to elucidate these processes, the dynamic composition and interplay of a large number of components and parallel processes must be evaluated. After genomics and transcriptomics, proteomics is the next logical step in the study of biological processes. The proteome is the entire complement of proteins produced or modified by an organism or cell at a particular time under particular circumstances (eg. *S. clavuligerus* while it is actively producing CA) (Wilkins et al. 1996). Investigating the expression of proteins can be more useful than mRNA analysis because mRNA is not always translated into protein and the amount of protein translated from a given amount of mRNA often depends on the specific gene (Rogers et al. 2008).

1.4.1: Isobaric tag for relative and absolute quantitation as a proteomics tool

Considering the degree of difficulty in accurately detecting and quantifying entire proteins, it becomes obvious that a "bottom up" sort of approach is necessary (Aebersold and Mann 2003; Chait 2006). Because of this the analysis of peptides derived from enzymatic cleavage, rather than of whole proteins, is becoming common. A quantitative mass spectrometry tool known as isobaric tag for relative and absolute quantitation (iTRAQ®) has been demonstrated to be very effective in this endeavor (Wiese et al. 2007). In this method of mass spectrometry, iTRAQ® reagents introduce stable isotopic tags onto peptides obtained by proteolysis. This method uses an *N*-hydroxysuccinimide ester derivative to modify the primary amino groups present in the peptide by linking a mass balance and a reporter group by the formation of an amide bond (Figure 1.5.1.1). The design of the reagents causes the differentially labeled peptides to appear as single peaks in mass spectrometry (MS) scans, an advantage because this reduces the chance of peak overlap (Wiese et al. 2007). When the iTRAQ® labeled peptides are run through tandem mass spectrometry (MS/MS) analysis, the mass balancing moiety is released as a neutral fragment, and this leads to the release of the reporter ions that actually supply the information on the relative quantity of proteins (Wiese et al. 2007).

Recent research has made a detailed temporal proteomic analysis of the different developmental stages of *S. coelicolor* grown on solid media using iTRAQ® coupled with LC-MS/MS. It was found that the initial compartmentalized mycelium (MI) proteome is rich in primary metabolism proteins and that the multinucleated hyphae (MII) are rich in proteins associated with secondary metabolism (Manteca et al. 2010). These results

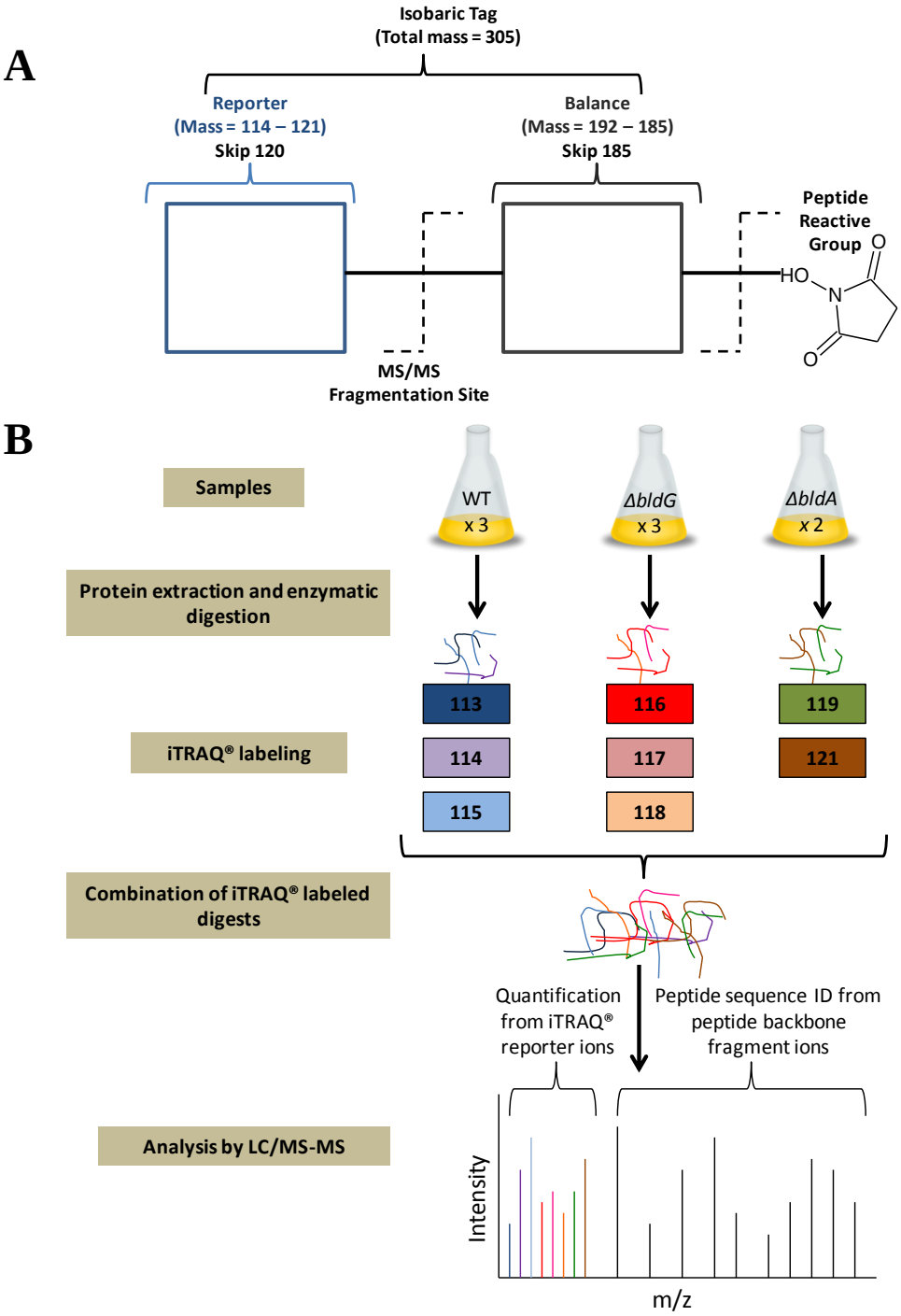

Figure 1.5.1.1: iTRAQ® labeling and LC/MS-MS analysis of WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus*. **(A)** Design of the 8-plex iTRAQ® tags and attachment to peptide reactive group. Dashed lines indicate MS/MS fragmentation sites. **(B)** General workflow and labeling strategy used in the described study.

indicate that the switch from primary to secondary metabolism occurs between the initial compartmentalized mycelium and the multinucleated hyphae, supporting the idea that secondary metabolism and hyphae differentiation are correlated. An even more recent iTRAQ®-based proteomic study of *S. coelicolor* found that allantoin catabolism influences the production of pigmented secondary metabolites in *S. coelicolor*, providing the first link between purine metabolism and secondary metabolism (Navone et al. 2014). These studies demonstrate the applicability of using iTRAQ® in studying secondary metabolism in the *Streptomyces*.

1.5: Main objectives of this thesis

Most of the proteomic research involving secondary metabolites, particularly antibiotics, has chosen to focus on how bacteria respond to antibiotic exposure (Bandow et al. 2003). Despite the increased use of proteomic strategies in antibiotic research, relatively little research has focused on specific organisms during the process of active secondary metabolism. Even fewer studies have chosen to compare a producing strain with a mutant that is defective or reduced in the production of a specific secondary metabolite, though these studies have yielded useful results that could be used to construct high-yielding producer strains (Gallo et al. 2010).

In its most simplified form, the goal of this research was to compare proteomic data from the WT CA-producing strain of *S. clavuligerus* with data from two developmental mutants, one of which is defective in CA production (*ΔbldG*) and the other not (*ΔbldA*) (Bignell et al. 2005; Trepanier et al. 2002), in order to gain a better understanding of the exact molecular processes behind the regulation of CA biosynthesis.

ΔbldA is included in this study for two reasons: first, inclusion of this strain will allow for protein expression differences between the mutant strains and the WT strain that are related to development to be filtered out so that focus can be turned to expression differences due to CA biosynthesis; and second, the *ΔbldA* protein data may help address questions related to TTA codon dependence in *S. clavuligerus*, which was not clear. As this research was primarily concerned with elucidating aspects of the regulatory cascade leading to CA production, proteins were extracted from all three strains during a time point in which the metabolite was being actively produced.

As one of the necessities of the research was to accurately identify and quantify as many proteins as possible from several different samples at once, iTRAQ® labeling and LC-MS/MS analysis was chosen due to its demonstrated applicability in such types of analyses (Figure 1.5.1.1) (Wiese et al. 2007). This method avoids the drawbacks of both traditional 2-D gel electrophoresis based methods, such as the unsuitability of the method in analysis of low abundance proteins, as well as other MS-based approaches such as ICAT or ICPL, which suffer from limited robustness or migration issues (Wu et al. 2006). While iTRAQ®-based methods do have some drawbacks – the stringent sample preparation protocol limits the ability to solubilize more hydrophobic proteome components, the reagents are costly and could in themselves be a source of variability, the method can be more susceptible to errors in precursor ion identification, and overall the data generated requires stringent manual validation - this method was chosen because of its high level of sensitivity and 8-plex tag design (Elliott et al. 2009). The fact that iTRAQ® allows for the analysis of up to 8 samples means that protein samples from

several replicates of each strain could be analyzed; these replicates represent an important validation tool in protein expression analysis.

While undoubtedly all of the collected protein expression data is useful for understanding *S. clavuligerus* secondary metabolism, the focus of this thesis is the regulation of CA production; therefore, special focus was placed on those proteins that may have regulatory functions such as sigma factors and transcriptional regulators. The underlying reasoning behind the experimental design of this research is that differences in protein expression between the WT and *ΔbldA* strains compared to the *ΔbldG* strain could reveal regulatory elements not previously known to have a role(s) in CA biosynthesis. Some of which may prove to be exciting candidates for over-expression or other manipulation experiments, which could lead to an increase in CA production.

Chapter 2: Materials and Methods

2.1: General procedures and supplies

All media and solutions were prepared with sterile MilliQ water and were sterilized after preparation by autoclaving or by filter sterilization using 2 μm filters (28145-481, VWR International). Antibiotics, reagents and dehydrated media were purchased from Sigma Aldrich, Fisher Scientific or VWR international, unless otherwise stated. All procedures involving bacterial cultures were performed using aseptic techniques and sterile reagents. All centrifugations were performed using an Eppendorf 5424 micro-centrifuge (022620401) or a Thermo Scientific Sorvall ST 16 R centrifuge (75004380) with a TX-400 Swinging Bucket Rotor (75003629). An Implen P300 NanoPhotometer was used to measure optical densities (ODs) and for determining protein/nucleic acid concentrations. All DNA was stored at -20°C and all glycerol stocks, supernatant samples, and protein samples were stored at -80°C.

2.2: *E. coli* procedures

2.2.1: Maintenance and stock preparation

E. coli cultures were grown overnight in 2 to 10 ml of Lennox broth (LB) and were maintained on LB agar (BP1427-2, Fisher Scientific) at 37°C. The following antibiotics were included when required at the stated final concentrations: ampicillin (100 μg/ml), apramycin (50 μg/ml), chloramphenicol (25 μg/ml) and kanamycin (50 μg/ml). Glycerol stocks for strain preservation were prepared by adding 600 μl of overnight cultures to 600 μl of sterile 40% glycerol in sterile microcentrifuge tubes. Cultures for the preparation of competent cells were grown in 2× yeast extract-tryptone media (YT)

(0.16% w/v tryptone, 0.1% w/v yeast extract, 0.05% w/v NaCl in MilliQ-H_2O). Chemically transformed cells were then grown on LB agar containing the appropriate antibiotics. Isopropyl-beta-D-thiogalactopyranoside (IPTG) (100 µl of 100mM stock) and 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside (X-Gal) (20 µl of a 50 µg/ml stock) were overlaid on the plates before use (Sambrook and Russell 2001). For conjugations, 50 mL of LB with the appropriate antibiotics was inoculated with 1 ml of a 5 ml overnight culture of ET12567/pUZ8002 containing pAU3-45-G or pAU3-45-A. All bacterial strains and plasmids used in this study are described in Table 2.2.1.1.

2.2.2: Plasmid and cosmid DNA isolation

For sequencing and sub-cloning purposes, plasmid and cosmid DNA were isolated using the EZ-10 Spin Column Plasmid DNA Miniprep kit (BS414, Biobasic Inc.) according to the manufacturer's instructions with the following modifications: room temperature incubations were not performed and DNA was eluted from the columns using 30 µl of sterile MilliQ water at 50°C. For routine screening purposes, plasmid and cosmid DNA was also isolated according to a modified alkaline lysis method (Birnboim and Doly 1979), as follows. One milliliter of overnight culture was transferred to a 1.5 ml microfuge tube and spun at 12,000 rpm for 30 seconds. After discarding the supernatant, 100 µl of ice-cold Solution I (50 mM glucose, 25mM Tris-Cl - pH8.0, 10 mM ethylenediaminetetraacetic acid (EDTA) - pH8.0) was added and the tube was vortexed. 200 µl of freshly prepared Solution II (0.2 M NaOH, 1% w/v SDS) was then added and the tube was inverted gently 5 to 7 times. Finally 150 µl of ice-cold Solution III (60 ml 5M potassium acetate, 11.5 ml glacial acetic acid, 28.5ml water yielding a

Table 2.1.1.1: Bacterial strains and plasmids used in this study.

Strain or plasmid	Final antibiotic concentrations used for selection	Description/relevant features	Reference
S. clavuligerus ATCC 27064		Wild type (WT) strain capable of normal development and CA production	American Type Culture Collection
S. clavuligerus ΔbldA	25µg/ml apramycin	*bldA* null mutant defective in development but produces CA	(Trepanier et al. 2002)
S. clavuligerus ΔbldG	25µg/ml apramycin	*bldG* null mutant defective in development and CA production	(Bignell et al. 2005)
K. pneumoniae ATCC 15380		Indicator organism for CA bioassays	(Reading and Cole 1977)
E. coli DH5-α		F^- general cloning host	Promega
E. coli ET12567	25µg/ml chloramphenicol	DNA methylation deficient host used for conjugate with *S. clavuligerus* or to passage DNA prior to *S. clavuligerus* transformation	(Gewain et al. 1992)
Cosmid clone 5D4	100µg/ml ampicillin	pWE15 derivative cosmid clone containing the *bldG* encompassing region from the *S. clavuligerus* chromosome	(Bignell et al. 2005)
pUZ8002	50µg/ml kanamycin	Encodes transfer functions for mobilization of *oriT*-containing plasmids in trans from *E. coli* to *S. clavuligerus*	(Gewain et al. 1992)
pGEM®-T Easy	100µg/ml ampicillin	Cloning vector for PCR products	Promega
pAU3-45	25µg/ml apramycin, 5µg/ml thiostrepton[a] (*S. clavuligerus*)	pSET152 derivative containing *tsr* resistance gene	(Bignell et al. 2005)
pAU3-45-G	25µg/ml apramycin, 5µg/ml thiostrepton[a] (*S. clavuligerus*)	pAU3-45 derivative containing *S. clavuligerus bldG* gene under the control of its native promoter	This study
pAU3-45-A	25µg/ml apramycin, 5µg/ml thiostrepton[a] (*S. clavuligerus*)	pAU3-45 derivative containing *S. clavuligerus bldA* gene under the control of its native promoter	This study

[a] Thiostrepton only used for selection in *S. clavuligerus* as it does not work in *E. coli*.

solution that is 3M acetate and 5M potassium - pH4.8) was added and the tube was inverted gently 5 to 7 times. After the addition of all three solutions, the tube was incubated on ice for 5 minutes and then spun at 10,000 rpm for 10 minutes. The resulting supernatant was then transferred to a fresh 1.5 ml microfuge tube containing 450 µl of isopropanol, and the contents were mixed by vortexing and allowed to stand for 5 minutes at room temperature. Following incubation, the tube was again spun at 10,000 rpm for 10 minutes and the supernatant was discarded. The nucleic acid pellet was washed with 300 µl of ice-cold 70% ethanol and was inverted gently 3 to 5 times before being spun at 10,000 rpm for 5 minutes. The supernatant was discarded and the tube was spun down once more at 10,000 rpm for 1 minute and any residual ethanol was removed via pipetting. This procedure was followed every time subsequently, when a nucleic pellet was washed with ethanol. The DNA pellet was allowed to air dry under a laminar flow hood for approximately 30 minutes and the dried pellet was re-suspended in 10 µl of 1× Tris-EDTA (TE: 10 mM Tris-HCl at pH 8.0 and 1mM EDTA at pH 8.0) buffer containing 20 µg/ml RNaseA (AC117, Omega Bio-Tek) and incubated at 37°C for approximately 20 minutes before storage.

2.2.3: Preparation and transformation of chemically competent cells

Five milliliters of 2× YT was inoculated with a single *E. coli* colony of either DH5α or ET12567/pUZ8002 and grown overnight at 37°C. Next, 200 ml of pre-warmed 2× YT was inoculated with 2 ml of the overnight culture and incubated with shaking at 37°C at 200 rpm until the OD_{600} reached 0.2. $MgCl_2$ was then added at a final concentration of 20 mM and the incubation was continued until the OD_{600} of the culture

was 0.45-0.55. The culture was transferred into 50 ml round bottom tubes (3119-0050, Nalgene) and incubated on ice for 2 hours. Following this, cells were pelleted by centrifugation at 3,500 rpm at 4°C for 5 minutes. The supernatant was discarded and the pellet was re-suspended in 100 ml of fresh, filter sterilized, 1× $Ca^{2+}Mn^{2+}$ solution (2× $Ca^{2+}Mn^{2+}$ was prepared using 50 ml water, 0.394 g $C_2H_3O_2Na.3H_2O$, 1.76 g $CaCl_2.2H_2O$, and 1.66 g $MnCl_2.4H_2O$, adjusted to pH5.5 and the volume brought up to 60 ml with MilliQ-H_2O), pre-chilled at 4°C and left on ice for 45 minutes. Next, the cells were pelleted at 3,500 rpm, at 4°C for 5 minutes and the supernatant was discarded. Cells were gently re-suspended in 10 ml of 1× $Ca^{2+}Mn^{2+}$ solution containing 15% glycerol, then rapidly aliquoted into pre-chilled 1.5 ml microfuge tubes and flash-frozen in liquid nitrogen.

DNA for transformation (10 µl ligation reactions or 2 µl plasmid/cosmid DNA preparations) was added to a chilled PCR microfuge tube on ice and the final volume was brought up to 50 µl with MilliQ water. Competent cells were thawed on ice and 100 µl of the cells were added to the tube containing the DNA. The transformation mixture was incubated on ice for 30 minutes, after which the cells were heat-shocked at 37°C for 5 minutes and then immediately placed back on ice for 2 minutes. The cells were then transferred to a microfuge tube containing 850 µl of LB and incubated with shaking at 37°C for 1 hour. The tubes were then centrifuged at 10,000 rpm for 2 minutes to pellet the cells. Finally, 900 µl of the supernatant was drawn off and the pellet was re-suspended in the remaining media and the entire contents plated onto a single LB plate containing the appropriate antibiotics. Plates were then incubated overnight at 37°C and

clones were identified based on blue/white colony selection using X-Gal and IPTG (Sambrook and Russell 2001).

2.3: *Streptomyces* procedures

2.3.1: Maintenance and stock preparation

Stocks of *S. clavuligerus* were prepared by growing strains on ISP-4 medium (277210, BD Biosciences) for 7 to 10 days and then scraping the growth with an ethanol flame sterilized steel spatula into 1.5 ml microfuge tubes containing 1 ml of sterile 20% glycerol. Apramycin (25µg/ml), nalidixic acid (25µg/ml) and/or thiostrepton (5µg/ml) were included in the growth media when required. Both spore and mycelial stocks were stored at -80°C. *S. clavuligerus* was maintained on ISP-4 or maltose-yeast extract-malt extract (MYM) media (0.4% w/v maltose, 0.4% w/v yeast extract, 1% w/v malt extract, 1.8% w/v agar in MilliQ water) containing the appropriate antibiotics. *S. clavuligerus* seed cultures for inoculating CA production cultures were grown in trypticase soy broth (211825, BD Biosciences) supplemented with 2% w/v starch (TSBS) for 48 hours before being transferred to starch asparagine (SA) medium (1% w/v soluble starch, 0.2% w/v L-asparagine, 2.1% w/v MOPS buffer, 0.06% w/v $MgSO_4$, 0.44% w/v K_2HPO_4 in MilliQ water, pH to 6.8; and 1ml of sterile trace elements solution: 0.10% w/v each $FeSO_4$, $MnCl_2$, $ZnSO_4$ and 0.13% w/v $CaCl_2$ - added after autoclaving). Apramycin (25 µg/ml) was included in the seed cultures used to grow the *ΔbldA* and *ΔbldG* mutants, but not for the WT strain. All ex-conjugates were allowed to recover on AS-1 medium (0.01% w/v yeast extract, 0.02% w/v L-alanine, 0.02% w/v L-arginine, 0.05% w/v L-asparagine, 0.5% soluble starch, 0.25% w/v NaCl, 1.0% w/v Na_2SO_4, 2.0% w/v agar, pH to 7.5 and

1% w/v 1M $MgCl_2$ added post-autoclaving) and were overlaid with 1 ml water containing 0.5 mg nalidixic acid to selectively kill *E. coli* and 1.25 mg apramycin for plasmid selection after 20-28 hours of initial incubation. All *S. clavuligerus* liquid cultures were grown at 28°C on a rotary shaker at 150 rpm and all plates with solid media were incubated at 28°C.

2.3.2: Chromosomal DNA extraction

Chromosomal DNA was extracted using a modified phenol-chloroform based method (Hopwood et al. 1985). Cells were grown in 25 ml TSBS for ~48 hours before being spun down at 3,500 rpm for 5 minutes and washed twice in 10 ml of 10.3% w/v sucrose. One milliliter of the pelleted cells was transferred to a polypropylene screw-cap tube (89004-310, VWR International) using a large bore 1000 µl tip (prepared by cutting off the tip prior to sterilization by autoclaving) and 2 ml lysozyme buffer (0.3 M sucrose, 25 mM EDTA, 25 mM Tris-HCl, pH 7.5, containing 50 µg/ml of RNaseA) was added along with 4 mg/ml of eggwhite lysozyme (0663-5G, Amresco). The tube was then incubated at 37°C for 30 to 45 minutes and gently inverted every 5 to 10 minutes. After incubation, 500 µl of 2% w/v sodium dodecyl sulfate (SDS) was added and the tube was shaken vigorously until the viscosity of the contents decreased. Following this, 500 µl of phenol-chloroform (BP1752-400, Fisher Scientific) was carefully added in a chemical safety cabinet and the tube was shaken until the liquid inside developed a "milky" appearance. The tube was then spun at 10,000 *g* for 5 minutes, after which 3 ml of the upper aqueous phase was transferred to a fresh tube to which 300 µl of 3M sodium acetate (pH5.2) and 3 ml of isopropanol were added. The tube was gently inverted and

incubated on ice for 10 minutes before vortexing until clumps of DNA became visible. During the incubation, a fresh microfuge tube was prepared which contained 1 ml of 70% ethanol. The DNA was then carefully spooled on a 200 µl pipette tip and transferred to the tube containing 70% ethanol, which was then stored at -20°C. After three days the DNA was transferred to a new microfuge tube containing 1 ml µl of 70% ethanol and was washed twice as previously mentioned. The DNA pellet was dried for ~10 minutes and then 200-500 µl of TE buffer was added, before incubation overnight at 37°C and final storage at -20°C.

2.3.3: Liquid cultures of *S. clavuligerus* for bioassays and HPLC

S. clavuligerus glycerol stocks (20 µl of WT spores and 50 µl of *ΔbldG* and *ΔbldA* mycelia) were used to start TSBS seed cultures. After 48 hours, 250 µl of these cultures were then used to inoculate 125 ml flasks with stainless steel springs containing 25 ml of SA with no antibiotics. Samples were taken from each flask every 24 hours for up to 120 hours as following: 1 ml of culture was aseptically transferred to a 1.5 ml microfuge tube and was centrifuged at 11,000 rpm for 5 minutes, 900 µl of the supernatant was transferred to a separate microfuge tube, and both the pellet and supernatant were stored until further use.

2.3.4: Liquid cultures for protein extraction

Seed cultures were inoculated as previously described. Following appropriate incubation, 500 ml flasks with stainless steel springs containing 100 ml of SA were

inoculated with 2 ml of each seed culture and incubated as previously described. A total of 4 culture replicates of each strain were prepared.

2.3.5: Mycelial conjugations

S. clavuligerus mycelia were grown in 50 ml of TSBS containing the appropriate antibiotics for 36-40 hours before being centrifuged at 3,500 rpm for 7 minutes and washed twice in 25 ml of 2× YT medium using standard conical 50 ml tubes (14-432-22, Fisher Scientific). Mycelia were then re-suspended in 5 ml of 2× YT and homogenized to break up the mycelia using a Duall Tissue Grinder with Glass Pestle (KT885450-0023, VWR International). In the meantime, a culture of the donor *E. coli* ET12567/pUZ8002 containing the plasmid to be transferred was grown to an OD of 0.4 after which the cells were centrifuged at 3,500 rpm and washed twice in 25 ml of LB before being re-suspended in 1 ml of LB. The homogenized *S. clavuligerus* mycelia were then spun down, re-suspended in 1 ml of 2× YT and heat-shocked at 40°C for 5 minutes. Immediately following this heat shock, 500 µl of this mixture was added to a sterile 1.5 ml microfuge tube containing 500 µl of the donor *E. coli* cells. The tube was then vortexed briefly and centrifuged at 10,000 rpm. The supernatant was removed and the pellet was re-suspended in the remaining medium and the entire contents were plated onto a single AS-1 plate. After 20-28 hours of incubation, plates were overlaid with the appropriate antibiotics. After ~7 days, S. *clavuligerus* colonies were usually seen on the AS-1 plates. Colonies were picked and homogenized with a sterile pipette tip in a PCR tube containing 10-20 µl sterile of MilliQ water, and were patched onto MYM containing the appropriate antibiotics. After 3-5 days of growth on MYM, patches would be picked

and plated onto ISP-4 media plates containing the appropriate antibiotics and incubated for ~10 days for the preparation of spore stocks.

2.4: DNA procedures

2.4.1: PCR and agarose gel electrophoresis conditions

Reactions were set up using 200 ng of DNA and the Phusion™ High Fidelity DNA Polymerase with High GC buffer and 3% dimethyl sulfoxide (DMSO) as per the manufacturer's instructions (F532S, Fisher Scientific). All PCRs were performed using an Eppendorf VapoProtect Mastercycler Pro (950040015). Gradient PCR cycles were set up as follows: 98°C for 30 seconds, followed by 30 cycles of: 98°C for 10 seconds, a gradient of 58-69°C for 30 seconds, and 72°C for 30 seconds; this was followed by a final extension step at 72°C for 5 minutes. Annealing temperatures from the gradient runs that produced the best results were used in all subsequent PCRs. Template for the PCR reactions consisted of 5D4 cosmid DNA, chromosomal DNA from the mutant or the WT strains, or PCR grade water in the case of the negative controls. All primers used are listed in Table 2.4.1.1. A total of 10 µl of the reactions were loaded onto 0.8% w/v (for *bldA* PCRs) or 1.5% w/v agarose gels (for *bldG* PCRs), respectively using 6× EZ-Vision® One DNA loading dye (N472, Amresco, Inc.) and either the GeneRuler™ 1 kb ladder (SM0312, Thermo Scientific) or the GeneRuler™ 100 bp Plus ladder (SM0321, Thermo Scientific). Gels were run at 90 V in constant V mode for one hour using 1× Tris-borate EDTA (TBE) buffer (89 mM Tris base, 89 mM Boric acid, 2 mM EDTA, pH 8). All gels were imaged using a UVP GelDoc-It® TS2 imager (71004-578). Extraction of products from agarose gels was performed using the Promega Wizard® SV Gel and PCR Clean-up

Table 2.4.1.1: Oligonucleotide primers used for strain verification and mutant complementation.

Primer name	Sequence (5`-3`)	Annealing Temperature[a]	Purpose
bldG-conf (F)	TGACGGACAATGGTCCCAAG	67°C	Confirming the presence of the *bldG* gene in *S. clavuligerus*
bldG-conf (R)	GTGTGGATCGGGAACACCTT		
bldA-conf (F)	TCCTCCTTGGGTATGACGGT	66°C	Confirming the presence of the *bldA* gene in *S. clavuligerus*
bldA-conf(R)	CGACGATGAGGCGATCTTGA		
apra (F)	AGAATGGTGCAGTGTCTCGG	63°C	Confirming the presence of the apramycin resistance cassette in *S. clavuligerus* mutants
apra (R)	CAGCTTCTCAACCTTGGGGT		
bldG-comp (F)	GTGAGGACGGGGGCGAGAT	61°C	Amplifying the *bldG* coding region for use in mutant complementation
bldG-comp (R)	GGGCGGTCCTGACATGCT		
bldA-comp (F)	CTCCGAGGACACACACCATC	69°C	Amplifying the *bldA* coding region for use in mutant complementation
bldA-comp (R)	CGACGATGAGGCGATCTTGA		

[a] Final Tm used with primer set selected based on best performance in a 58-69°C gradient; gradient was between Tm suggested by Integrated DNA Technologies and Tm as calculated by the Thermo Scientific Tm Calculator for Phusion using modified Breslauer's thermodynamics, dH and dS parameters.

System (A9281) as per the manufacturers' instructions, except DNA was eluted using 20 µl MilliQ water heated to 50°C.

2.4.2: Ligations

Ligation of PCR products with the pGEM®-T Easy vector (A1360, Promega) was carried out according to the manufacturer's recommendations. Since a proof reading polymerase was used for PCR, A overhangs were added to the PCR products prior to ligation with pGEM®-T using the Thermo Scientific *Taq* DNA polymerase (EP0402) in 10 µl reactions with the following components: 1× Taq buffer with KCl, 0.2 mM dNTPs, 2.25 mM MgCl, 0.5 µl enzyme and up to 6 µl of PCR product. The reactions were incubated at 72°C for 10 minutes, after which the PCR products with A overhangs were used immediately in ligation reactions with the pGEM®-T Easy vector. Other ligations were carried out using the Fermentas Rapid DNA Ligation Kit (K1422, Thermo Scientific) according to the manufacturer's protocol, and all ligation reactions were incubated overnight at 4°C.

2.4.3: Complementation of mutant strains

For complementation of the *ΔbldA* and *ΔbldG* mutants, the respective coding sequences were PCR amplified using WT *S. clavuligerus* chromosomal DNA (*bldA*) or a *bldG* containing cosmid (5D4) and the gene specific primer sets (Table 2.4.1.1). The PCR products were then ligated into the pGEM®-T Easy vector as described above and the ligations were used to transform *E. coli* DH5α cells. White colonies were picked and used to inoculate tubes containing 2 ml of LB+ampicillin, which were then incubated overnight. Plasmid DNA was isolated from these cultures using the modified alkyline-

lysis method and glycerol stocks were also prepared simultaneously. Plasmids were then screened for the presence of the insert by restriction digestion overnight using the EcoRI enzyme (BO101S, New England BioLabs Inc.) in 20 µl reactions according to the manufacturer's recommendations. Glycerol stocks from identified positive clones were used to inoculate 5 ml of LB+ampicillin, and plasmid DNA was isolated using the EZ-10 kit after overnight incubation. The isolated DNA was digested with EcoRI to purify the insert after agarose gel electrophoresis and gel extraction, and the insert was ligated with similarly digested pAU3-45. This led to the *bldA* and *bldG* complementation constructs pAU3-45-A and pAU3-45-G, respectively. The inserts were then sequenced to confirm that no errors were present. Confirmed constructs were then introduced into *S. clavuligerus ΔbldA* and *ΔbldG* strains, respectively, via mycelial conjugation as described previously.

2.5: Detection of CA in supernatants

2.5.1: Bioassays for the detection of CA

To detect the presence of CA in the supernatants, 200 ml of TSB agar (TSBA) containing 6 µg/ml penicillin G was inoculated with 1 ml of a *Klebsiella pneumoniae* stock (grown in TSB and prepared as per the *E. coli* protocol) and was poured into an ethanol sterilized 22 × 22 cm plastic bioassay tray. The same volume of TSBA was inoculated with only *K. pneumoniae* and was poured into a second sterile tray to serve as a control so that only the effect of CA is measured. Sterile paper discs (10mm) were then placed onto the agar and carefully spotted with 10 µl of *S. clavuligerus* culture

supernatants after which the trays were incubated overnight at 37°C. After incubation, zones of inhibition were measured (in mm) and recorded.

2.5.2: HPLC for the detection of CA

Reversed-phase high performance liquid chromatography (HPLC) was carried out on an Agilent Technologies 1260 Infinity Quaternary LC system using a 100 × 8 mm Bondclone™ 10 µm C18 148 Å LC Column (00D-2117-L0, Phenomenex Inc). Supernatants were analyzed as follows: 100 µl of the supernatant was derivitized in the dark for 15 minutes with 25 µl of 20.6% imidazole (10284730, Fisher Scientific), which was adjusted to pH6.8 using 5M HCl. Control blank samples were set up using the same amount of supernatant with 25 µl of filter-sterilized MilliQ water. Derivitized samples were spun at 10,000 rpm to remove particulate matter. The samples were carefully transferred to 100 µl mandrel point inserts with polymer feet (5181-1270, Agilent Technologies), which were placed in screw-cap glass vials (5181-3377, Agilent Technologies) and loaded onto the LC system. Of these samples, 25 µl was injected onto the column with a flow rate of 2.5 ml/min and were run for 20 minutes using phosphate buffer as the mobile phase (0.1M KH_2PO_4, 6% MeOH, pH to 3.2 with phosphoric acid). The diode array detector (DAD) was set to detect at 311nm, 317nm, and 320 nm. Chromatographic data was analyzed using Agilent ChemStation for LC 3-D Systems (G2170BA, revision: B.04.03, Agilent Technologies).

2.6: Proteomic sample preparation procedures

2.6.1: Protein extraction

Based on the results of the bioassays and HPLC analysis described earlier, the 48 hour time point was selected for protein extraction. Cultures were spun down at 4,500 rpm for 10 minutes each time in 50 ml tubes (89039-658, VWR International), and 1 ml of the resulting supernatant was saved for HPLC and bioassay analysis while the rest was discarded. A third spin was performed to remove any residual media. The cell pellets were re-suspended in 2 to 3 ml 1× phosphate buffered saline (PBS: 0.8% w/v NaCl, 0.02% w/v KCl, 0.14% w/v Na_2HPO_4, 0.02% w/v KH_2PO_4, MilliQ water; pH to 7.4) + 0.01% w/v SDS by vigorous vortexing. The suspensions were then transferred to 3 ml screw-cap cryovials (0566965, Fisher Scientific) and were sonicated on ice using a QSonica (Q125-110,VWR International) sonicator with a 5/64 inch probe (FB4423, Fisher Scientific) set on 50% power setting. The sonication program consisted of 6 cycles of 15 seconds on and 15 seconds off for a total of 3 minutes. The sonicated cells were then transferred to fresh tubes, and 100 µl of each sample was transferred to 1.5 ml tubes and was stored at -20°C for quantification and SDS-PAGE. The remaining samples were transferred to fresh 3 ml cyrovials and were stored at -80°C until they were shipped to the University of Victoria British Columbia Proteomics Centre. Protein quantification was performed using the OmniPur Bradford Method Protein Assay (2740-OP, EMD Millipore) with different amounts of bovine serum albumin (BSA) as the standard according to the manufacturer's protocol.

2.6.2: Visualization of proteins by SDS-PAGE

The appropriate amount of protein (145.2 µg), 6.6 µl of 5× protein loading dye (EC-887, National Diagnostics), 1 µl of dithiothreitol (DTT), and 1× PBS to 34 µl was

added to a PCR tube and was heated to 100°C for three minutes. A total of 15 µl of each sample was loaded onto an SDS 10% PAG (resolving gel consisted of: 10% w/v acrylamide/bis-acrylamide, 26% w/v 1.5 M Tris-HCl-pH8.8, 0.01% w/v each of SDS and ammonium persulfate (APS) and 0.00004% v/v tetramethylethylenediamine (TEMED); stacking gel consisted of: 4% w/v acrylamide/bis-acrylamide, 25% w/v 0.5 M Tris-HCl-pH6.8, 0.01% w/v each of SDS and APS, and 0.001% v/v TEMED), which was run at 4°C and 45V for 5 hours using a BioRad Mini-PROTEAN® Tetra System gel system (165-8001, BioRad) with 1× Tris-glycine electrophoresis buffer (25 mM Tris, 200 mM Glycine, 0.1% w/v SDS, pH 8.5). The Thermo Scientific PageRuler Prestained Protein Ladder (26619) was used as the marker. Gels were then stained on a rocking platform overnight in at least 5 volumes of staining solution (50% v/v MeOH, 40% v/v H_20, 10% v/v glacial acetic acid, 0.25g Coomassie Brilliant Blue R-250 per 100 ml solution), after which they were allowed to destain for at least 2 hours in destaining solution (25% MeOH, 10% glacial acetic acid). After destaining, gels were imaged and stored in MilliQ water in a sealed plastic container.

2.6.3: Shipping to University of Victoria British Columbia Proteomics Centre

A total of 2 ml of each cellular lysate was shipped on dry ice by air mail to the University of Victoria British Columbia Proteomics Centre, Saanich, BC V8Z 7X8. As there were originally 4 replicate protein preparations for each strain and the 8-plex method chosen for further analysis can only analyze up to eight samples, three each of the WT and *ΔbldG* mutant strain lysates and 2 of the *ΔbldA* mutant strain lysates were chosen

based on the protein concentrations determined by the Bradford assay as well as the clarity of the banding patterns on the SDS-PAGs.

2.7: iTRAQ® labeling and LC-MS/MS analysis

The following procedures regarding iTRAQ® labeling and LC-MS/MS analysis were conducted at the University of Victoria British Columbia Proteomics Centre.

2.7.1: iTRAQ® labeling

On arrival, protein concentrations were re-determined using a bicinchoninic acid (BCA) protein assay. Samples were then precipitated overnight in acetone followed by resolubilization in triethylammonium bicarbonate (TEAB) and 0.2% w/v SDS. Next, proteins were reduced with Tris(2-carboxyethyl)phosphine hydrochloride (TCEP) and alkylated with methyl methanethiosulfonate (MMTS). Finally, proteins were digested in-solution with trypsin and labeled with the appropriate 8-plex iTRAQ® label. WT samples were labeled with the 113,114, and 115 labels; *ΔbldG* samples were labeled with the 116, 117, and 118 labels; and *ΔbldA* samples were labeled with the 119 and 121 labels (Figure 1.5.1.1) (Kuzyk et al. 2009).

2.7.2: Fractionation via HPLC

The iTRAQ® labeled peptides were combined, desalted, and concentrated on an Oasis HLB cartridge, and speed vacuum centrifuged to dryness before separation by high pH reversed phase HPLC (Kuzyk et al. 2009). Fractions were collected every 30 seconds for 96 minutes and were concatenated into 24 fractions by combining every 24th fraction (e.g fractions 1, 25, 49, 73 were combined). The length of the reverse gradient was 2

hours per HPLC fraction. The HPLC fractions were then reduced in volume by lyophilization and were analyzed by LC-MS/MS.

2.7.3: Conditions for LC-MS/MS

Each of the samples was rehydrated to 110 µl (2% v/v acetonitrile, 0.1% v/v formic acid). Following rehydration, 15 µl aliquots of the peptide solutions were separated by on-line reversed phase liquid chromatography using a Thermo Scientific EASY-nLCII system with a reversed phase Magic C-18AQ (75µm I.D., 2 cm length, 5µm, 100Å, Michrom BioResources Inc) pre-column and a Magic C-18AQ nano-analytical column (75µm I.D., 15 cm length, 5µm, 100Å, Michrom BioResources Inc) at a flow rate of 300 nl/min. The chromatography system was coupled on-line to an LTQ Orbitrap Velos mass spectrometer equipped with a Nanospray Flex source (Thermo Scientific). The solvents that were used are as follows: A: 2% v/v acetonitrile, 0.1% v/v formic acid; B: 90% v/v acetonitrile, 0.1% v/v formic acid (Manteca et al. 2010). After a 249 bar (~5µL) pre-column equilibration and a 249 bar (~8µL) nanocolumn equilibration, samples were separated using a 120 minute gradient (0 min: 5% B; 100 min: 40% B; 5 min: 80% B; 2 min: 95% B; 13 min: 95% B). The parameters for the LTQ Orbitrap Velos (Thermo Scientific) were as follows: Nano-electrospray ion source with spray voltage 2.1kV; capillary temperature 250°C; Survey MS1 scan *m/z* range 400-1800 profile mode; resolution 30,000 @ *m/z* 400 with AGC target 1E6; and one microscan with maximum inject time 500 ms. A siloxane *m/z* 445.120024 lock mass was used for internal calibration. Other settings were: Preview mode for FTMS master scans: on; injection waveforms: on; monoisotopic precursor selection: on; rejection of charge state:

1. The experiment was acquired as a top 10 data dependent analysis of the most abundant ions with charge states of 2-4, exceeding 5,000 counts, being selected for higher-energy collisional dissociation (HCD) FT MSMS fragmentation (scans 2-11) and detection in centroid mode. Dynamic exclusion settings were: repeat count: 1; repeat duration: 15 seconds; exclusion list size: 500; exclusion duration: 15 seconds with a 10ppm mass window. The FT HCD settings were: resolution 7,500 @ *m/z* 400 in centroid mode with AGC target 1E5, amu isolation width, and normalized collision energy 50%, 0.1 msec activation time (Casado-Vela et al. 2010).

2.8: Data analysis

Initial analysis of the raw file data was conducted at the University of Victoria British Columbia Proteomics Centre and subsequent analysis was conducted at Memorial University of Newfoundland by the author with assistance from Dr. Lourdes Peña-Castillo, Department of Computer Science, Memorial University of Newfoundland.

2.8.1: Proteome Discoverer 4.1 parameters

The raw files generated from LC-MS/MS were analyzed by the University of Victoria British Columbia Proteomics Centre using Proteome Discoverer 4.1 software suite (Thermo Scientific). Spectrum Selection was used to generate peak lists of the HCD spectra (parameters: activation type: HCD; s/n cut-off: 1.5; total intensity threshold: 0; minimum peak count: 1; precursor mass: 350-5,000 Da). The peak lists were submitted to a database search using Mascot 2.4 and were searched against a database of *S. clavuligerus* proteins that had been created using both of the available *S. clavuligerus* full genome sequences (NZ_ADWJ01000000 and NZ_ADGD01000000) as well as the

four plasmids (NZ_CM001016.1, NZ_CM001017.1, NZ_CM001018.1, and NZ_CM001019.1) with the Artemis genome browser and annotation tool from the Wellcome Trust Sanger Institute (Medema et al. 2010; Song et al. 2010). Search parameters were: precursor tolerance: 10 ppm; MS/MS tolerance 20 mmu for FT MS/MS HCD data; enzyme Trypsin; 2 missed cleavages; instrument type FT-ICR ESI; fixed modification: Methylthio (C), iTRAQ® 8-plex (K), and iTRAQ® 8-plex (N-term); variable modifications: Oxidation (M), Deamidated (NQ), iTRAQ® 8-plex (Y)(Casado-Vela et al. 2010). The HCD Percolator settings were: Max delta Cn 0.05; Target false discovery rate (FDR) strict 0.01, Target FDR relaxed 0.05 with validation based on q-Value (Casado-Vela et al. 2010).

2.8.2: Normalization and differential expression

Abundance measurements for 36,780 peptides uniquely mapped to a single protein were obtained. To ensure that only data that was included by Proteome Discoverer during quantitation analysis were used, peptides had to be classified as "used," which requires the presence of an iTRAQ® label and at least one valid iTRAQ® reporter ion ratio. The median abundance of multiple peptides uniquely mapped to a protein was used as the abundance measurement for that protein. All protein abundance measurements <1 or missing were set to 1, and measurements were $\log_2$ transformed. Replicates for each strain were normalized using quantile normalization available in the normalize between arrays function in the R package Limma (version 3.16.3) (Smyth 2005). Pairwise differential protein expression between the three strains (i.e. *ΔbldG*-WT, *ΔbldA*-WT, *ΔbldA-ΔbldG*) was identified by means of a moderated paired t-test (Smyth

2004) available in Limma. P-values were corrected for multiple testing using the FDR approach. Proteins with a FDR-corrected P-value of less than 0.01 in any given comparison were deemed to have a statistically significant differential expression in that comparison.

2.9: TTA-dependence in *S. clavuligerus*

2.9.1: Identification of TTA codon containing genes in *S. clavuligerus*

The full sequence data of the *S. clavuligerus* chromosome (NZ_CM001015), as well as the four plasmids, pSCL1 (NZ_CM001016), pSCL2 (NZ_CM001017), pSCL3 (NZ_CM001018), and pSCL4 (NZ_CM001019), were obtained in FASTA format from NCBI and uploaded to the TTA Lynx (http://ttalynx.bio.lnu.edu.ua/cgi-bin/index.pl) server. Once uploaded to the server, TTA Lynx filtered out all genes containing TTA codons. The proteins encoded by these genes were then manually searched for in the data set. For proteins present in our dataset that are encoded by genes containing TTA codons, homologues of these genes from other *Streptomyces* species were also found using the StrepDB (http://strepdb.streptomyces.org.uk/) for comparison. The location and context of each TTA codon was also determined manually.

Chapter 3: Results

3.1: Verification of strains prior to proteomics analysis

3.1.1: Strain morphology

Both the *ΔbldA* and *ΔbldG* mutant strains used in this study are developmental mutants, i.e. they cannot form aerial mycelia or sporulate (Bignell et al. 2005; Trepanier et al. 2002). Therefore, a simple preliminary step was to observe the morphological characteristics of the strains grown on solid media for verification. To accomplish this, the wild-type (WT) strain and the two mutants were plated onto ISP-4 media, which is known to support sporulation. As expected, after approximately one week the *ΔbldA* and *ΔbldG* mutants failed to produce the characteristic fuzzy white aerial mycelia or grey spores as compared to the WT strain (Figure 3.1.1.1).

To ensure that the observed morphological phenotypes were caused by the disruption of the respective genes, each mutant was also subjected to complementation studies. Wild-type copies of the genes were cloned into the integrative plasmid pAU3-45, resulting in pAU3-45-G and pAU3-45-A, which contained the *bldG* and *bldA* genes under the control of their native promoters, respectively. These plasmids were then introduced into the respective mutant strains via mycelial conjugation. As seen in Figure 3.1.1.1, both *ΔbldA* and *ΔbldG* mutants could be successfully complemented by the introduction of the respective gene, clearly demonstrating that the phenotypic defect in each mutant is caused solely by the disruption of the respective gene as reported previously (Bignell et al. 2005; Trepanier et al. 2002).

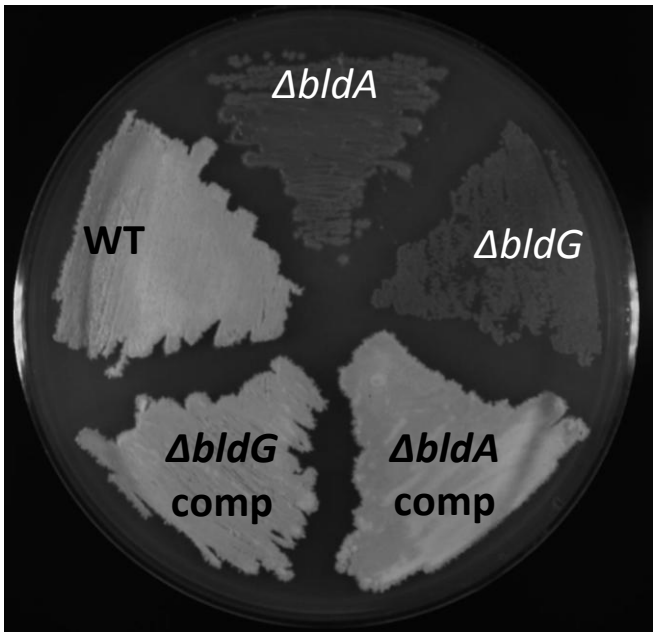

Figure 3.1.1.1: Morphology of *S. clavuligerus* WT strain as compared to the *ΔbldA* and *ΔbldG* developmental mutants before and after complementation (*ΔbldA*-comp and *ΔbldG*-comp) by reintroduction of the respective gene under the control of its native promoter. The WT and complemented mutants clearly show fuzzy grey/white spores, whereas the developmental mutants display the characteristic "bald" phenotype.

3.1.2: CA production by different strains

Previous studies have demonstrated that the *ΔbldG* mutant is completely blocked in CA production (Bignell et al. 2005), whereas the metabolite is still produced by the *ΔbldA* mutant and the WT strain (Trepanier et al. 2002). To verify that the strains being subjected to detailed proteomics analysis displayed the same phenotype, a survey of CA production was performed. Bioassays and HPLC using culture supernatants were employed for this purpose. The three strains were grown in SA medium for up to 120 hours and samples were collected every 24 hours for analysis by bioassays as described in section 2.5.1. Since the WT and the *ΔbldA* mutant strains are capable of producing CA, zones of inhibition were observed surrounding discs that were infused with culture supernatants from these strains (Figure 3.1.2.1). The *ΔbldG* mutant, on the other hand, is incapable of producing CA, which was confirmed by the absence of zones of inhibition around discs that were infused with culture supernatants from this strain (Figure 3.1.2.1). The complemented mutants were also capable of producing CA as determined by bioassays (data not shown).

For HPLC analysis, supernatant samples taken after 48 hours of growth of the respective strains in SA medium were derivatized with imidazole prior to injection, and CA production was monitored by following the absorbance at 311nm (Figure 3.1.2.2). A 10 μg/μl CA standard was also included as a positive control, and HPLC analysis was performed using supernatants from four different replicates of each strain. Derivatized culture supernatants from the WT and the *ΔbldA* mutant strains showed a detectable peak absorbing at 311nm at ~7 min (Figure 3.1.2.2 A). A small peak with a similar retention

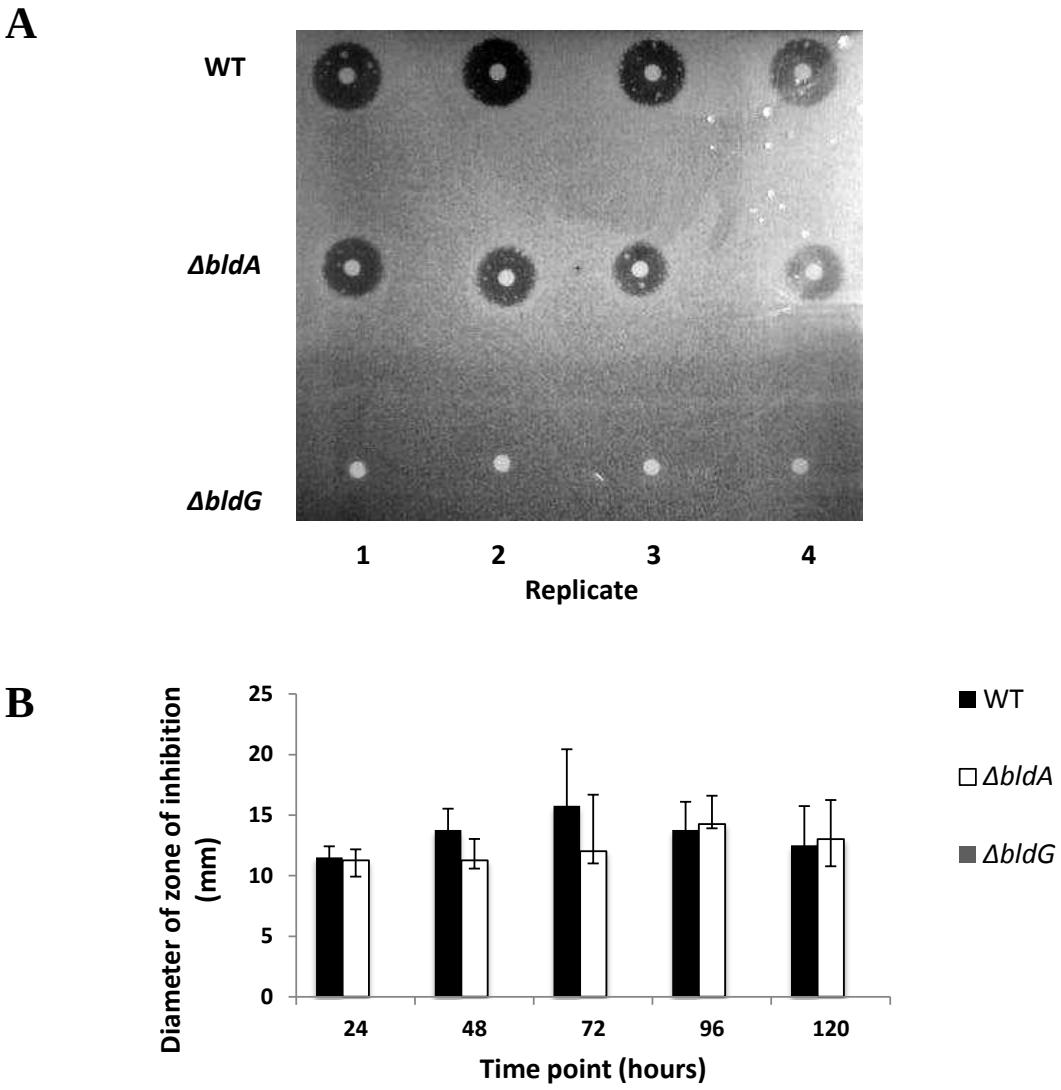

Figure 3.1.2.1: Bioassay for the detection of CA in liquid culture supernatants from WT, *ΔbldA*, and *ΔbldG S. clavuligerus* strains grown for up to 120 hours in SA medium. **(A)** Image of CA bioassay plate using four replicates of each *S. clavuligerus* strain showing results from the 48 hour sampling. **(B)** Bar graph showing average size of the zones of inhibition (in mm) on bioassay plates using culture supernatants from the three respective *S. clavuligerus* strains (n=4) sampled between 24 to 120 hours when grown in SA. Note that no CA activity was detected in the culture supernatants from the *ΔbldG* mutant. Error bars indicate standard error.

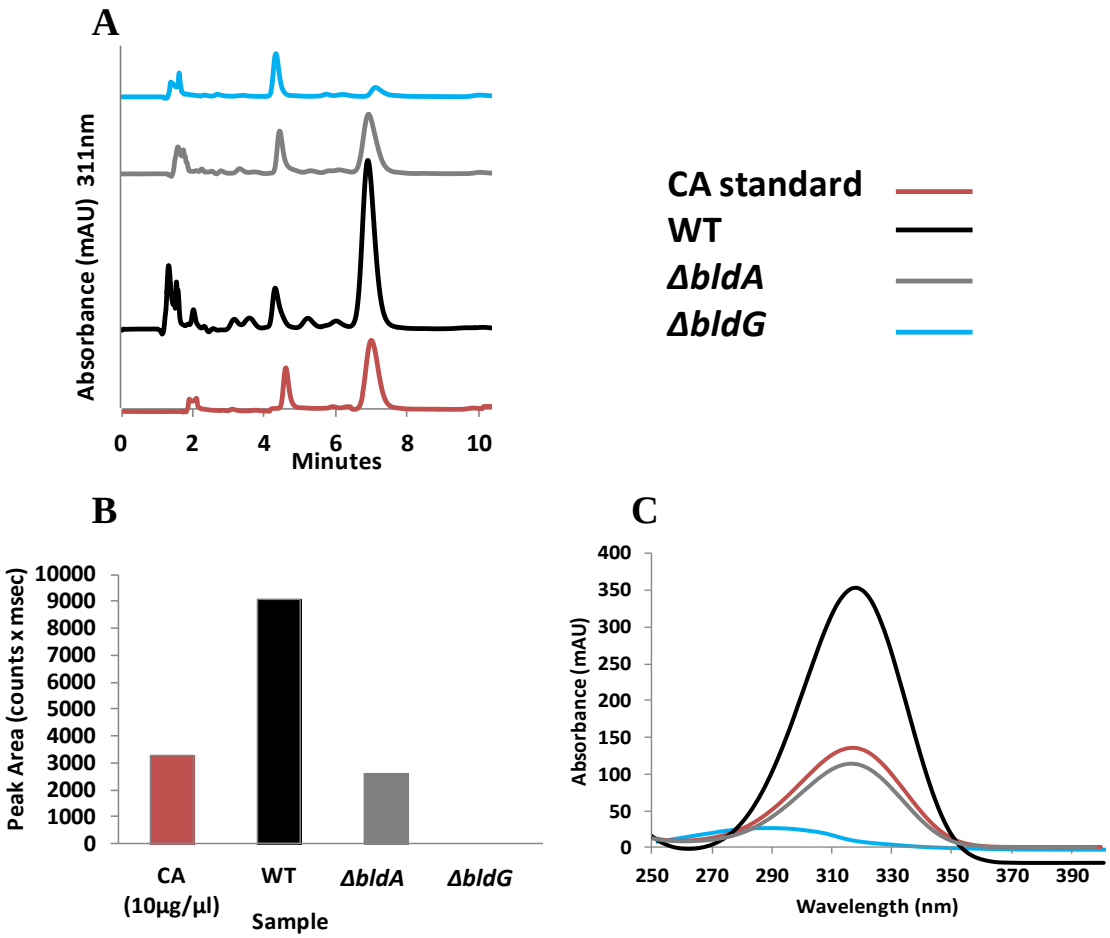

Figure 3.1.2.2: HPLC analysis of imidazole derived culture supernatants from the WT, *ΔbldA*, and *ΔbldG S. clavuligerus* strains grown for 48 hours in SA medium. **(A)** Chromatograms obtained, including one from a pure CA standard, are shown. **(B)** Bar graph showing peak area for CA detected in each supernatant. **(C)** Absorbance (nm) of the suspected CA peaks in the three strains compared to a pure CA standard, which absorbs at 310-330nm. Note that none of the supernatants form the *ΔbldG* showed bonafide peaks corresponding to CA.

time was also observed in the *ΔbldG* supernatant samples as well (Figure 3.1.2.2 A).

The presence of a small peak in the *ΔbldG* supernatant samples was cause for initial concern. The use of diode array detection technology in the HPLC system allowed for closer examination of the absorbance spectrum of the peak for comparison with that of a pure derivatized CA standard, and this demonstrated that the peak observed in the *ΔbldG* supernatant samples was not CA (Figure 3.1.2.2 C). Pure CA derivitized with imidazole had a maximum absorbance at ~311nm, whereas the peak observed in the *ΔbldG* supernatant samples had a maximum absorbance closer to 280nm. Based on the bioassay, HPLC and absorbance data, it was therefore verified that the WT and *ΔbldA* mutant produced CA and the *ΔbldG* mutant did not.

3.1.3: Strain verification by genomic DNA PCR

Primer sets were designed to PCR amplify the *bldA* and *bldG* genes as well as the apramycin resistance cassette (*apra*) that was used to disrupt the respective genes in the mutant strains. When chromosomal DNA from the *ΔbldG* mutant was used as template, no PCR product was observed using the *bldG* specific primers (*bldG*-conf) and a 500 bp product was observed using the *apra* specific primers, as expected (Figure 3.1.3.1 A). While using chromosomal DNA as template from the *ΔbldA* mutant, a product of 1.8 kb was expected using the *bldA* specific primers (*bldA*-conf) because these primers amplify a portion of the disrupted *bldA* gene and surrounding area (400 bp in size) as well as the entire 1.4 kb *apra* cassette that was used to prepare this mutant (Figure 3.1.3.1.B). On the other hand, as for the *ΔbldG* mutant, a 500 bp PCR product was observed when the *apra* specific primers were used with the same *ΔbldA* chromosomal DNA as template (Figure

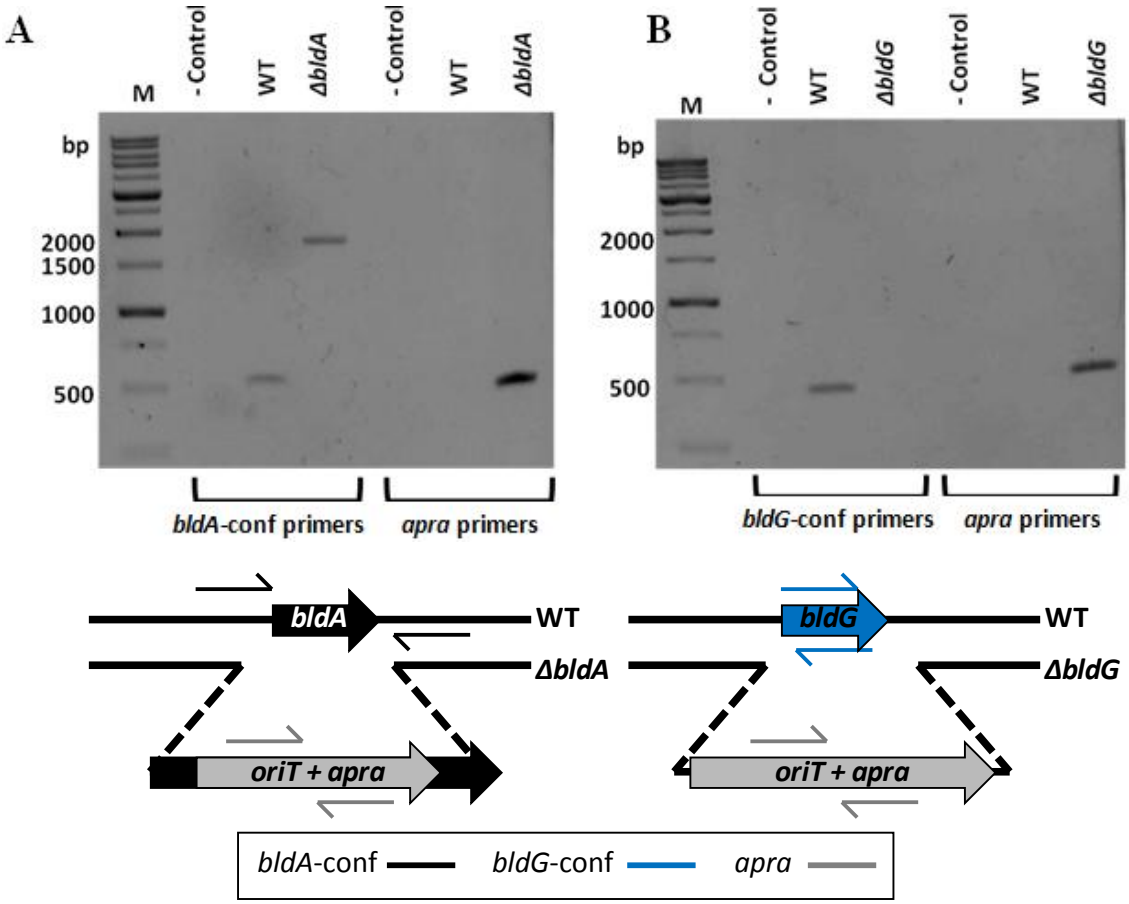

Figure 3.1.3.1: Confirmation of gene mutants using genomic DNA PCR. **(A)** PCR products were separated using 0.8% w/v agarose gel electrophoresis. A 500 bp product corresponding to the *bldA* gene and surrounding area was amplified using WT genomic DNA as the template and the *bldA*-conf primers, whereas no product was detected for the *apra* resistance cassette using the *apra* primers with the same template. A 1.8 kb product corresponding to a portion of the *bldA* gene and the *apra* disruption cassette was amplified using the *ΔbldA* genomic DNA as template and the *bldA*-conf primers, and a 500 bp product corresponding to the *apra* resistance cassette was amplified from the same product using the *apra* primers. **(B)** PCR products were separated using 1.5% w/v agarose gel electrophoresis. A 457 bp product corresponding to the *bldG* gene was amplified using WT genomic DNA as the template and the *bldG*-conf primers, whereas no product was detected for the *apra* resistance cassette using the *apra* primers with the same template. The *ΔbldG* genomic template did not yield a product using the *bldG*-conf primers, whereas a 500 bp product was obtained for the *apra* resistance cassette using the *apra* primers with the same template. Negative control reactions consisted of sterile distilled water in place of genomic DNA.

3.1.3.1 B). As a control, genomic DNA from the WT strain was also used in reactions with all three primer sets. As expected, for the *bldG* and *bldA* specific primer sets, PCR products of 457 bp and 500 bp were observed using WT chromosomal DNA as template, respectively, and no product was seen when the *apra* specific primers were used (Figure 3.1.3.1). A negative control using sterile distilled water as template was also included to ensure that there was no contaminating DNA in any of the PCR reagents.

3.2: Culture sampling and proteomics analysis

3.2.1: Determination of sampling time point for protein extraction

Bioassays were performed using four replicates of each *S. clavuligerus* strain. Samples were taken every 24 hours for up to 120 hours, the measurements were averaged and the standard error was calculated (Figure 3.1.2.1B). There was no significant difference in the size of the zones of inhibition between any of the time points; however, it has been reported in the literature that CA production is well established after 48 hours growth in SA medium with peak production taking place after approximately 96 hours of growth (Paradkar and Jensen 1995). Therefore, the 48 hour time point was selected for protein isolation to sample the proteome during the period when active CA production is taking place in *S. clavuligerus*.

3.2.2: Protein extraction

S. clavuligerus cell pellets suspended in PBS + 0.01% w/v SDS were subjected to sonication, resulting in crude cellular lysates with protein concentrations between 7 and 15 µg/µl (Table 3.2.2.1). Four replicate cultures of each strain were used for protein extraction, even though only 8 samples were to be sent for further analysis for 8-plex

Table 3.2.2.1: Protein concentrations of crude cellular lysates from the WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus* selected for iTRAQ® labeling as determined by Bradford assay.

Strain and replicate	Protein concentration (µg/µl)
WT-1	14.9
WT-2	9.00
WT-3	8.84
ΔbldA-1	7.00
ΔbldA-2	8.80
ΔbldG-1	9.74
ΔbldG-2	9.38
ΔbldG-3	9.52

iTRAQ®. This was done to ensure there were enough samples with a high enough protein concentration (150 μg total protein at 2 mg/ml) for further analysis in case some cultures did not grow optimally. All protein samples were also visualized using standard SDS-PAGE and staining with coomassie brilliant blue in order to verify the quality of the extracted proteins as well as for relative quantification (Figure 3.2.2.1). The samples that had the highest protein concentrations and clearest banding patterns by SDS-PAGE were chosen for further 8-plex iTRAQ® analysis and were sent to the University of Victoria British Columbia Proteomics Centre. The CA production status of all cultures used for protein isolation was also determined using bioassays and HPLC (Table 3.2.2.2).

3.3: Analysis of proteomics data

3.3.1: Results of normalization and differential expression

The main goal of this study was to investigate differences in protein expression patterns among the different biological samples to better understand the regulatory cascade involved in CA production in *S. clavuligerus*. A general approach to accomplish this is through identifying proteins that are differentially expressed between or among samples. A total of 2,496 *Streptomyces clavuligerus* proteins were detected in the iTRAQ® analysis at the University of Victoria British Columbia Proteomics Centre, 2,442 of which met the strict confidence criteria as described in the methods section, and were therefore included for further analysis. This corresponds to approximately 33.5% of the entire *S. clavuligerus* proteome, as the *S. clavuligerus* genome has been estimated to encode 7,281 proteins (Medema et al. 2010). The Proteome Discoverer software (version 4.1, Thermo-Scientific) provides ratios that represent the relative abundance of each

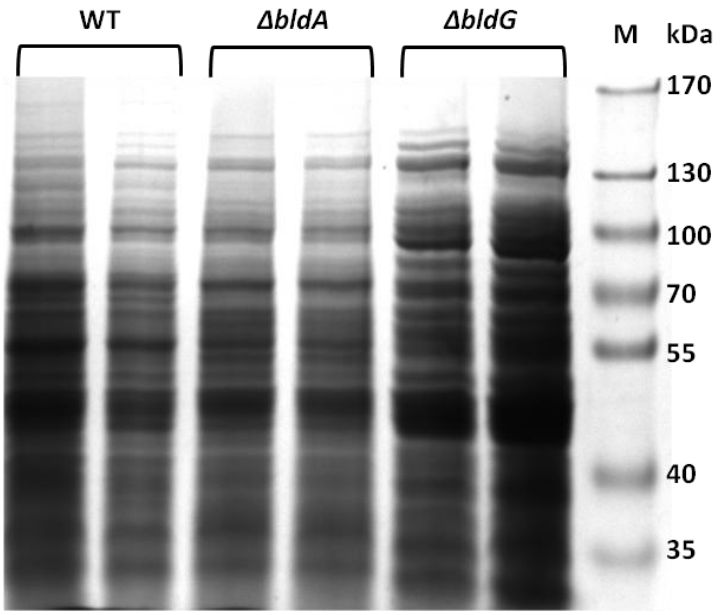

Figure 3.2.2.1: SDS-PAGE analysis of crude protein extracts from 2 replicates each of the WT, *ΔbldA*, and *ΔbldG S. clavuligerus* strains using 10% w/v acrylamide/bisacrylamide gels. A total of 145 µg of protein was loaded in each lane, and the electrophoresis was carried out at 45V constant mode for 5 hours at 4°C. Thermo Scientific PageRuler Prestained Protein ladder was used as the marker, indicated by 'M'.

Table 3.2.2.2: Amount of clavulanic acid detected in 48 hour supernatants from WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus* based on HPLC peak area and bioassay zones of inhibition.

Sample	Peak area (counts × msec)	Zone of inhibition (mm)
WT-1	9319.01	17
WT-2	9588.01	13
WT-3	7802.18	14
ΔbldA-1	2748.57	12
ΔbldA-2	2637.55	12
ΔbldG-1	0	0
ΔbldG-2	0	0
ΔbldG-3	0	0

protein between samples based on detected peptide fragments. Quantile normalization of the replicates of each strain was performed prior to further analysis to correct for variations in protein abundance using the statistical package R (version 3.0.0). A $\log_2$ scale for intensity was used as the variation in the log-ratios is less dependent on absolute magnitudes/concentrations of the detected peptides preventing skewed distribution (Boehm et al. 2007). As seen in Figure 3.3.1.1, when quantile normalization was carried out on the expression data, replicates from each strain clustered together, suggesting that protein expression levels between the replicates were significantly similar. Therefore, the quantile normalized data was used for further analysis.

Pair-wise differential protein expression patterns between strains was determined using a moderated paired t-test with FDR-corrected P-values, in which P-values of less than 0.05 in any given comparison were deemed to be statistically significant (Figure 3.3.1.2). The criteria for under and over expression was adjusted by setting a $\log_2$ fold change cut-off at -0.8 for under-expressed proteins and +1.2 for over-expressed proteins, respectively, as reported in previous studies (Davalos et al. 2010). A total of 283 proteins were over-expressed and 677 were under-expressed in the *ΔbldG* mutant as compared to the WT strain (adjusted P-value = 0.05), whereas a total of 275 and 641 proteins were respectively expressed in the same comparison when the P-value was reduced to 0.01 (Table A.1.1 and A.1.2). For the *ΔbldA* mutant, a total of 60 proteins were over-expressed and 1,345 proteins were under-expressed when compared to the WT strain (P-value = 0.05), which was reduced to 57 and 1279, respectively, when the P-value was set to 0.01 (Table A.1.3 and A.1.4). A total of 235 proteins were over-expressed and 1,296

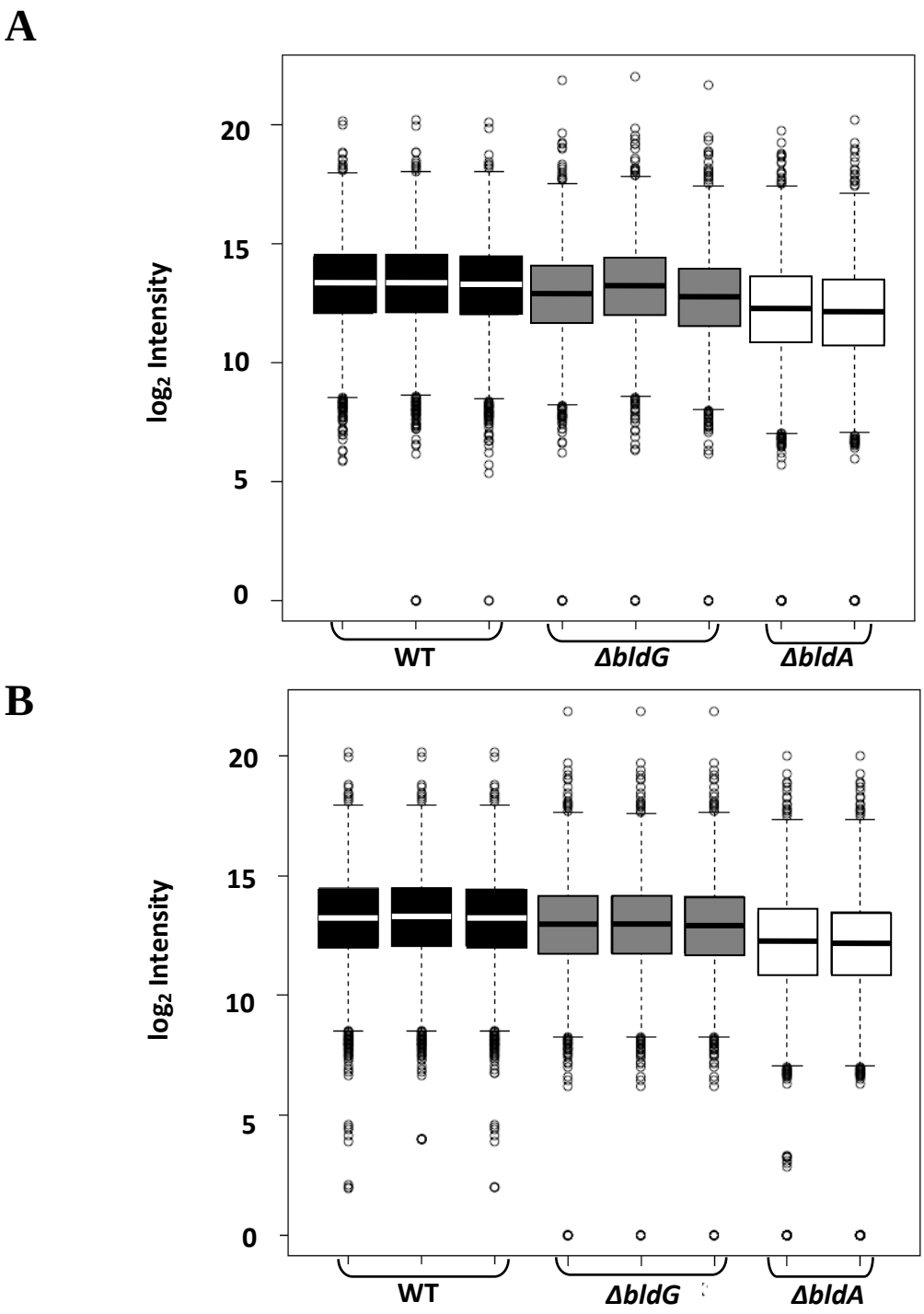

Figure 3.3.1.1: Raw and normalized aggregated median intensity values per peptide of $\log_2$ transformed iTRAQ® generated protein abundance measurements for the WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus*. (**A)** Raw intensities prior to quantile normalization. **(B)** Intensities following quantile normalization to remove technical variation between strains.

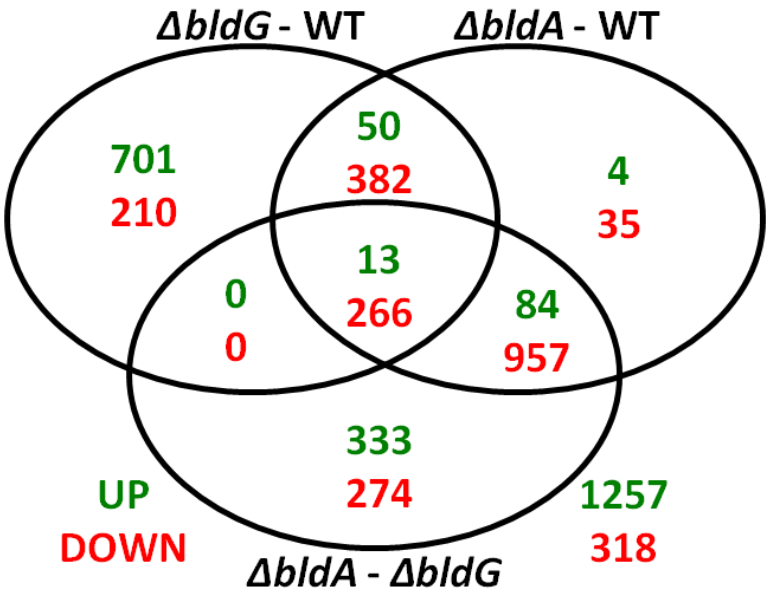

Figure 3.3.1.2: Venn diagram of proteins found to be differentially expressed (P=0.05) per comparison in *S. clavuligerus* (*ΔbldG*-WT, *ΔbldA*-WT, *ΔbldA*-*ΔbldG*). Numerals in green represent the number of proteins that were determined to be over-expressed and numerals in red represent those proteins found to be under-expressed. Each differentially expressed protein is represented twice. For example 490051386, the protein encoded by *bldG*, is represented both in the green-333 group and the red-382 group meaning that this protein is under-expressed in both *ΔbldG* and *ΔbldA* compared to WT, but it is expressed more in *ΔbldA* compared to *ΔbldG*.

were under-expressed in *ΔbldA* when compared to the *ΔbldG* strain (P-value = 0.05), which was reduced to 224 and 1,240, respectively, when the P-value was set at 0.01 (Table A.1.5 and A.1.6). Furthermore, 426, 222 and 227 proteins were expressed at similar levels between *ΔbldG* and WT, *ΔbldA* and WT and *ΔbldA* and *ΔbldG* respectively when the P-value was set to 0.01 (Tables A.1.7-A.1.9). Only proteins with P-values of 0.01 are considered further.

3.3.2: Differential expression of regulatory proteins

Of particular interest to this study was the identification of proteins higher up than CcaR in the regulatory cascade leading to CA biosynthesis. This includes sigma factors and other transcriptional regulators that could potentially be involved in regulating secondary metabolism in *S. clavuligerus*. Those proteins found to be simultaneously under-expressed in *ΔbldG* compared to the WT stain and over-expressed in *ΔbldA* compared to *ΔbldG* are of importance as they could be potential positive regulators of secondary metabolism rather than of differentiation based on the phenotypes of the *ΔbldG* and *ΔbldA* mutants. Similarly, those proteins found to be over-expressed in *ΔbldG* compared to WT and under-expressed in *ΔbldA* compared to *ΔbldG* are of interest as potential negative regulators or repressors of secondary metabolism.

3.3.2.1: Sigma factors and related proteins

Elaborate networks of sigma factors, anti-sigma factors, and anti-anti-sigma factors have been shown to be involved in cellular differentiation, stress responses and antibiotic production in the *Streptomyces* (Bibb et al. 2000; Kelemen et al. 1996; Kim et al. 2008; Sevcikova et al. 2001; Viollier et al. 2003). A total of ten sigma factors, three

anti-sigma factors, and one anti-anti-sigma factor were detected in the dataset collected using iTRAQ® analysis (Table 3.3.2.1.1). Among these were the anti-anti-sigma factor encoded by *bldG*, two of the anti-sigma factors with which BldG interacts (Orf3/ApgA and RshA) and the sigma factor SigH (regulated by the anti-sigma factor RshA). BldG is under-expressed in both *S. clavuligerus ΔbldG* and *ΔbldA* strains as compared to the WT strain and over-expressed in *ΔbldA* as compared to *ΔbldG*, however, neither the anti-sigma factors Orf3/ApgA and RshA nor SigH were significantly under or over-expressed in the same pair-wise comparisons.

Two additional sigma factors (AdsA and 490052605, both belonging to the sigma 70-family) were significantly under-expressed in *ΔbldG* and were unaffected in *ΔbldA* when compared to the WT strain. A second sigma 70-family protein (490061073) was found to be significantly under-expressed in both the *ΔbldG* and *ΔbldA* strains as compared to WT. Additionally, four various sigma factors were under-expressed in the *ΔbldA* strain when compared to WT and not differentially expressed between *ΔbldG* and WT: RpoE (known as SigR in *S. coelicolor*), which is a key regulator of the oxidative stress response (Paget et al. 1998); HrdD, the function of which is yet unknown and is partially dependent upon SigE for its expression (Buttner et al. 1990; Paget et al. 1999); a sigma factor (490058906) that is homologous to *S. coelicolor* SigF which is required for proper sporulation in other *Streptomyces* spp. (Tzanis et al. 2014) and sigma factor HrdB which is the principle sigma factor responsible for transcribing housekeeping genes. In addition, two sigma 24-family proteins (497683136 and 490056752) were over-expressed in *ΔbldG* and under-expressed in *ΔbldA* when compared to the WT strain.

Table 3.3.2.1.1: Sigma factors, anti-sigma factors, and anti-anti-sigma factors detected in proteins extracted from the WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus.*

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G-WT[e]	logFC A-WT[f]	adj.P.Val A-WT[g]	logFC A-G[h]	adj.P.Val A-G[i]
490058537	RNA polymerase subunit sigma-24 AdsA	1.13E+01	-3.42E+00	3.40E-06	-6.56E-01	1.41E-02	2.77E+00	9.80E-06
490052605	RNA polymerase sigma-70 factor	1.16E+01	-2.48E+00	2.19E-06	-1.70E-01	2.28E-01	2.31E+00	3.74E-06
490061073	RNA polymerase subunit sigma-70	1.45E+01	-1.38E+00	3.19E-05	-1.57E+00	2.73E-05	-1.87E-01	2.03E-01
490058906	RNA polymerase sigma factor	9.61E+00	-7.00E-01	8.32E-03	-1.67E+00	1.60E-04	-9.67E-01	2.30E-03
497683309	RNA polymerase sigma factor SigH	1.20E+01	-5.61E-01	3.22E-02	-1.32E-01	5.88E-01	4.29E-01	9.81E-02
497683562	RNA polymerase sigma factor HrdB	1.33E+01	6.66E-02	6.48E-01	-8.16E-01	1.05E-03	-8.83E-01	6.08E-04
497683136	RNA polymerase subunit sigma-24	1.51E+01	3.12E+00	1.16E-05	-1.43E+00	8.69E-04	-4.56E+00	3.24E-06
490056752	RNA polymerase subunit sigma24	1.23E+01	1.23E+00	2.64E-04	-1.34E+00	2.51E-04	-2.57E+00	8.67E-06
490051619	RNA polymerase sigma factor RpoE	1.31E+01	9.53E-01	7.17E-03	-1.75E+00	5.17E-04	-2.70E+00	4.58E-05
490051497	RNA polymerase sigma factor HrdD	1.11E+01	9.76E-01	7.37E-03	-1.40E+00	1.92E-03	-2.38E+00	1.04E-04
490051386	anti-sigma B factor antagonist BldG	1.54E+01	-5.23E+00	2.60E-06	-3.00E+00	4.11E-05	2.23E+00	1.49E-04
490051385	anti-sigma regulatory factor Orf3	1.36E+01	-6.92E-01	1.57E-03	-7.06E-03	9.64E-01	6.85E-01	2.17E-03
490051650	anti-sigma regulatory factor RshA	1.33E+01	-6.78E-01	2.13E-03	-5.45E-01	8.94E-03	1.33E-01	4.04E-01
490059496	anti-sigma factor	1.56E+01	5.11E-01	1.84E-01	-6.62E-01	1.20E-01	-1.17E+00	1.60E-02

[a] Identification is based on annotation by NCBI. [b] Description is based on NCBI annotation of protein similarity by BLAST. [c] Average normalized expression in the WT strain. [d] Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. [e]Adjusted P-value in *ΔbldG* as compared to the WT strain. [f] Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. [g] Adjusted P-value in *ΔbldA* as compared to the WT strain. [h] Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and [i] Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

3.3.2.2: Transcriptional regulators

A total of 196 transcriptional regulators of various families were also present in the dataset. Sixty-eight and 110 of these regulators were under- or over-expressed (P = 0.01) in *ΔbldG* (Table 3.3.2.2.1) or in *ΔbldA* (Table A.10), respectively, when compared to the WT strain. In addition, 89 regulators were under or over-expressed in *ΔbldA* when compared to *ΔbldG* (Table 3.3.2.2.2). Several regulatory elements with known roles in regulating CA biosynthesis (Figure 1.3.1.1) were detected in the protein samples. One AraC family protein (490055879/AdpA) is under-expressed in both *ΔbldG* and *ΔbldA* compared to the WT strain and under-expressed in *ΔbldA* as compared to *ΔbldG*. AdpA has a role in the positive regulation of *ccaR* and therefore indirectly regulates CA biosynthesis (Table 3.3.2.2.1) (Lopez-Garcia et al. 2010). A homologue of *S. coelicolor* RNaseIII (490059733/AbsB) was under-expressed in both *ΔbldG* and *ΔbldA* when compared to the WT strain and is similarly expressed between *ΔbldA* and *ΔbldG*. AbsB autoregulates its own expression and that of other genes by cleaving transcripts, and mutation of the gene encoding it results in the loss of secondary metabolite production (Price et al. 1999; Xu et al. 2008) (Table A.1.2). A pleiotropic regulator (490054092/BldD) was found to be similarly expressed among the three strains (Tables A.1.7-A.1.9). BldD is known to repress the pre-mature expression of multiple genes involved in differentiation and antibiotic biosynthesis (Elliot et al. 1998; Elliot et al. 2001; Hunt et al. 2005). Finally, a protein identified as an AfsR-like regulator (497683347) was found to be similarly under-expressed in both *ΔbldG* and *ΔbldA* compared to the WT strain. On closer examination the protein was identified to be a

Table 3.3.2.2.1: Regulators found to be significantly under or over-expressed in the *ΔbldG* strain of *S. clavuligerus* compared to the WT strain.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G-WT[e]	logFC A-WT[f]	adj.P.Val A-WT[g]	logFC A-G[h]	adj.P.Val A-G[i]
490056196	transcriptional regulator	1.42E+01	-3.38E+00	8.89E-05	1.07E+00	3.26E-02	4.45E+00	2.73E-05
497681787	regulator	1.49E+01	-3.15E+00	1.46E-04	7.25E-01	1.22E-01	3.88E+00	6.24E-05
497683074	XRE family transcriptional regulator	1.34E+01	-3.13E+00	4.47E-03	-1.98E+00	4.41E-02	1.16E+00	1.90E-01
490055141	DNA-binding protein	1.45E+01	-3.10E+00	1.30E-05	-1.41E+00	1.02E-03	1.69E+00	3.37E-04
497682610	transcriptional regulator	1.27E+01	-2.96E+00	1.09E-04	-9.56E-01	3.47E-02	2.01E+00	1.05E-03
497685222	DNA-binding protein	1.24E+01	-2.80E+00	1.67E-06	-3.28E+00	1.68E-06	-4.73E-01	7.42E-03
497682597	XRE family transcriptional regulator	1.22E+01	-2.70E+00	2.76E-05	-1.00E+00	6.34E-03	1.70E+00	3.87E-04
497683559	TerD-family protein	1.39E+01	-2.67E+00	1.17E-05	-2.17E+00	4.81E-05	5.04E-01	4.50E-02
490058590	XRE family transcriptional regulator	1.26E+01	-2.65E+00	1.06E-03	-7.51E-01	1.83E-01	1.90E+00	7.20E-03
497683347	putative regulatory protein (AfsR-like protein)	1.52E+01	-2.64E+00	8.11E-06	-2.57E+00	1.59E-05	7.25E-02	7.22E-01
490050159	PbsX family transcriptional regulator	1.38E+01	-2.52E+00	3.03E-06	-2.45E+00	5.79E-06	7.16E-02	6.35E-01
490057023	regulatory protein	1.28E+01	-2.47E+00	1.39E-05	-2.75E-01	2.15E-01	2.20E+00	2.98E-05
497682848	TetR family transcriptional regulator	1.27E+01	-2.37E+00	1.13E-03	-2.72E+00	8.42E-04	-3.44E-01	4.81E-01
490052791	transcriptional regulator	1.40E+01	-2.16E+00	1.90E-05	-1.87E+00	5.82E-05	2.97E-01	1.54E-01
497683124	Fis family transcriptional regulator	1.30E+01	-2.11E+00	1.70E-05	-1.48E+00	1.42E-04	6.27E-01	9.53E-03
490056694	GntR family transcriptional regulator	1.35E+01	-2.01E+00	1.28E-03	-3.04E+00	2.22E-04	-1.03E+00	3.40E-02
497681584	DNA-binding protein	1.42E+01	-1.99E+00	1.14E-05	-4.00E-01	3.74E-02	1.59E+00	4.05E-05
490058790	IclR family transcriptional regulator	1.23E+01	-1.97E+00	1.35E-03	-1.82E+00	2.95E-03	1.43E-01	7.33E-01
490055317	AsnC family transcriptional regulator	1.37E+01	-1.94E+00	1.49E-05	-1.48E+00	8.36E-05	4.68E-01	2.14E-02
497682129	IclR family transcriptional regulator	1.52E+01	-1.93E+00	3.86E-05	-1.86E+00	6.86E-05	6.58E-02	7.49E-01
490056384	LuxR family transcriptional regulator	1.50E+01	-1.79E+00	5.87E-03	-3.24E+00	4.38E-04	-1.45E+00	1.94E-02
490055173	LuxR family transcriptional regulator	1.36E+01	-1.77E+00	9.21E-05	-1.59E+00	2.32E-04	1.79E-01	4.27E-01
490057927	transcriptional regulator	1.51E+01	-1.74E+00	1.66E-04	-2.32E+00	5.72E-05	-5.80E-01	3.91E-02
497685265	LuxR family transcriptional regulator	1.04E+01	-1.61E+00	2.70E-05	-2.69E+00	5.34E-06	-1.08E+00	2.72E-04
490057423	GntR family transcriptional regulator	1.54E+01	-1.45E+00	2.39E-04	-1.61E+00	2.10E-04	-1.59E-01	4.75E-01
490052137	IclR family transcriptional regulator	1.43E+01	-1.44E+00	2.44E-05	-8.78E-02	5.35E-01	1.36E+00	4.10E-05

497681972	Fur family transcriptional regulator	1.37E+01	-1.38E+00	2.36E-03	-4.25E+00	1.46E-05	-2.87E+00	6.96E-05
490053914	LuxR family transcriptional regulator	1.37E+01	-1.33E+00	1.36E-04	-2.22E+00	1.81E-05	-8.91E-01	1.40E-03
490058041	XRE family transcriptional regulator	1.05E+01	-1.32E+00	1.75E-04	-2.26E+00	1.96E-05	-9.43E-01	1.30E-03
490055879	AraC family transcriptional regulator	1.36E+01	-1.26E+00	8.85E-05	-2.52E+00	5.93E-06	-1.26E+00	1.09E-04
490060245	TetR family transcriptional regulator	1.54E+01	-1.26E+00	6.86E-05	-3.74E-01	3.43E-02	8.84E-01	5.42E-04
490051029	DtxR family transcriptional regulator	1.42E+01	-1.25E+00	4.95E-04	-2.53E+00	2.28E-05	-1.29E+00	5.52E-04
490055876	response regulator	1.44E+01	-1.24E+00	2.76E-05	-1.10E+00	7.59E-05	1.40E-01	2.68E-01
497683042	transcriptional regulator	1.36E+01	-1.24E+00	2.64E-04	3.94E-01	6.69E-02	1.63E+00	7.95E-05
490055478	DNA-binding protein	1.26E+01	-1.23E+00	5.29E-05	6.14E-01	2.77E-03	1.84E+00	9.37E-06
490050197	DNA-binding protein	9.67E+00	-1.17E+00	9.20E-04	-2.34E+00	4.11E-05	-1.17E+00	1.24E-03
497681565	IclR family transcriptional regulator	1.34E+01	-1.07E+00	1.77E-04	-1.06E+00	2.75E-04	1.05E-02	9.45E-01
490057267	transcriptional activator	1.45E+01	-1.07E+00	3.96E-03	9.80E-01	8.66E-03	2.05E+00	1.82E-04
490054231	MarR family transcriptional regulator	1.37E+01	-1.06E+00	3.31E-03	-1.42E+00	1.12E-03	-3.65E-01	1.92E-01
490057935	LuxR family transcriptional regulator	1.51E+01	-1.05E+00	6.12E-05	-6.00E-01	1.61E-03	4.47E-01	6.15E-03
490052578	DeoR family transcripitonal regulator	8.23E+00	-9.72E-01	1.87E-03	-2.11E+00	5.35E-05	-1.14E+00	1.11E-03
497683061	NmrA family protein	1.21E+01	-9.51E-01	1.66E-03	-2.76E+00	1.39E-05	-1.81E+00	7.54E-05
490051193	LacI family transcriptional regulator	1.35E+01	-9.46E-01	2.79E-03	-2.84E+00	1.84E-05	-1.89E+00	1.00E-04
490052594	transcriptional regulator	1.52E+01	-9.31E-01	1.57E-04	-1.04E+00	1.34E-04	-1.05E-01	4.26E-01
497681703	DNA-binding protein	1.09E+01	-9.07E-01	1.41E-02	1.19E+00	6.14E-03	2.10E+00	3.02E-04
490054541	DNA-binding protein	1.52E+01	-8.79E-01	3.19E-04	1.02E+00	2.20E-04	1.90E+00	8.76E-06
490057306	TetR family transcriptional regulator	1.15E+01	-8.32E-01	1.18E-03	-2.64E+00	7.11E-06	-1.81E+00	2.78E-05
490051829	LysR family transcriptional regulator	1.42E+01	-7.73E-01	1.06E-02	-2.54E+00	4.30E-05	-1.76E+00	2.31E-04
490056872	AsnC family transcriptional regulator	1.32E+01	-7.50E-01	1.10E-02	-2.67E+00	3.10E-05	-1.92E+00	1.29E-04
497681723	TetR family transcriptional regulator	1.37E+01	1.16E+00	1.09E-04	-2.37E-01	1.39E-01	-1.39E+00	5.04E-05
490053359	GntR family transcriptional regulator	1.33E+01	1.16E+00	2.11E-04	-5.93E-01	9.10E-03	-1.75E+00	3.24E-05
490055041	DNA-binding protein	1.33E+01	1.30E+00	2.15E-04	-6.71E-01	8.73E-03	-1.97E+00	3.24E-05
497682165	XRE family transcriptional regulator	1.04E+01	1.38E+00	5.22E-03	-2.96E+00	1.61E-04	-4.34E+00	2.01E-05
490058535	REX family transcriptional regulator	1.26E+01	1.38E+00	4.17E-04	-8.76E-01	6.13E-03	-2.26E+00	4.11E-05
490051647	DeoR family transcriptional regulator	1.14E+01	1.41E+00	4.00E-05	-1.96E+00	1.46E-05	-3.37E+00	1.73E-06
497682237	transcriptional regulator	1.18E+01	1.48E+00	1.64E-04	-6.86E-01	1.12E-02	-2.17E+00	2.97E-05
490059014	XRE family transcriptional regulator	1.23E+01	1.57E+00	3.97E-04	-5.10E-01	8.01E-02	-2.08E+00	1.15E-04

497683062	TetR family transcriptional regulator	1.45E+01	1.75E+00	6.19E-05	-8.82E-01	3.13E-03	-2.63E+00	1.08E-05
490054741	transcriptional regulator	1.33E+01	1.80E+00	4.34E-06	-4.35E-01	7.05E-03	-2.24E+00	2.62E-06
490060648	LuxR family transcriptional regulator	9.47E+00	1.80E+00	9.31E-03	-1.80E+00	1.33E-02	-3.61E+00	3.88E-04
490060239	XRE family transcriptional regulator	1.31E+01	2.06E+00	1.32E-03	7.31E-01	1.19E-01	-1.32E+00	1.43E-02
497682584	XRE family transcriptional regulator	1.16E+01	2.11E+00	1.14E-05	-1.74E+00	4.30E-05	-3.86E+00	1.73E-06
490059687	transcriptional regulator	1.33E+01	2.13E+00	1.16E-05	-9.34E-01	1.10E-03	-3.06E+00	3.40E-06
490051466	TetR family transcriptional regulator	1.14E+01	2.53E+00	1.23E-04	-1.65E-01	6.28E-01	-2.69E+00	1.09E-04
497683951	LysR family transcriptional regulator	1.13E+01	2.81E+00	1.45E-05	-2.30E+00	5.62E-05	-5.11E+00	2.03E-06
497683598	transcriptional regulator	1.26E+01	3.14E+00	1.67E-06	-3.96E-01	2.79E-02	-3.53E+00	1.57E-06
497685319	DNA-binding protein	1.60E+01	3.16E+00	1.11E-04	-7.51E-01	9.48E-02	-3.91E+00	4.51E-05
490055325	DNA-binding protein	1.43E+01	4.66E+00	5.43E-06	1.08E+00	1.10E-02	-3.58E+00	2.27E-05

[a] Identification is based on annotation by NCBI. **[b]** Description is based on NCBI annotation of protein similarity by BLAST. **[c]** Average normalized expression in the WT strain. **[d]** Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. **[e]** Adjusted P-value in *ΔbldG* as compared to the WT strain. **[f]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. **[g]** Adjusted P-value in *ΔbldA* as compared to the WT strain. **[h]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and **[i]** Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Figure 3.3.2.2.2: Regulators found to be significantly under or over-expressed in the *ΔbldA* strain *S. clavuligerus* compared to the *ΔbldG* strain.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G-WT[e]	logFC A-WT[f]	adj.P.val A-WT[g]	logFC A-G[h]	adj.P.Val A-G[i]
497683951	LysR family transcriptional regulator	1.13E+01	2.81E+00	1.45E-05	-2.30E+00	5.62E-05	-5.11E+00	2.03E-06
490051238	MarR family transcriptional regulator	1.17E+01	6.92E-01	1.12E-03	-4.10E+00	1.11E-06	-4.79E+00	4.00E-07
497682165	XRE family transcriptional regulator	1.04E+01	1.38E+00	5.22E-03	-2.96E+00	1.61E-04	-4.34E+00	2.01E-05
497685319	DNA-binding protein	1.60E+01	3.16E+00	1.11E-04	-7.51E-01	9.48E-02	-3.91E+00	4.51E-05
497682584	XRE family transcriptional regulator	1.16E+01	2.11E+00	1.14E-05	-1.74E+00	4.30E-05	-3.86E+00	1.73E-06
490060648	LuxR family transcriptional regulator	9.47E+00	1.80E+00	9.31E-03	-1.80E+00	1.33E-02	-3.61E+00	3.88E-04
490055325	DNA-binding protein	1.43E+01	4.66E+00	5.43E-06	1.08E+00	1.10E-02	-3.58E+00	2.27E-05
497683598	transcriptional regulator	1.26E+01	3.14E+00	1.67E-06	-3.96E-01	2.79E-02	-3.53E+00	1.57E-06
497681275	GntR family transcriptional regulator	9.47E+00	1.08E+00	2.23E-04	-2.31E+00	9.05E-06	-3.39E+00	2.03E-06
490051647	DeoR family transcriptional regulator	1.14E+01	1.41E+00	4.00E-05	-1.96E+00	1.46E-05	-3.37E+00	1.73E-06
490051912	GntR family transcriptional regulator	1.33E+01	2.78E-01	4.90E-02	-2.81E+00	2.74E-06	-3.09E+00	1.61E-06
497684806	GntR family transcriptional regulator	1.16E+01	3.93E-01	1.33E-01	-2.68E+00	4.05E-05	-3.07E+00	1.72E-05
490059687	transcriptional regulator	1.33E+01	2.13E+00	1.16E-05	-9.34E-01	1.10E-03	-3.06E+00	3.40E-06
490055448	HrcA family transcriptional regulator	1.07E+01	3.86E-01	3.54E-01	-2.66E+00	5.65E-04	-3.04E+00	2.40E-04
490050038	MarR family transcriptional regulator	1.08E+01	4.89E-01	1.09E-02	-2.43E+00	7.49E-06	-2.92E+00	2.96E-06
497682579	transcriptional regulator	1.15E+01	3.14E-01	2.33E-01	-2.56E+00	6.05E-05	-2.87E+00	2.82E-05
497681972	Fur family transcriptional regulator	1.37E+01	-1.38E+00	2.36E-03	-4.25E+00	1.46E-05	-2.87E+00	6.96E-05
497683509	PucR family transcriptional regulator	1.36E+01	8.44E-01	4.39E-04	-1.89E+00	1.39E-05	-2.74E+00	2.57E-06
490060004	regulatory protein	1.09E+01	3.90E-01	2.38E-02	-2.32E+00	7.67E-06	-2.71E+00	3.34E-06
490051466	TetR family transcriptional regulator	1.14E+01	2.53E+00	1.23E-04	-1.65E-01	6.28E-01	-2.69E+00	1.09E-04
497683062	TetR family transcriptional regulator	1.45E+01	1.75E+00	6.19E-05	-8.82E-01	3.13E-03	-2.63E+00	1.08E-05

490057572	regulatory protein	1.34E+01	3.88E-01	4.78E-02	-2.09E+00	2.58E-05	-2.47E+00	9.23E-06
490047179	MerR-family transcriptional regulator	1.03E+01	-3.17E-02	9.63E-01	-2.45E+00	3.27E-03	-2.42E+00	3.06E-03
497683714	GntR family transcriptional regulator	1.31E+01	2.23E-01	1.18E-01	-2.12E+00	7.83E-06	-2.34E+00	4.06E-06
490058894	LuxR family transcriptional regulator	1.50E+01	9.10E-01	2.18E-04	-1.37E+00	4.24E-05	-2.28E+00	3.85E-06
490055493	MarR family transcriptional regulator	1.44E+01	-3.44E-01	3.60E-02	-2.61E+00	5.07E-06	-2.27E+00	5.80E-06
490051417	MarR family transcriptional regulator	1.43E+01	-5.68E-01	1.79E-02	-2.83E+00	1.23E-05	-2.26E+00	2.46E-05
490058535	REX family transcriptional regulator	1.26E+01	1.38E+00	4.17E-04	-8.76E-01	6.13E-03	-2.26E+00	4.11E-05
490054741	transcriptional regulator	1.33E+01	1.80E+00	4.34E-06	-4.35E-01	7.05E-03	-2.24E+00	2.62E-06
497682237	transcriptional regulator	1.18E+01	1.48E+00	1.64E-04	-6.86E-01	1.12E-02	-2.17E+00	2.97E-05
497681422	LuxR family transcriptional regulator	1.18E+01	4.68E-01	3.73E-02	-1.70E+00	1.22E-04	-2.16E+00	3.01E-05
490057686	transcriptional regulator	1.31E+01	5.10E-01	9.20E-03	-1.65E+00	3.92E-05	-2.16E+00	8.94E-06
490059014	XRE family transcriptional regulator	1.23E+01	1.57E+00	3.97E-04	-5.10E-01	8.01E-02	-2.08E+00	1.15E-04
497685129	ArsR family transcriptional regulator	1.09E+01	-2.57E-01	6.16E-02	-2.27E+00	5.07E-06	-2.02E+00	5.57E-06
490056617	transcriptional regulator	1.15E+01	-1.14E-01	7.77E-01	-2.12E+00	1.24E-03	-2.00E+00	1.46E-03
490055041	DNA-binding protein	1.33E+01	1.30E+00	2.15E-04	-6.71E-01	8.73E-03	-1.97E+00	3.24E-05
490056872	AsnC family transcriptional regulator	1.32E+01	-7.50E-01	1.10E-02	-2.67E+00	3.10E-05	-1.92E+00	1.29E-04
490059720	IclR family transcriptional regulator	1.49E+01	8.09E-01	1.51E-02	-1.11E+00	5.43E-03	-1.91E+00	2.88E-04
490055603	GntR family transcriptional regulator	1.33E+01	9.18E-01	1.12E-03	-9.84E-01	1.17E-03	-1.90E+00	3.33E-05
490053558	XRE family transcriptional regulator	9.14E+00	-7.75E-04	9.97E-01	-1.90E+00	1.11E-04	-1.90E+00	9.26E-05
490056868	RpiR family transcriptional regulator	1.24E+01	2.35E-01	1.33E-01	-1.66E+00	3.44E-05	-1.89E+00	1.48E-05
490051193	LacI family transcriptional regulator	1.35E+01	-9.46E-01	2.79E-03	-2.84E+00	1.84E-05	-1.89E+00	1.00E-04
490051556	TetR family transcriptional regulator	1.23E+01	2.83E-02	9.42E-01	-1.86E+00	1.02E-03	-1.89E+00	8.35E-04
490054315	transcriptional regulator	1.28E+01	5.07E-01	5.32E-02	-1.32E+00	1.14E-03	-1.82E+00	1.79E-04
490058107	LuxR family transcriptional regulator	1.25E+01	-8.07E-01	6.02E-02	-2.61E+00	4.37E-04	-1.81E+00	2.57E-03
497683061	NmrA family protein	1.21E+01	-9.51E-01	1.66E-03	-2.76E+00	1.39E-05	-1.81E+00	7.54E-05

490057306	TetR family transcriptional regulator	1.15E+01	-8.32E-01	1.18E-03	-2.64E+00	7.11E-06	-1.81E+00	2.78E-05
490060107	XRE family transcriptional regulator	1.33E+01	3.99E-01	4.45E-02	-1.41E+00	1.82E-04	-1.81E+00	4.19E-05
490051829	LysR family transcriptional regulator	1.42E+01	-7.73E-01	1.06E-02	-2.54E+00	4.30E-05	-1.76E+00	2.31E-04
490053359	GntR family transcriptional regulator	1.33E+01	1.16E+00	2.11E-04	-5.93E-01	9.10E-03	-1.75E+00	3.24E-05
490057142	regulatory protein	1.14E+01	-8.91E-03	9.61E-01	-1.69E+00	2.60E-05	-1.68E+00	2.10E-05
497685154	regulatory protein	1.58E+01	3.41E-01	3.10E-01	-1.27E+00	7.49E-03	-1.61E+00	2.09E-03
490055137	transcriptional regulator	1.37E+01	-2.42E-01	3.25E-01	-1.84E+00	2.43E-04	-1.60E+00	4.39E-04
490059040	RpiR family transcriptional regulator	1.34E+01	-4.70E-01	9.60E-02	-1.97E+00	2.50E-04	-1.50E+00	9.01E-04
497681563	MarR family transcriptional regulator	1.47E+01	4.56E-01	1.46E-02	-1.03E+00	4.01E-04	-1.49E+00	5.06E-05
497683496	AsnC family transcriptional regulator	1.32E+01	7.81E-01	8.57E-04	-6.98E-01	2.28E-03	-1.48E+00	4.02E-05
490054063	transcriptional regulator	1.41E+01	-2.86E-01	4.34E-02	-1.76E+00	1.34E-05	-1.48E+00	2.15E-05
490053058	DNA-binding protein	1.48E+01	5.15E-01	1.69E-02	-9.51E-01	1.40E-03	-1.47E+00	1.25E-04
497683736	GntR family transcriptional regulator	1.22E+01	1.07E+00	2.57E-04	-3.83E-01	4.42E-02	-1.45E+00	6.58E-05
490053695	transcriptional regulator	1.32E+01	-3.07E-03	9.87E-01	-1.41E+00	1.09E-04	-1.41E+00	9.22E-05
497681723	TetR family transcriptional regulator	1.37E+01	1.16E+00	1.09E-04	-2.37E-01	1.39E-01	-1.39E+00	5.04E-05
490051191	transcriptional regulator	1.30E+01	-3.64E-01	3.28E-01	-1.72E+00	2.89E-03	-1.36E+00	8.09E-03
497681284	AsnC family transcriptional regulator	1.29E+01	4.10E-01	1.30E-01	-9.35E-01	9.10E-03	-1.35E+00	1.38E-03
490060239	XRE family transcriptional regulator	1.31E+01	2.06E+00	1.32E-03	7.31E-01	1.19E-01	-1.32E+00	1.43E-02
497681220	GntR family transcriptional regulator	1.35E+01	8.34E-01	1.98E-02	-4.89E-01	1.47E-01	-1.32E+00	3.23E-03
497681302	transcriptional regulator	1.19E+01	1.10E+00	3.67E-04	-1.91E-01	3.04E-01	-1.29E+00	2.03E-04
490051029	DtxR family transcriptional regulator	1.42E+01	-1.25E+00	4.95E-04	-2.53E+00	2.28E-05	-1.29E+00	5.52E-04
490058573	LuxR family transcriptional regulator	1.28E+01	-8.38E-01	4.13E-02	-2.10E+00	9.46E-04	-1.26E+00	1.02E-02
490055879	AraC family transcriptional regulator	1.36E+01	-1.26E+00	8.85E-05	-2.52E+00	5.93E-06	-1.26E+00	1.09E-04
497681429	GntR family transcriptional regulator	1.44E+01	-4.61E-01	1.73E-01	-1.69E+00	1.70E-03	-1.23E+00	7.27E-03
497685379	DNA-binding protein	1.54E+01	1.18E-01	6.46E-01	-1.09E+00	4.16E-03	-1.21E+00	2.19E-03

490060366	TetR family transcriptional regulator	1.56E+01	3.13E-01	2.35E-02	-8.64E-01	2.68E-04	-1.18E+00	4.52E-05
490051741	PucR family transcriptional regulator	1.12E+01	-5.67E-01	2.83E-02	-1.74E+00	1.97E-04	-1.18E+00	1.32E-03
490050197	DNA-binding protein	9.67E+00	-1.17E+00	9.20E-04	-2.34E+00	4.11E-05	-1.17E+00	1.24E-03
490052137	IclR family transcriptional regulator	1.43E+01	-1.44E+00	2.44E-05	-8.78E-02	5.35E-01	1.36E+00	4.10E-05
497681584	DNA-binding protein	1.42E+01	-1.99E+00	1.14E-05	-4.00E-01	3.74E-02	1.59E+00	4.05E-05
497683042	transcriptional regulator	1.36E+01	-1.24E+00	2.64E-04	3.94E-01	6.69E-02	1.63E+00	7.95E-05
490055141	DNA-binding protein	1.45E+01	-3.10E+00	1.30E-05	-1.41E+00	1.02E-03	1.69E+00	3.37E-04
497682597	XRE family transcriptional regulator	1.22E+01	-2.70E+00	2.76E-05	-1.00E+00	6.34E-03	1.70E+00	3.87E-04
490055478	DNA-binding protein	1.26E+01	-1.23E+00	5.29E-05	6.14E-01	2.77E-03	1.84E+00	9.37E-06
490054541	DNA-binding protein	1.52E+01	-8.79E-01	3.19E-04	1.02E+00	2.20E-04	1.90E+00	8.76E-06
490058590	XRE family transcriptional regulator	1.26E+01	-2.65E+00	1.06E-03	-7.51E-01	1.83E-01	1.90E+00	7.20E-03
497682610	transcriptional regulator	1.27E+01	-2.96E+00	1.09E-04	-9.56E-01	3.47E-02	2.01E+00	1.05E-03
490057267	transcriptional activator	1.45E+01	-1.07E+00	3.96E-03	9.80E-01	8.66E-03	2.05E+00	1.82E-04
497681703	DNA-binding protein	1.09E+01	-9.07E-01	1.41E-02	1.19E+00	6.14E-03	2.10E+00	3.02E-04
490057023	regulatory protein	1.28E+01	-2.47E+00	1.39E-05	-2.75E-01	2.15E-01	2.20E+00	2.98E-05
497681787	regulator	1.49E+01	-3.15E+00	1.46E-04	7.25E-01	1.22E-01	3.88E+00	6.24E-05
490059845	GntR family transcriptional regulator	1.37E+01	-2.52E-01	7.66E-01	3.85E+00	2.66E-03	4.10E+00	1.68E-03
490056196	transcriptional regulator	1.42E+01	-3.38E+00	8.89E-05	1.07E+00	3.26E-02	4.45E+00	2.73E-05

[a] Identification is based on annotation by NCBI. [b] Description is based on NCBI annotation of protein similarity by BLAST. [c] Average normalized expression in the WT strain. [d] Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. [e]Adjusted P-value in *ΔbldG* as compared to the WT strain. [f] Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. [g] Adjusted P-value in *ΔbldA* as compared to the WT strain. [h] Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and [i] Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

partial entry for CcaR (Alexander and Jensen 1998), the positive regulator for both cephamycin C and CA biosynthesis in *S. clavuligerus*. The transcription of *ccaR* is abolished in *ΔbldG* mutants (Bignell et al. 2005) and despite the presence of a TTA codon in the encoding gene (SCLAV_4204), CcaR is effectively mistranslated in *S. clavuligerus ΔbldA* mutants (Trepanier et al. 2002). Additionally, several of the biosynthetic proteins from the CA biosynthetic gene cluster (490050161/Bls2, 490059562/Cas2, 490050162/Pah2, 490050165/OppA1, and 497683335/Gcas) were found to be under-expressed in both *ΔbldG* and *ΔbldA* as compared to the WT strain with the exception of Pah2, which was only under-expressed in *ΔbldG* when compared to the WT strain (Table A.1.2).

Next, attention was turned to identifying potential regulators of interest based on the differential expression profiles between *ΔbldG* and the WT strain. First to be addressed will be regulators found to be the most under-expressed in *ΔbldG* and unaffected in *ΔbldA* when compared to the WT strain. Next, a number of transcriptional regulators belonging to families that are known to have roles in the regulation of secondary metabolism, such as SARPs (Martin and Liras 2010; Perez-Llarena et al. 1997), LysR (Perez-Redondo et al. 1998), and IcIR (Santamarta et al. 2005; Yang et al. 2009), will be addressed. Additionally, those proteins belonging to regulatory families that were under-represented in the samples will be addressed. Protein families represented by multiple proteins in the dataset will be addressed last.

The most under-expressed transcriptional regulator in *ΔbldG* compared to the WT strain is a homologue of *S. coelicolor* BdtA (490056196), which has been previously demonstrated to be repressed by BldD in wild-type *S. coelicolor* (Elliot et al. 2001) (Table 3.3.2.2.1). This protein is also over-expressed in *ΔbldA* when compared to the WT strain. Three other regulatory proteins were under-expressed in *ΔbldG* and similarly expressed in *ΔbldA* when compared to the WT strain. The second most under-expressed transcriptional regulator in the set (497681787) contains a TPR motif and is homologous to a sporulation-associated protein in *S. coelicolor* (SCO2192). Two additional regulators meeting the above criteria and were over-expressed in *ΔbldA* as compared to *ΔbldG* (490057023 and 497683042) are homologous to sporulation-associated proteins in *S. griseus* and *S. coelicolor*.

A putative AfsR-like protein (490057267) was under-expressed in *ΔbldG* as compared to the WT strain (Table 3.3.2.2.1). This protein is encoded by SCLAV_0462 and is located in a secondary metabolite gene cluster containing a polyketide synthase (PKS) gene (SCLAV_0446-0497) designated SMC5, making it likely that this protein is a SARP (Medema et al. 2010). A single LysR-family transcriptional regulator (497683951) was over-expressed in *ΔbldG* and under-expressed in *ΔbldA* compared when to the WT strain and the gene encoding this protein (SCLAV_5537) is situated in front of two co-transcribed genes of unknown function. Four IclR transcriptional regulators were detected in the dataset (490058790, 497682129, 490052137 and 497681565) were under-expressed in *ΔbldG* compared to the WT strain. All of these proteins with the exception of a regulator of glyoxylate bypass (490052137) were also

under-expressed in *ΔbldA* when compared to the WT strain. The glyoxylate bypass regulator (SCLAV_5007) likely negatively regulates a malate synthase (490052131: SCLAV_5001) which was over-expressed in *ΔbldG* compared to WT (Table A.1.1) (Navone et al. 2014).

Several protein families were represented by only one or two proteins in the dataset (Table 3.3.2.2.1). Four of these are similarly under-expressed in both *ΔbldG* and *ΔbldA* when compared to the WT strain, including proteins belonging to the TerD-family (497683559), MarR-family (490054231 and 490051238), Fis-family (497683124) and DtxR-family (490051029). TerD-family proteins are thought to confer resistance to tellerium and have been implicated in differentiation in *S. coelicolor* (Sanssouci et al. 2011). MarR-family proteins are known to regulate the expression of proteins conferring resistance to multiple antibiotics (Alekshun and Levy 1999) and the gene encoding the MarR-family protein (SCLAV_2873) is located divergently next to a gene (SCLAV_2874) encoding a putative β-lactamase. Fis-family proteins normally function as accessory transcriptional activators of MarR-family proteins (Martin and Rosner 1997), whereas DtxR-family proteins regulate gene expression in response to iron (Oram et al. 2004).

Six additional regulators were under-expressed in both the *ΔbldG* and *ΔbldA* strains compared to WT and under-expressed in *ΔbldA* compared to *ΔbldG*. This included proteins belonging to the AsnC-family (490055317 and 490056872), Fur-family (497681972), the PbsX-family (490050159/PcbR), NmrA-family (497683061) and

DeoR-family (490052578) (Table 3.3.2.2.1 and 3.3.2.2.2). The AsnC-family of proteins regulate cellular metabolism at both the global and pathway specific level in response to amino acid effectors (Thaw et al. 2006). The gene encoding 490055317 (AsnC-family, SCLAV_4510) is divergently located next to genes encoding proteins involved in thiamine metabolism (SCLAV_4511-12) and peptidoglycan biosynthesis (SCLAV_4509). The Fur-family protein designated as 490056872 is encoded by SCLAV_0369, which is divergently oriented next to an operon containing an ABC-type antimicrobial peptide transport system and a putative peptidoglycan binding protein (SCLAV_0366-0368). Fur-family proteins normally regulate iron-uptake and the gene encoding the second protein from this family (497681972: SCLAV_1702) is located downstream from genes encoding an ABC-type metal ion transport system (SCLAV_1699-1702). PbsX-family proteins are normally involved in the regulation of post-exponential phase responses. The identification of PcbR as a PbsX-family protein is a mis-annotation as this protein is a secreted penicillin binding protein (penicillin binding protein right) the gene for which is located in the cephamycin C cluster (Paradkar et al. 1996a). NmrA-family proteins are involved in nitrogen metabolite repression (Andrianopoulos et al. 1998). DeoR-family proteins generally function to repress sugar metabolism and have been found to be involved in morphological differentiation and secondary metabolite production in *S. avermitilis* (Ulanova et al. 2013). A second protein annotated as a DeoR-family protein (490051647) was found to be over-expressed in *ΔbldG* and under-expressed in *ΔbldA* as compared to the WT strain, but it is possibly a misannotation as the amino acid sequence of the protein is lacking the domains typically

found in DeoR-family regulators (namely pfam00455). In addition, 490051647 is most likely related to diacylglycerol kinases based on the presence of a predicted DAGK_cat domain (pfam00781). A single REX-family transcriptional regulator (490058535), which in other *Streptomyces* regulates genes encoding components of the respiratory chain, was found to be over-expressed in *ΔbldG* and under-expressed in *ΔbldA* when compared to the WT strain (Brekasis and Paget 2003).

Multiple GntR-family transcriptional regulators, which have various functions including gluconate repression, were also detected (Table 3.3.2.2.1). Two of the detected GntR-family regulators (490056694 and 490057423) were under-expressed in both *ΔbldG* and *ΔbldA* as compared to the WT strain. The latter of these, as well as nine other GntR-family transcriptional regulators (490056694, 490057423, 497681386, 497683714, 490051912, 497684806, 497681220, 490055603, 497683736, 497681275 and 490053359) were also under-expressed in *ΔbldA* as compared to *ΔbldG* and one, an autoregulatory sporulation specific transcriptional factor (490059845/WhiH) (Persson et al. 2013), was over-expressed in *ΔbldA* as compared to *ΔbldG*.

Five members of the TetR-family (490060245, 497682848/AtrA, 490057306, 490051466, 497681723), members of which are involved in the transcriptional regulation of multidrug efflux, antibiotic biosynthesis pathways, osmotic stress response, catabolic pathways and differentiation processes (Ramos et al. 2005), were under-expressed in *ΔbldG* compared as compared to the WT strain (Table 3.3.2.2.1). One TetR-family protein (490060245) was under-expressed in *ΔbldG* and was unaffected in *ΔbldA* when

compared to the WT strain and over-expressed in *ΔbldA* compared to *ΔbldG*. The gene encoding 490060245 (SCLAV_5246) is located downstream from the gene encoding RocG/GdhA, the deletion of which increases production of the immunosuppressant FK506 in *S. tsukubaensis* (Huang et al. 2013). Two of the TetR-family proteins (497682848/AtrA and 490057306) were under-expressed in both *ΔbldG* and *ΔbldA* as compared to the WT strain. In *S. coelicolor*, AtrA regulates the transcription of *act*II-ORF4, the pathway specific activator of actinorhodin biosynthesis (Uguru et al. 2005). The gene encoding the second TetR-family regulator (490057306: SCLAV_0504) is located upstream of genes involved in peptidoglycan synthesis (SCLAV_0506-0507). Two TetR-family regulators (490051466 and 497681723) were over-expressed in *ΔbldG* as compared to the WT and under-expressed in *ΔbldA* as compared to *ΔbldG*. The protein designated as 490051466 is listed in StrepDB as AmfC, a mycelia formation protein that lacks any TetR-family regulatory domains. The gene encoding the second protein (497681723) lies downstream of putative genes encoding components of an ABC-type transport system (SCLAV1312-1313). An additional TetR-family regulator (497683062) was over-expressed in *ΔbldG* and under-expressed in *ΔbldA* as compared to the WT strain. The gene encoding 497683062 (SCLAV_3466) is located in the opposite orientation next to genes encoding two putative serine/threonine protein kinases homologous to *S. griseus* AfsK (SCLAV_3467a and 3467b), as well as a gene encoding a hypothetical regulatory protein with a DUF397 domain (SCLAV_3468). Proteins containing the DUF397 domain have been previously implicated in regulating antibiotic production in *S. coelicolor* (Fernandez-Moreno et al. 1992; Pope et al. 1998).

A total of eight XRE-family transcriptional regulators, which control various and diverse metabolic functions, were also found to be differentially expressed in *ΔbldG* as compared to the WT strain (Table 3.3.2.2.1). Four of these (497683074, 497682597, 490058590 and 490058041) were under-expressed in both *ΔbldG* and *ΔbldA* strains as compared to WT, one of which (490058590) was found to over-expressed in *ΔbldA* as compared to *ΔbldG*. Two XRE-family transcriptional regulators (490059014 and 490060239) were found to be over-expressed in *ΔbldG* as compared to the WT strain and under-expressed in *ΔbldA* when compared to *ΔbldG*. Furthermore, two proteins (497682165 and 497682584) were found to be over-expressed in *ΔbldG* and under-expressed in *ΔbldA* when compared to the WT strain. Four additional XRE family transcriptional regulators (490061322, 490052695, 490053558 and 490060107) were found to be under-expressed in *ΔbldA* compared to the WT and *ΔbldG*, respectively. The last XRE-family regulator detected in the dataset (490054092/BldD), which is a pleiotropic regulator controlling both differentiation and antibiotic production in *S. coelicolor*, was not differentially expressed in either the *ΔbldG* or the *ΔbldA* when compared to the WT strain, but was significantly under-expressed in *ΔbldA* as compared to *ΔbldG*.

3.3.2.3: Putative regulatory elements

Six proteins (490051454, 490054446, 490059100, 490051359, 490051928 and 490058168) with possible regulatory functions (based on the presence of HTH and other DNA-binding domains) were found to be differentially expressed among the three strains (Table 3.3.2.3.1). Three of these (490051454, 490054446 and 490059100) were found to

Table 3.3.2.3.1: Hypothetical proteins with possible regulatory functions found to be significantly under or over-expressed in the *ΔbldG* strain of *S. clavuligerus* compared to the WT strain.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G-WT[e]	logFC A-WT[f]	adj.P.val A-WT[g]	logFC A-G[h]	adj.P.Val A-G[i]
490051454	conserved hypothetical protein	1.23E+01	-5.21E+00	6.60E-05	-3.32E-01	5.94E-01	4.87E+00	1.13E-04
490054446	conserved hypothetical protein	1.22E+01	-3.59E+00	2.48E-05	-7.67E-01	5.42E-02	2.82E+00	1.04E-04
490051359	conserved hypothetical protein	1.25E+01	-2.79E+00	3.55E-05	-2.96E+00	4.05E-05	-1.71E-01	5.57E-01
490059100	hypothetical protein	1.58E+01	-1.32E+00	2.88E-05	-5.20E-01	4.99E-03	7.99E-01	4.90E-04
490051928	hypothetical protein	1.44E+01	-1.23E+00	9.76E-05	-1.64E+00	3.55E-05	-4.08E-01	2.72E-02
490058168	hypothetical protein	1.02E+01	2.43E+00	7.44E-05	-9.51E-01	1.18E-02	-3.38E+00	1.81E-05

[a] Identification is based on annotation by NCBI. [b] Description is based on NCBI annotation of protein similarity by BLAST. [c] Average normalized expression in the WT strain. [d] Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. [e]Adjusted P-value in *ΔbldG* as compared to the WT strain. [f] Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. [g] Adjusted P-value in *ΔbldA* as compared to the WT strain. [h] Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and [i] Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

be under-expressed in *ΔbldG* as compared to the WT strain, the last of these was also over-expressed in *ΔbldA* compared to *ΔbldG*. Two of the proteins (490051359 and 490051928) were under-expressed in both *ΔbldG* and *ΔbldA* as compared to the WT strain. A single protein (490058168) was over-expressed in *ΔbldG* as compared to the WT strain and was under-expressed in *ΔbldA* when compared to *ΔbldG*.

Additionally, putative regulators such as 490051454 and 490054446 and other regulators containing a HTH_XRE domain (497683074, 497682597, 490058590, 497681584, 490058041, 490055478, 490050197 and 490054541) are encoded by genes commonly found coupled to or upstream of genes encoding predicted proteins containing a DUF397 domain (Table 3.3.2.3.2). For example, the gene encoding the protein designated as 490051454 (SCLAV_2291) is coupled to SCLAV_2292 followed by SCLAV_2293 (Figure 3.3.2.3.1), with the latter two encoding hypothetical proteins containing DUF397 domains. The gene encoding 490054446 (SCLAV_2153) is similarly arranged, being coupled to and in the vicinity of genes encoding hypothetical proteins predicted to contain DUF397 domains (SCLAV_2136 and 2137, respectively). Only a single DUF397 domain containing protein was found in the dataset (497683523). The protein is 74% similar to the BldB protein, which has a known function in differentiation and secondary metabolite biosynthesis (Pope et al. 1998). This BldB-like protein was only slightly under-expressed in *ΔbldG* as compared to the WT strain and not differentially expressed in *ΔbldA* compared to WT (Table A.1.2).

Table 3.3.2.3.2: XRE-HTH regulators and hypothetical proteins encoded by genes located near or coupled to genes encoding DUF397-containing proteins from the WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr -WT[c]	logFC G-WT[d]	adj.P.Val G-WT[e]	logFC A-WT[f]	adj.P.Val A-WT[g]	logFC A-G[h]	adj.P.Val A-G[i]
490051454	conserved hypothetical protein	1.23E+01	-5.21E+00	6.60E-05	-3.32E-01	5.94E-01	4.87E+00	1.13E-04
490054446	conserved hypothetical protein	1.22E+01	-3.59E+00	2.48E-05	-7.67E-01	5.42E-02	2.82E+00	1.04E-04
497683074	XRE family transcriptional regulator	1.34E+01	-3.13E+00	4.47E-03	-1.98E+00	4.41E-02	1.16E+00	1.90E-01
497682597	XRE family transcriptional regulator	1.22E+01	-2.70E+00	2.76E-05	-1.00E+00	6.34E-03	1.70E+00	3.87E-04
490058590	XRE family transcriptional regulator	1.26E+01	-2.65E+00	1.06E-03	-7.51E-01	1.83E-01	1.90E+00	7.20E-03
497681584	DNA-binding protein	1.42E+01	-1.99E+00	1.14E-05	-4.00E-01	3.74E-02	1.59E+00	4.05E-05
490058041	XRE family transcriptional regulator	1.05E+01	-1.32E+00	1.75E-04	-2.26E+00	1.96E-05	-9.43E-01	1.30E-03
490055478	DNA-binding protein	1.26E+01	-1.23E+00	5.29E-05	6.14E-01	2.77E-03	1.84E+00	9.37E-06
490050197	DNA-binding protein	9.67E+00	-1.17E+00	9.20E-04	-2.34E+00	4.11E-05	-1.17E+00	1.24E-03
490054541	DNA-binding protein	1.52E+01	-8.79E-01	3.19E-04	1.02E+00	2.20E-04	1.90E+00	8.76E-06

[a] Identification is based on annotation by NCBI. [b] Description is based on NCBI annotation of protein similarity by BLAST. [c] Average normalized expression in the WT strain. [d] Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. [e] Adjusted P-value in *ΔbldG* as compared to the WT strain. [f] Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. [g] Adjusted P-value in *ΔbldA* as compared to the WT strain. [h] Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and [i] Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

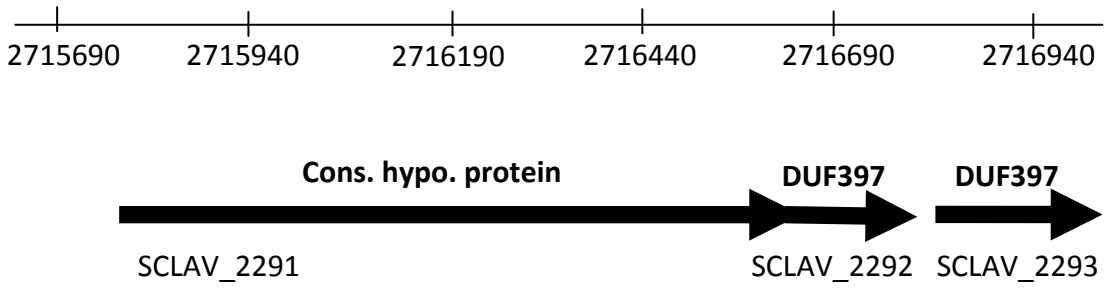

Figure 3.3.2.3.1: Arrangement of genes on *S. clavuligerus* chromosome showing the location of SCLAV_2291 and two genes encoding DUF397-domain proteins. The SCLAV_2291 protein shows similar domain architecture to XRE family transcriptional regulators and was under-expressed in *ΔbldG* compared to WT.

3.3.2.4: Two-component systems

Two-component systems (TCS), typically consisting of a sensor kinase and a response regulator, have also been found to regulate antibiotic production as well as cellular development (Aceti and Champness 1998; Martin 2004; Ryding et al. 2002; Sola-Landa et al. 2003). PhoP (490059014), a response regulator known to be involved in the phosphate mediated regulation of antibiotic biosynthesis, was found to be over-expressed in *ΔbldG* and unaffected in *ΔbldA* as compared to the WT strain, and under-expressed in *ΔbldA* when compared to *ΔbldG* (Tables 3.3.2.2.1 and 3.3.2.2.2). Several of the proteins known to be under the control of PhoP were also observed to be differentially expressed, including PstB (490058978), which was under-expressed in *ΔbldG* as compared to the WT strain and PhoU (490051157), which was under-expressed in *ΔbldA* when compared to the WT strain (Tables A.1.2 and A.1.3). A sensor kinase (49005442/DraK) was found to be similarly expressed among all three strains (Table A.1.7-A.1.9). This kinase belongs to the DraKR system, deletion of which results in reduced actinorhodin and increased levels of undecylprodigiosin production in *S. coelicolor* when grown in high nitrogen concentrations (Yu et al. 2012).

Several other response regulators were over-expressed in *ΔbldG*, including the regulator of a vancomycin resistance system (490054741/VanR) and 497682237, which is a putative orphan response regulator (without a associated kinase gene). The gene encoding 497682237 (SCLAV_2253) is located near the *gal* operon (SCLAV_2254-2256). Several other putative response regulator proteins belonging to the LuxR family (490056384, 490055173, 497685265, 490053914, 490057935, 490058723, 490058573,

and 490058107) were found to be under-expressed in both *ΔbldG* and *ΔbldA* compared to the WT strain (Tables 3.3.2.2.1 and 3.3.2.2.2). Genes for all of these proteins were located in the vicinity of genes encoding putative sensor kinases with the exception of 490056384, which is annotated in StrepDB as a protein involved in differentiation.

3.3.2.5: Serine/threonine kinases

Serine/threonine kinases are also of interest as regulatory elements. A number of proteins in *Streptomyces* spp. are phosphorylated on their serine/threonine and tyrosine residues during cellular development and some serine/threonine kinases are known to phosphorylate transcriptional factors involved in secondary metabolism (Lee et al. 2002). A total of nine serine/threonine kinases were detected in the dataset (Table 3.3.2.5.1). One kinase (497683065/AfsK) with a known role in the regulation of secondary metabolism was similarly expressed among the three strains. The AfsK/AfsR/AfsS system controls both differentiation and secondary metabolism and disruption of any of the encoding genes results in decreased antibiotic production (Horinouchi et al. 1983) (Floriano and Bibb 1996; Lee et al. 2007; Rajkarnikar et al. 2006). The kinase designated as 497683146 was over-expressed in *ΔbldG* and under-expressed in *ΔbldA* as compared to the WT strain and is homologous to *S. coelicolor* PkaD, which is thought to be a positive regulator of actinorhodin production in that species (Urabe et al. 2008). Three other kinases (490060020/AmfT/RamC, 497683145, and 497682612) were under-expressed in *ΔbldG* and *ΔbldA* as compared to the WT strain and are annotated in StrepDB as being involved in differentiation. The serine/threonine kinase 497683929, which was over-expressed in *ΔbldG* and unchanged in *ΔbldA* as compared to the WT

Table 3.3.2.5.1: Serine/threonine kinases detected in proteins extracted from the WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus.*

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G -WT[e]	logFC A -WT[f]	adj.P.Val A-WT[g]	logFC A -G[h]	adj.P.Val A -G[i]
490060020	serine/threonine protein kinase	1.19E+01	-3.48E+00	2.61E-06	-3.28E+00	5.46E-06	1.94E-01	3.34E-01
497683145	serine/threonine protein kinase	1.19E+01	-3.20E+00	8.16E-03	-3.04E+00	1.47E-02	1.62E-01	8.67E-01
497682612	serine/threonine protein kinase	1.44E+01	-1.13E+00	4.09E-05	-1.22E+00	4.25E-05	-9.05E-02	4.61E-01
490055158	serine/threonine protein kinase	1.31E+01	4.61E-02	7.03E-01	-7.01E-01	8.52E-04	-7.48E-01	5.30E-04
490058391	serine/threonine-protein kinase	1.12E+01	3.09E-01	1.74E-02	-6.52E-01	7.28E-04	-9.61E-01	8.19E-05
497683065	serine/threonine protein kinase	1.63E+01	3.75E-01	2.83E-02	-2.28E-03	9.88E-01	-3.77E-01	3.60E-02
490057932	serine/threonine protein kinase	9.92E+00	6.43E-01	1.97E-02	-7.07E-01	1.90E-02	-1.35E+00	7.71E-04
497683929	serine/threonine protein kinase	1.02E+01	1.34E+00	8.24E-04	-2.46E-01	3.52E-01	-1.59E+00	4.51E-04
497683146	serine/threonine protein kinase	1.25E+01	1.89E+00	1.59E-01	-1.93E+00	1.81E-01	-3.82E+00	2.06E-02

[a] Identification is based on annotation by NCBI. [b] Description is based on NCBI annotation of protein similarity by BLAST. [c] Average normalized expression in the WT strain. [d] Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. [e] Adjusted P-value in *ΔbldG* as compared to the WT strain. [f] Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. [g] Adjusted P-value in *ΔbldA* as compared to the WT strain. [h] Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and [i] Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

strain, is encoded by a gene (SCLAV_5481) that does not have any homologues in other *Streptomyces* spp. in the StrepDB. The gene encoding 497683929 is located in a predicted secondary metabolite gene cluster containing a putative non-ribosomal peptide synthetase (NRPS) (SCLAV_5463-5497) (Medema et al. 2010).

3.3.3: Identification and expression of proteins encoded by TTA codon containing genes

Also of interest to this study were those proteins encoded by TTA codon-containing genes as most of these genes, with the exception of *ccaR*, are thought to be *bldA*-dependent for their translation. It has been suggested that effective mistranslation of these genes can take place when the TTA codon is followed by a G or an A, whereas codons followed by C or T are predicted to be *bldA* dependent (Trepanier et al. 2002). The protein expression data for the *ΔbldA* mutant and WT strains generated in this study (Table A.1.3 and A.1.4) allowed the testing of this hypothesis in *S. clavuligerus*.

Analysis of the *S. clavuligerus* chromosome and plasmids (pSCL1, pSCL2, pSCL3 and pSCL4) nucleotide sequences revealed a total of 243 TTA codon-containing genes. Twenty-four proteins present in the dataset are encoded by genes containing TTA codons, including 8 transcriptional regulators/DNA binding proteins, 3 cytochrome P-450s and 6 hypothetical proteins (Table 3.3.3.1). Genes for 8 of the 23 proteins are located on the 1.8-Mb mega-plasmid pSCL4 and the rest are located on the *S. clavuligerus* chromosome. There were two proteins (497684176 and 497684177) for which there were no StrepDB gene entries at the time of writing. The protein identified as CcaR (497683347) is missing the first 73 amino acids including the leucine encoded

Table 3.3.3.1: Proteins encoded by TTA codon containing genes detected in proteins extracted from WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus*

Protein ID/StrepDB gene ID/length of gene[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G-WT[e]	logFC A-WT[f]	adj.P.Val A-WT[g]	logFC A-G[h]	adj.P.Val A-G[i]	TTA codon context[j]
497682856 SCLAV_3157 292 codons	hypothetical protein	1.35E+01	-4.12E+00	1.99E-06	-5.46E+00	1.64E-06	-1.35E+00	4.45E-04	GAC**TTA**CGC 27 - 28 - 29
497685093 SCLAV_p0750 691 codons	1,4-dihydropyridine enantioselective esterase	1.04E+01	-2.43E+00	6.60E-04	-4.31E+00	5.24E-05	-1.89E+00	3.13E-03	ATG**TTA**CAG 120-121-122
497684176 N/A	dihydrouridine synthase	1.42E+01	-1.66E+00	1.58E-05	-4.12E+00	1.11E-06	-2.46E+00	3.82E-06	N/A
490052143 SCLAV_5015 391 codons	cytochrome P450	1.13E+01	-2.39E+00	3.93E-06	-4.08E+00	1.24E-06	-1.69E+00	2.13E-05	CGA**TTA**CCC 359-360-361
490060866 SCLAV_p0471 398 codons	UDP-glucose 6-dehydrogenase	1.38E+01	-2.33E+00	1.38E-01	-4.07E+00	3.11E-02	-1.74E+00	2.83E-01	TTG**TTA**CGC 388-389-390
490050309 SCLAV_p1442 233 codons	hypothetical protein	1.04E+01	-2.91E+00	1.57E-05	-3.64E+00	9.05E-06	-7.38E-01	1.80E-02	GGC**TTA**CGG 55 - 56 - 57
497685222 SCLAV_p1005 3437 codons	DNA-binding protein	1.24E+01	-2.80E+00	1.67E-06	-3.28E+00	1.68E-06	-4.73E-01	7.42E-03	GAG**TTA**TCC 251-252-253
497681088 SCLAV_0315 462 codons	UDP-N-acetylglucosamine 2-epimerase	1.30E+01	-1.97E+00	2.00E-05	-3.07E+00	5.34E-06	-1.10E+00	4.95E-04	TCC**TTA**AGC 11 - 12 - 13
490051696 SCLAV_1663 529 codons	ABC transporter permease	1.14E+01	-2.33E+00	6.15E-06	-2.90E+00	5.07E-06	-5.72E-01	8.66E-03	CAG**TTA**CTG 75 - 76 - 77
490057169 SCLAV_0317 627 codons	hypothetical protein	1.02E+01	-2.27E+00	9.65E-05	-2.75E+00	5.41E-05	-4.83E-01	1.16E-01	CTG**TTA**GGC 23 - 24 - 25
490059108 SCLAV_3389 440 codons	cytochrome P450	1.34E+01	-3.79E+00	1.15E-06	-2.71E+00	2.89E-06	1.08E+00	1.02E-04	GTC**TTA**CCC 16 - 17 - 18
497685265 SCLAV_p1082 282 codons	LuxR family transcriptional regulator	1.04E+01	-1.61E+00	2.70E-05	-2.69E+00	5.34E-06	-1.08E+00	2.72E-04	GCG**TTA**GTG 205-206-207

490060901 SCLAV_p0539 2332 codons	hypothetical protein	1.20E+01	-2.56E+00	1.99E-06	-2.65E+00	3.17E-06	-8.39E-02	5.40E-01	GAG**TTA**TCC 78 - 79 - 80
490061051 SCLAV_p0799 453 codons	protein kinase	1.24E+01	-4.02E+00	3.11E-04	-2.59E+00	4.41E-03	1.43E+00	4.86E-02	GGG**TTA**CGC 161-162-163
497683347* SLAV_4204 262 codons	putative regulatory protein (AfsR-like protein)	1.52E+01	-2.64E+00	8.11E-06	-2.57E+00	1.95E-05	7.25E-02	7.22E-01	TCA**TTA**GCG 37 - 38 - 39
490055879 SCLAV_1957/*adpA* 400 codons	AraC family transcriptional regulator	1.36E+01	-1.26E+00	8.85E-05	-2.52E+00	5.93E-06	-1.26E+00	1.09E-04	TCT**TTA**CCA 222-223-224
490057035 SCLAV_0166 436 codons	alpha/beta hydrolase	1.40E+01	-2.67E+00	4.16E-06	-2.43E+00	1.04E-05	2.35E-01	1.96E-01	CGG**TTA**CGG 282-283-284
490058041 SCLAV_1516 295 codons	XRE family transcriptional regulator	1.05E+01	-1.32E+00	1.75E-04	-2.26E+00	1.96E-05	-9.43E-01	1.30E-03	GAG**TTA**AGG 20 - 21 - 22
497684177 N/A	hypothetical protein	1.38E+01	-1.75E+00	2.85E-05	-1.74E+00	4.43E-05	6.74E-03	9.69E-01	N/A
497682597 SCLAV_2845 295 codons	XRE family transcriptional regulator	1.22E+01	-2.70E+00	2.76E-05	-1.00E+00	6.34E-03	1.70E+00	3.87E-04	CCT**TTA**CGT 129-130-131
497681584 SCLAV_1107 288 codons	DNA-binding protein	1.42E+01	-1.99E+00	1.14E-05	-4.00E-01	3.74E-02	1.59E+00	4.05E-05	CAG**TTA**CGA 281-282-283
497685280 SCLAV_p1103 1317 codons	hypothetical protein	1.83E+01	5.08E-01	7.00E-02	2.07E-01	4.52E-01	-3.01E-01	2.79E-01	CGT**TTA**TGG 925-926-927
490058513 SCLAV_2310 323 codons	transcriptional regulator	1.60E+01	8.65E-01	7.60E-02	9.37E-01	7.64E-02	7.18E-02	8.79E-01	CCG**TTA**CGC 4 - 5 - 6
490060397 SCLAV_5461 407 codons	cytochrome P450	1.73E+01	4.76E-01	1.44E-01	1.76E+00	1.06E-03	1.28E+00	4.64E-03	CGG**TTA**CGG 268-269-270

*** Protein identification is a partial CcaR missing the first 73 amino acids. The TTA codon is located at position 38 in *S. clavuligerus ccaR*.**

[a] Identification is based on annotation by NCBI and StrepDB. [b] Description is based on NCBI annotation of protein similarity by BLAST. [c] Average normalized expression in the WT strain. [d] Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. [e] Adjusted P-value in *ΔbldG* as compared to the WT strain. [f] Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. [g] Adjusted P-value in *ΔbldA* as compared to the WT strain. [h] Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain. [i] Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain and [j] Location and frame of TTA codon in encoding gene based on StrepDB.

by the TTA codon, however it is included in this analysis. Twenty proteins were under-expressed in both the *ΔbldA* and *ΔbldG* mutant strains compared to WT and surprisingly no proteins were under-expressed solely in *ΔbldA* compared to WT. A putative cytochrome P450 (490060397) was over-expressed in *ΔbldA* compared to WT. A total of 13 of the identified TTA codon containing genes in the data set have homologues in other *Streptomyces* species with identities ranging from 31%-98% similarity. Of these 13, only 5 genes were found to retain the TTA codon in homologous genes in the other species (Table 3.3.3.2).

Table 3.3.1.2: *S. clavuligerus* TTA-containing genes encoding proteins detected in the WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus* and homologues in other *Streptomyces* that retain the TTA codon.

***S. clavuligerus* gene and TTA frame**[a]	**Homologues and TTA frame**[b]	**% conserved/ E-value**[c]
SCLAV_1107 CAG**TTA**CGA 281-282-283	SGR_2944 CAG**TTA**CGA 270-271-273	75% 1e-144
SCLAV_2310 CCG**TTA**CGC 4 - 5 - 6	SAV_2269 CTC**TTA**CGG 178-179-180	39% 6e-37
SCLAV_5015 CGA**TTA**CCC 359-360-361	SGR_1279 CTG**TTA**CTG 225-226-227	54% 5e-144
	SCO3770 CGT**TTA**ATT 6 - 7 - 8	51% 5e-117
SCLAV_p1005 GAG**TTA**TCC 251-252-253	SGR_6776 GGG**TTA**CCC 241-242-243	34% 0.0
SCLAV_1957/*adpA* TCT**TTA**CCA 222-223-224	SVEN_2580 TCT**TTA**CCG 222-223-224	98% 0.0
	SCAB57831 TCT**TTA**CCC 224-225-226	86% 0.0
	STRS4_01466 TCT**TTA**CCG 224-225-226	83% 0.0
	SAV_5261 TCT**TTA**CCC 224-225-226	84% 0.0
	SGR_4742 TCT**TTA**CCG 223-224-225	88% 0.0
	SLI_3139 TCT**TTA**CCG 224-225-226	83% 0.0
	SCO2792 TCT**TTA**CCG 224-225-226	86% 0.0

[a] Identification is based on StrepDB gene entries and nucleotide sequences. [b] Identification based on StrepDB homologues and nucleotide sequences. [c] Based on StrepDB BLAST function's determination of identities and E-value.

Chapter 4: Discussion

In this study, protein expression data was collected using iTRAQ® labeled peptides from the *ΔbldG*, *ΔbldA* and WT strains of *S. clavuligerus* grown under CA production conditions. A total of 2,442 proteins were detected that met the strict criteria for identification (Tables A.1.1 - A.1.9). The primary goal of this research was to elucidate previously unknown aspects of the regulation of CA biosynthesis in *S. clavuligerus* and because of this, special attention was given to regulatory proteins such as sigma factors, transcriptional regulators, TCSs and serine/threonine kinases. Those potential regulatory elements found to be over or under-expressed in *ΔbldG* compared to the WT strain and *ΔbldG* compared to *ΔbldA* could potentially be under the direct or indirect control of the pleiotropic regulator BldG and are considered in the following sections.

4.1: The positive activator of CA biosynthesis is under-expressed in the *ΔbldA* and *ΔbldG* mutants

Proteins involved in the direct regulation of CA biosynthesis (including BldG and CcaR) as well as several of the enzymes involved in its production, were found to be under-expressed in both *ΔbldG* and *ΔbldA* when compared to the WT strain (Figure 4.1.1) (Bachmann et al. 1998; Bignell et al. 2005; Paradkar and Jensen 1995; Perez-Llarena et al. 1997; Santamarta et al. 2011). While CcaR is required for the activation of CA biosynthesis (Alexander and Jensen 1998), *ΔbldA* was clearly able to produce CA (Figure 3.1.2.2), though at a reduced level as compared to the WT strain (Figure 3.1.2.2 B). Other work has found that CcaR transcripts may be slightly reduced and CA

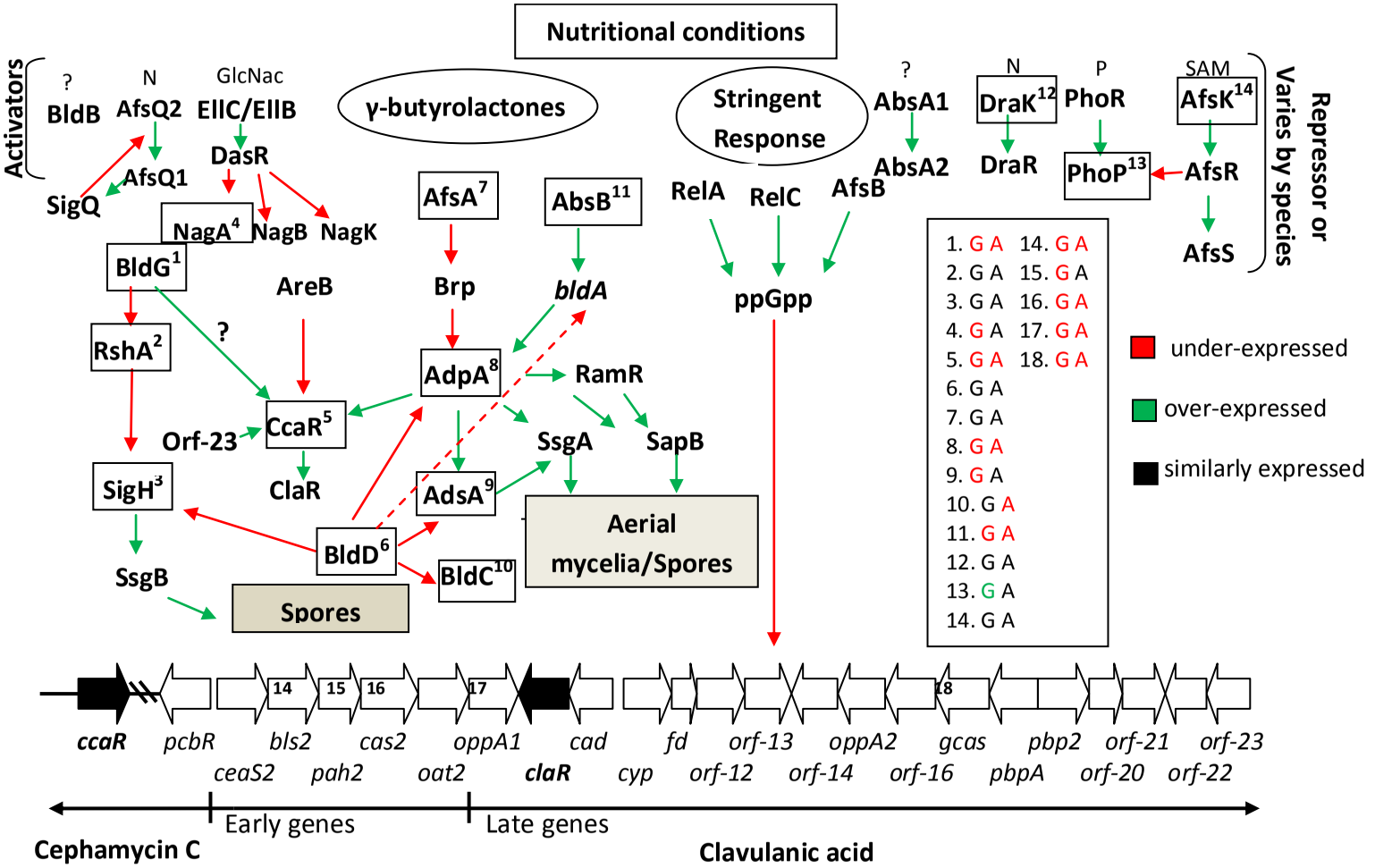

Figure 4.1.1: Regulatory cascade leading to CA production in *S. clavuligerus* based on published and current work. Proteins detected in this study are indicated by boxes with numbers. G or A in the key indicate expression levels between *ΔbldG* or *ΔbldA* and WT with red indicating proteins under-expressed and green indicating proteins over-expressed in the comparison.

production was delayed in *S. clavuligerus ΔbldA*, which in other *Streptomyces* species could be attributed to the effect of cell density on secondary metabolite production; this is unlikely to be the case in *S. clavuligerus* as secondary metabolism occurs during exponential growth phase (Sanchez and Brana 1996; Trepanier et al. 2002). While qualitative analysis seemed to show that the *ΔbldA* cultures were slightly less dense than the *ΔbldG* or WT cultures, this did not cause a delay in CA production in that strain (Figure 3.1.2.2).

As CcaR was very slightly but not significantly under-expressed in *ΔbldG* as compared to *ΔbldA* (Table A.1.9), another possibility is that very low copy numbers of CcaR are required for CA biosynthesis and that the threshold for detecting this is too low for traditional transcriptional analyses. Again, this seems unlikely as other work has found *ccaR* transcripts to be highly abundant in both WT and *ΔbldA S. clavuligerus* after 48 hours growth in liquid medium, though these studies were conducted using TSBS medium (Trepanier et al. 2002). Other research has found that growth media has been shown to effect secondary metabolism. For example, a pattern of failure for many mutants of early genes in the CA pathway (*bls2*, *pah2*, *cas2*) to produce CA in SA medium has been reported and that partial restoration of the ability occurs in soy-based media (Jensen et al. 2000). This is because the paralogues for these genes in the paralogue gene cluster are regulated differently from the CA cluster genes and can be expressed in soy medium but not in SA (Tahlan et al. 2004a). Without further validation of CcaR expression levels, the best possible explanation for its under-expression in *ΔbldA* is that *ΔbldA* had already stopped actively producing CA by the time the proteins were

extracted. Further experiments, including Western analysis of CcaR protein levels in all three strains grown in SA, TSBS, and soy-based media, are currently underway, as there have been no such experiments conducted previously on SA-grown *S. clavuligerus*.

4.2: Additional sigma factor targets of BldG remain elusive

In *Streptomyces*, both differentiation and secondary metabolism are regulated by various sigma factors (Bibb et al. 2000; Kelemen et al. 1996; Sevcikova et al. 2001; Sevcikova et al. 2010; Viollier et al. 2003), and therefore it is only natural to look to these regulatory elements as a means of further elucidating these pathways and eventually improving industrial production of desirable secondary metabolites. Additionally, the sigma factor that is regulated by BldG to control *ccaR* transcription and thereby CA and cephamycin C biosynthesis is still unknown (Bignell et al. 2005).

Thus far BldG has been found to regulate several anti-sigma factor partners, including the anti-sigma factor encoded by *orf3/apgA* as well as the anti-sigma factor regulating SigH (RshA), which has a dual role in differentiation and the osmotic stress response and the anti-sigma factor regulating SigF (RsfA), which is involved in sporulation (Figure 4.1.1) (Parashar et al. 2009; Sevcikova et al. 2010; Mingyar et al. 2014). In the SigH system in *S. coelicolor*, the osmotic induction of the SigH-dependent promoter *sigHp2* is abolished in *ΔbldG* mutants (Sevcikova et al. 2010). The protein expression data obtained in the current research shows that BldG is under-expressed in both *S. clavuligerus ΔbldG* and *ΔbldA* strains compared to the WT strain; however, the anti-sigma factors encoded by *orf3/apgA* and *rshA* and the sigma factor SigH are not differentially expressed among the three strains (Table 3.3.2.1.1 and Figure 4.1.1).

More attention has been placed on identifying σ^B and σ^F homologues for BldG to interact with as the sigma factors in the RsbV/RsbW and SpoIIAA/SpoIIAB systems are homologues to these sigma factors, respectively (Benson and Haldenwang 1993; Duncan and Losick 1993). The only σ^B homologue to be detected in the protein samples was HrdD, which was not differentially expressed in *ΔbldG* and was under-expressed in *ΔbldA* as compared to the WT strain (Table 3.3.2.2.1). Mutants for *hrdD* have no distinct phenotype in *S. coelicolor* with neither differentiation nor secondary metabolism being affected (Buttner et al. 1990) making it unlikely that this is a target of *S. clavuligerus* BldG.

A sigma factor designated 490058906 is homologous to *S. coelicolor* SigF, which is required for proper sporulation in other *Streptomyces* (Table 3.3.2.1.1) (Tzanis et al. 2014). SigF was recently found to be regulated by BldG in *S. coelicolor* as BldG interacts with the SigF anti-sigma factor RsfA, which was not detected in this study (Mingyar et al. 2014). The reversible phosphorylation of BldG is necessary for proper development of *S. coelicolor* and RsfA has been shown to play this role during early developmental stages (Bignell et al. 2003; Mingyar et al. 2014), whereas neither Orf3/ApgA or RshA contain the necessary HATPase_c kinase domain. (Parashar et al. 2009; Sevcikova et al. 2010). Only one promoter (*whiEp2*),which directs the expression of a gene for spore pigment biosynthesis (*whiE-ORFVIII*), has been found to be dependent on SigF, but no direct role of SigF in the recognition of this promoter has been identified (Kelemen et al. 1998). It is likely that BldG has an additional sigma factor partner to interact with, as both *sigH* and *sigF* mutants exhibit a Whi phenotype in which

aerial hyphae septation or maturation is affected, in contrast to the *bld* phenotype of *ΔbldG*, which lack aerial hyphae altogether (Bignell et al. 2000; Sevcikova et al. 2001). It is also likely that BldG has an additional anti-sigma factor partner to interact with as *in vivo* phosphorylation of BldG was not affected in a *rsfA* mutant (Mingyar et al. 2014).

Additionally, the protein expression data collected in this research may point to a possible role of BldG in the regulation of AdsA, the most under-expressed sigma factor found in the *ΔbldG*-WT comparison. Both AdsA and the transcriptional regulator AdpA are required for the transcription of *ssgA*, which is necessary for spore formation at a step after aerial mycelia have formed (Yamazaki et al. 2000, 2003). AdpA also has a role in the positive regulation of CcaR and therefore indirectly of CA biosynthesis (Lopez-Garcia et al. 2010). AdsA, which is part of an operon controlled by AdpA (Yamazaki et al. 2000), was not differentially expressed between *ΔbldA* and the WT strain, but it was under-expressed in *ΔbldG* compared to WT (Table 3.3.2.1.1). AdpA is *ΔbldA* dependent (Takano et al. 2003) and this protein was under-expressed in *ΔbldA* as well as *ΔbldG* compared to the WT strain (Figure 4.1.1). As AdpA was under-expressed in *ΔbldA* it would be expected for AdsA to be under-expressed as well. Rather, AdsA is relatively unaffected in the *ΔbldA* mutant but severely reduced in the *ΔbldG* background, perhaps indicating that BldG is somehow indirectly involved in the regulation of AdsA. This is consistent with previous work that found *adsA* transcripts are not detectable in *bldG* mutants in *S. coelicolor* (Bibb et al. 2000).

4.3: BldG may indirectly regulate a PKS and an NRPS

Polyketides and non-ribosomal peptides are two large classes of natural products that are synthesized by PKSs, NRPSs or hybrids of both, many of which have clinically important biological activities. The *Streptomyces* are capable of producing a large number of these metabolites and *S. clavuligerus* is a known producer of multiple polyketide and non-ribosomal peptide antibiotics including cephamycin C, penicillin N and holomycin (Figure 1.1.2.1) (Li and Walsh 2010; Martin 1998; Paradkar et al. 1996b). The genome of *S. clavuligerus* contains over 20 known and putative secondary metabolite gene clusters containing PKSs, NRPSs or PKS-NRPS hybrids (Medema et al. 2010) and putative regulators of two of these clusters were identified in the protein samples.

A SARP-family regulatory protein AfsR is known to control secondary metabolite biosynthesis in *S. coelicolor* when it is activated by a serine/threonine kinase (Lee et al. 2007; Matsumoto et al. 1994; Umeyama et al. 2002). A putative AfsR-like SARP whose encoding gene is located within a putative secondary metabolite gene cluster was under-expressed in *ΔbldG* as compared to the WT strain (Table 3.3.2.2.1). Although no serine/threonine kinase was found in the cluster, a PKS lies downstream of the AfsR-like protein-encoding gene (SCLAV_0462). Homologues for both SCLAV_0462 and most of the linked PKS cluster genes exist in *Streptomyces scabies*. Two genes encoding putative AfsA-domain containing γ-butyrolactone biosynthesis proteins (SCLAV_0463 and SCLAV_0471), which are not conserved in *S. scabies* or present in any other sequenced *Streptomyces* species, are located near the AfsR-like SARP gene. γ-butyrolactones bind

to BRPs which are known to negatively regulate antibiotic biosynthesis in *Streptomyces* as is the case with the indirect negative regulatory effect on *ccaR* by Brp *via* the AdpA pathway (Kim et al. 2004; Lopez-Garcia et al. 2010; Paradkar 2013; Santamarta et al. 2005). Perhaps, as suggested by Medema, *et al*., one or both of these γ-butyrolactones work indirectly to regulate the PKS cluster (Medema et al. 2010). Of greater interest is the possibility that BldG indirectly regulates the AfsR-like SARP of this system similarly to how it regulates CcaR expression in the CA/cephamycin C supercluster.

Additionally, a serine/threonine kinase whose encoding gene is located in a putative secondary metabolite cluster containing an NRPS (Medema et al. 2010) was over-expressed in *ΔbldG* when compared to the WT strain (Table 3.3.2.5.1). Unfortunately neither of the NRPSs (SCLAV_5484 or SCLAV_5485), the SARP (SCLAV_5476) or a PKS (SCLAV_5492) were detected in the dataset. Without additional data it is not possible to ascribe a function to this kinase, though it is possible that it could activate the SARP, which in turn may regulate expression of the NRPS. Based on the differential expression data, perhaps BldG has an indirect role in positively regulating expression of the serine/threonine kinase making this the first example of BldG negatively regulating biosynthesis of a secondary metabolite. It is also possible that this particular NRPS cluster is silent in *S. clavuligerus* in general or under the particular growth conditions used in this study.

4.4: A possible system of XRE-family transcriptional regulators and DUF397-domain containing proteins

Several proteins that were under-expressed in *ΔbldG* when compared to the WT strain (Table 3.3.2.3.1), have putative regulatory functions based on the presence of HTH or other DNA binding domains. Two of these (490051454 and 490054446) are DNA-binding proteins containing HipB conserved domains (COG1396), HTH-XRE domains (cd00093) and HTH_31 domains (PF13560), indicating that these are related to XRE-family transcriptional regulators, which show a similar domain architecture. Both of the proteins are encoded by genes found to be coupled to or located slightly upstream of genes encoding DUF397 domain proteins, which have been implicated in the regulation of secondary metabolism (Pope et al. 1998). These DUF397 domain containing hypothetical protein encoding genes were found coupled to or downstream of the genes encoding all but one of the HTH_XRE domain containing protein genes found to be under-expressed in *ΔbldG* when compared to the WT strain (Table 3.3.2.3.2). *S. clavuligerus* has 45 genes encoding putative DUF397-containing proteins though unfortunately only one (497683523) was present in the dataset (Table A.1.4). This protein was under-expressed in *ΔbldG* when compared to the WT strain (Table A.1.2) and is 74% similar to BldB, which has a known function in regulating differentiation and secondary metabolism (Pope et al. 1998). Other work has found that BldB and BldB-like proteins likely require a partner to interact with (Eccleston et al. 2002; Eccleston et al. 2006).

Studies in *S. coelicolor* of an XRE-family regulator (WhiJ) and a small acidic protein of unknown function with a DUF397 domain (SCO4542) may provide clues as to how BldB and potentially other DUF397 proteins regulate expression of other products. Deletion of *SCO4542*, immediately downstream of *whiJ*, resulted in a bald phenotype but this phenotype was completely reversed by the deletion of *whiJ* (Ainsa et al. 2010). This suggests that WhiJ represses differentiation and that the *SCO4542* product counteracts this effect. It is possible that the function of these DUF397 proteins is to interact antagonistically with XRE-family proteins (McCormick and Flardh 2012). Given that genes encoding so many of the HTH_XRE domain proteins under-expressed in *ΔbldG* were coupled to or located near genes encoding DUF397 proteins (Table 3.3.2.3.2), it is possible that these systems have some role in the regulation of secondary metabolism and may themselves be under indirect regulation by BldG.

4.5: Evidence for an overlapping BldG and BldD regulon

The most under-expressed regulator in *ΔbldG* compared to WT is BdtA, a DNA-binding protein originally thought to have a role in differentiation in *S. coelicolor* as transcript levels for this protein increase between 36 and 48 hours when aerial mycelia are abundant and sporulation begins (Elliot et al. 2001). Further analysis found that a *bdtA* mutant has no distinctive phenotype (den Hengst et al. 2010; Hunt et al. 2005). BldC is the only BdtA homologue in *S. coelicolor* and it is required for both differentiation and secondary metabolite biosynthesis (Hunt et al. 2005). The *bdtA* gene is negatively regulated by the pleiotropic regulator BldD, which is known to repress the pre-mature expression of multiple genes involved in differentiation, including the genes

encoding the sigma factors WhiG and AdsA, as well genes involved in secondary metabolite biosynthesis, such as *bldC* (Figure 4.1.1) (den Hengst et al. 2010). In. *S. coelicolor*, *bdtA* transcripts are three-fold over-expressed between 15 and 36 hours in a *bldD* mutant compared to the WT strain but fall significantly between 36 and 48 hours when *bdtA* transcripts are highest in the WT strain (Elliot et al. 2001). Both BldD and BldC were detected in the dataset, with BldD not being differentially expressed between the WT strain and either of the two mutants and BldC being under-expressed in *ΔbldA* when compared to the WT strain (Figure 4.1.1).

At this point, it is not possible to know whether *S. clavuligerus* BdtA is critical for either differentiation or secondary metabolite biosynthesis in *S. clavuligerus* without further mutational studies of this locus. However based on the expression data, a possible indirect role of BldG in the regulation of *bdtA* can be proposed in which BldG has some role in switching on the transcription of *bdtA* at an appropriate time in development. BldG and BldD are already known to indirectly or directly regulate the same product in at least one case, namely SigH. BldG interacts with the SigH anti-sigma factor RshA and transcription from the SigH dependent promoter *sigHp2* is abolished in *ΔbldG* (Parashar et al. 2009; Sevcikova et al. 2010). BldD negatively regulates SigH through the same promoter, which is significantly up-regulated in a *bldD* mutant (Kelemen et al. 2001). BldD and BldG may work to repress and activate certain genes involved in differentiation and/or secondary metabolism, respectively. This could perhaps explain why the *bldD* and *bldC* mutants are able to complement *bldG* mutants in *S. coelicolor* (Molle and Buttner 2000; Nodwell et al. 1999; Willey et al. 1993).

4.6: BldG may indirectly regulate diverse two-component systems

A large number of two-component systems exist in the genomes of *Streptomyces* species. Although the stress signals and other environmental inputs that these systems recognize are unknown, several of them have an effect on differentiation and antibiotic production (Hutchings et al. 2004; Martin et al. 2012). The genome of *S. clavuligerus* contains 51 paired TCSs, 21 orphan response regulators, and 8 orphan sensor kinases (Medema et al. 2010).

4.6.1: BldG may have effects on phosphate regulation of secondary metabolism

PhoP, a TCS response regulator, was found to be over-expressed in *ΔbldG* when compared to the WT strain (Table 3.3.2.2.1 and Figure 4.1.1). The PhoR-PhoP TCS is involved in the phosphate mediated regulation of secondary metabolism. Deletions of the system result in different phenotypes depending on the *Streptomyces* suggesting that phosphate control of secondary metabolism is stricter in some species (Ghorbel et al. 2006; Sola-Landa et al. 2003). For example, PhoP deletion mutants over-produce pigmented secondary metabolites in *S. lividans* (Sola-Landa et al. 2003), but no such increase is seen in *S. coelicolor* mutants (Santos-Beneit et al. 2009). Additionally, proteins involved in phosphate transport that are positively regulated by PhoP under conditions of phosphate limitation were also found to be differentially expressed, including the pathway specific activator PhoU (under-expressed in *ΔbldA* when compared to WT) and PstB (under-expressed in *ΔbldG* when compared to WT) (Tables A.1.4 and A.1.1)(Ghorbel et al. 2006; Salehghamari et al. 2012). PhoU is a modulator of the phosphate response genes and its expression has previously been found to be induced

when PhoP is phosphorylated (Sola-Landa et al. 2005) and PstB is a member of the phosphate transporter system and is also dependent on PhoP for expression (Rodriguez-Garcia et al. 2007). In a CA over-producing mutant, the genes encoding these proteins were found to be more highly transcribed, likely to overcome nitrogen and phosphate limitations (Medema et al. 2011), and in a *ΔccaR:tsr* mutant strain they were found to be slightly under-expressed (Alvarez-Alvarez et al. 2014).

The *pho* regulon was recently characterized in *S. clavuligerus* and although CA production is negatively regulated by phosphate (Lebrihi et al. 1987), no PHO binding boxes were observed near any of the CA cluster genes or in the promoter regions of *ccaR* or *claR* (Salehghamari et al. 2012). The lack of identifiable PHO boxes indicates that PhoP may not have a direct role in the regulation of CA biosynthesis. It is interesting that PhoP is over-expressed in *ΔbldG* compared to the WT strain, though it is difficult to explain why PhoU and PstB, which are both regulated directly or indirectly by PhoP, are not also over-expressed.

4.6.2: Additional TCS potentially affected by BldG

Several other TCS response regulators were over-expressed in *ΔbldG* (Table 3.3.2.2.1). One is homologous to *S. coelicolor* VanR, which is the regulator of the VanRS TCS that controls a gene cluster conferring inducible high-resistance to vancomycin (Hong et al. 2004; Hutchings et al. 2006a). Genes encoding both VanR and VanS are present in *S. clavuligerus* but the rest of the *van* cluster is absent. It is uncertain as to why this protein is over-expressed in the CA non-producing *ΔbldG* strain or what role VanRS may have in *S. clavuligerus*. A second response regulator over-expressed in

ΔbldG is encoded by a gene located only 11 base pairs downstream from the *gal* operon. There are homologues to this regulator in multiple *Streptomyces* species and it is one of the orphan response regulators that lacks a sensor kinase (Hutchings et al. 2004; Medema et al. 2010); however, in none of the other species is the regulator located so close to the *gal* operon (Adams et al. 1988). None of the proteins encoded by the *gal* operon were detected in the *S. clavuligerus* protein samples and nothing definitive can be said about the role of the regulator. However, as induction of the *gal* operon is normally repressed by glucose (Adams et al. 1988), which *S. clavuligerus* is incapable of utilizing (Perez-Redondo et al. 2010), it is possible that *S. clavuligerus* employs a novel mechanism of *gal* regulation that could involve this orphan response regulator.

4.7: TTA dependence is re-evaluated in *S. clavuligerus*

A total of 24 out of 243 proteins (~10%) encoded by TTA containing genes were present in the dataset, which is lower than the percent coverage of the dataset as a whole. This is likely in part due to the fact that TTA codons only occur in genes involved in secondary metabolism and morphological differentiation, and therefore were not expressed under the provided growth conditions (Leskiw et al. 1991). In *Streptomyces* species the *bldA* gene encodes the only t-RNA for translating the leucine codon TTA, which is the rarest codon in *Streptomyces* genes (Piret and Chater 1985; Wright and Bibb 1992). Mutations in *bldA*, first described in *S. coelicolor*, result in lack of aerial hyphae formation and secondary metabolite production in that species (Hopwood 1967; Merrick 1976). It was previously shown that certain TTA codon containing genes were dependent upon *bldA* for expression (Lawlor et al. 1987). This, coupled with the accumulation of

bldA t-RNA in stationary phase, led to the hypothesis that levels of charged *bldA* t-RNA might determine the levels of the products of the TTA-containing genes (Leskiw et al. 1993). Later, *adpA* (the pleiotropic regulatory gene responsible for the *ΔbldA* mutant developmental phenotype) and several other TTA-containing genes were identified that were required for the biosynthesis of the blue-pigmented secondary metabolite actinorhodin (Fernandez-Moreno et al. 1991; Takano et al. 2003).

bldA mutants have since been described in other diverse *Streptomyces* species and these mutants generally have been found to have similar phenotypes to *S. coelicolor* mutants (Kwak et al. 1996; Tao et al. 2007), although this is not always the case. While in *S. coelicolor* and other species such as *S. griseus* both normal development and secondary metabolite production are affected, only hyphae formation and sporulation is abolished in *S. clavuligerus* (Trepanier et al. 2002). This was surprising as *ccaR* contains a TTA codon (Trepanier et al. 2002). Trepanier, *et al*. suggested several possible explanations for effective mistranslation, including location of the TTA codon and the individual nucleotides flanking the TTA codon (Trepanier et al. 2002).

The relative position of some rare codons has been shown to have a more severe effect on translation when located in the first 25-50 codons and a less severe effect when located further away towards the 3′ end of the transcript (Chen and Inouye 1990). This is unlikely to be the case in *S. clavuligerus*, as the TTA codon in the *ccaR* transcriptional regulator is located at codon position 38 (Trepanier et al. 2002). The possibility that the identity of the nucleotides flanking the codon may allow it to be mistranslated was

suggested because flanking nucleotides have been linked to frame shifting in some other systems, including yeasts and viruses (Belcourt and Farabaugh 1990; Brierley et al. 1992; Trepanier et al. 2002). They found that while there was no apparent pattern for the nucleotide at the 5′ end for the assayed TTA containing genes, at the 3' end the TTA codons were followed by a C or a T with one exception - the *bldA* independent *ccaR*, which had a G following the TTA codon (Trepanier et al. 2002). At this time, *ccaR* was the only known *bldA*-independent TTA containing gene, therefore it was hypothesized that *bldA*-dependent genes would have a C or a T immediately 3′ of the TTA codon and *bldA*-independent genes would have a G or potentially an A 3′ of the codon.

The results of this work do not support the abovementioned hypothesis. CcaR, previously believed to be *bldA*-independent in *S. clavuligerus*, was found to be similarly under-expressed in the *ΔbldA* and *ΔbldG* mutants compared to the WT strain despite the presence of a G immediately 3′ of the TTA codon. As *ΔbldA* did produce genuine CA (Figure 3.1.2.2), the most likely explanation is that *ΔbldA* had already stopped producing CA at the time of protein extraction and *ccaR* was not being transcribed (discussed in section 4.1). Four additional proteins found to be more under-expressed in Δ*bldA* than in Δ*bldG* when compared to the WT strain are also encoded by genes with Gs or As immediately 3′ to a TTA codon, suggesting that the presence of a G or A 3′ of the codon does not necessarily allow for effective mistranslation.

A protein encoded by a gene (SCLAV_5461) with a C immediately 3′ of the TTA codon was over-expressed in *ΔbldA* compared to the WT strain (Table 3.3.3.1). The

over-expressed protein is a cytochrome P450 (490060397), which is predicted to be involved in limonene, pinene, napthalene, anthracene and gamma-Hexachlorocyclohexan degradation based on the KEGG pathway information available on StrepDB. At this time it is uncertain why this particular protein is over-expressed in the *ΔbldA* mutant. Two other products that are slightly but not significantly over-expressed in Δ*bldA* when compared to the WT strain are encoded by genes (SCLAV_2310 and SCLAV_p1103) that also contain Cs immediately 3′ of the TTA codon (Table 3.3.3.1), suggesting that genes with Cs following the TTA codon are not *bldA*-dependent.

4.8: Summary

A total of 2,442 proteins corresponding to 33.5% of the *S. clavuligerus* proteome were detected from cellular lysates extracted from WT, *ΔbldA* and *ΔbldG S. clavuligerus* strains at a time point consistent with CA production. There are only three previously published reports on the analysis of *Streptomyces* proteomes using iTRAQ® in the literature, and these were only able to detect up to 15% of the predicted proteome of *S. coelicolor* (Jayapal et al. 2008; Manteca et al. 2010; Navone et al. 2014). Therefore, iTRAQ® analysis conducted at the University of Victoria British Columbia Proteomics Centre was considered to have worked successfully, although some protein descriptions were mis-annotated. Additional sigma factor partners for BldG were not identified, as there is no way to detect sigma factors or cognate anti-sigma factors using this method unless the sigma factor regulates its own expression. However, several hundred transcriptional regulators and other potential regulator elements were detected, some of which are likely under direct or indirect control by BldG. These include an AfsR-like

SARP potentially involved in the regulation of a large PKS containing gene cluster, a potentially novel system involving XRE and XRE-like transcriptional regulators and DUF397 domain proteins, as well as a transcriptional regulator with an as of yet unknown function in *S. clavuligerus* that lends further support to an overlapping regulon between *bldD* and *bldG*. Further, the analysis of proteins encoded by TTA codon containing genes suggests that the role of *bldA* and TTA dependence in *S. clavuligerus* should be re-evaluated.

Though further research, including transcriptional and mutational analysis, will be necessary to elucidate the functions of some of the regulators of interest detected in this study, some of the encoding genes may prove to be exciting candidates for over-expression or other manipulation experiments. This could lead to developments in the industrial fermentation of the organism that in turn could lead to an increase in CA production and a reduction in cost, both valuable commercial and pharmaceutical possibilities. This study represents the only proteomic analysis of a CA producing and a non-producing strain of *S. clavuligerus* to date and has provided insight into the complex regulatory cascades controlling antibiotic biosynthesis in this species. It also represents the most complete proteomic analysis of *S. clavuligerus* to date, to the author's knowledge. This set of protein data will serve in the future as a useful tool to direct research into aspects of CA biosynthesis and secondary metabolism, as well as into aspects of development and primary metabolism.

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Appendix 1: Additional tables showing differential protein expression in WT, *ΔbldA*, and *ΔbldG* strains of *S. clavuligerus*

Table A.1.1: Proteins determined to be significantly (p=0.01) over-expressed in the *ΔbldG* compared to the WT strain of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G -WT[e]	logFC A -WT[f]	adj.P.Val A-WT[g]	logFC A -G[h]	adj.P.Val A -G[i]
490053486	hypothetical protein	8.52E+00	5.99E+00	1.17E-02	5.19E+00	3.01E-02	-7.99E-01	6.92E-01
490050479	ABC transporter	6.25E+00	5.68E+00	1.36E-03	-3.59E+00	1.70E-02	-9.28E+00	1.35E-04
490058488	trans-aconitate 2-methyltransferase	6.45E+00	5.05E+00	8.06E-04	-6.08E+00	4.59E-04	-1.11E+01	1.87E-05
490055325	DNA-binding protein	1.43E+01	4.66E+00	5.43E-06	1.08E+00	1.10E-02	-3.58E+00	2.27E-05
490052915	catalase	1.15E+01	4.54E+00	5.45E-05	-8.57E-01	1.23E-01	-5.40E+00	2.88E-05
490054418	amino acid transporter	1.53E+01	4.43E+00	2.11E-05	-3.60E-02	9.35E-01	-4.46E+00	2.51E-05
497683953	cytosine deaminase	1.09E+01	4.41E+00	6.74E-03	1.16E+00	3.81E-01	-3.25E+00	3.20E-02
497682270	molybdenum cofactor biosynthesis protein MoaC	3.62E+00	4.35E+00	3.75E-04	-2.65E+00	6.72E-03	-7.00E+00	4.05E-05
490055769	carbon-nitrogen hydrolase	1.15E+01	3.89E+00	2.79E-06	-6.96E-01	1.47E-02	-4.58E+00	2.23E-06
490056767	PTS glucose transporter subunit IIA	9.90E+00	3.86E+00	1.67E-06	1.96E+00	3.03E-05	-1.91E+00	2.71E-05
490052448	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	9.98E+00	3.75E+00	1.80E-04	2.28E+00	3.45E-03	-1.47E+00	2.24E-02
490050037	hypothetical protein	9.80E+00	3.73E+00	1.29E-06	5.67E-01	6.96E-03	-3.16E+00	2.23E-06
497681691	hypothetical protein	1.43E+01	3.71E+00	7.44E-05	-3.44E-01	4.49E-01	-4.06E+00	5.72E-05
497681074	hypothetical protein	1.10E+01	3.68E+00	1.87E-06	-2.98E-01	1.39E-01	-3.97E+00	2.03E-06
497683354	HAD-superfamily hydrolase	5.38E+00	3.57E+00	2.17E-03	-5.39E+00	3.89E-04	-8.95E+00	2.46E-05
490053866	sodium:proton antiporter	1.28E+01	3.55E+00	8.97E-05	1.11E-01	8.06E-01	-3.44E+00	1.29E-04
490054729	dihydrodipicolinate synthase	1.31E+01	3.48E+00	3.93E-06	-1.23E+00	9.06E-04	-4.71E+00	2.03E-06
490058356	PTS sugar transporter subunit IIA	1.30E+01	3.43E+00	2.19E-06	-3.62E-01	8.10E-02	-3.79E+00	2.23E-06
490057723	DNA polymerase III subunit epsilon	3.92E+00	3.41E+00	1.47E-03	-3.53E+00	1.85E-03	-6.93E+00	4.66E-05
497681532	stress protein	1.39E+01	3.37E+00	1.55E-05	1.47E+00	1.54E-03	-1.90E+00	3.51E-04
490053822	epimerase	1.08E+01	3.36E+00	1.57E-06	4.61E-01	1.63E-02	-2.90E+00	2.57E-06
490051538	magnesium transporter CorA	1.33E+01	3.34E+00	1.50E-05	-9.63E-01	1.07E-02	-4.30E+00	5.94E-06
490060637	2-methylisocitrate lyase	1.09E+01	3.27E+00	1.36E-02	-1.09E-01	9.27E-01	-3.38E+00	1.57E-02
490060232	phytoene synthase	1.19E+01	3.25E+00	2.39E-05	-1.93E+00	5.09E-04	-5.18E+00	4.05E-06
490055599	phosphohistidine phosphatase	9.98E+00	3.17E+00	2.02E-05	-9.05E-01	1.49E-02	-4.08E+00	7.86E-06

497681919	ACP S-malonyltransferase	1.02E+01	3.17E+00	7.78E-05	8.18E-01	6.06E-02	-2.36E+00	4.61E-04
497685319	DNA-binding protein	1.60E+01	3.16E+00	1.11E-04	-7.51E-01	9.48E-02	-3.91E+00	4.51E-05
497683598	transcriptional regulator	1.26E+01	3.14E+00	1.67E-06	-3.96E-01	2.79E-02	-3.53E+00	1.57E-06
490054953	hypothetical protein	9.23E+00	3.13E+00	6.47E-06	7.00E-01	1.52E-02	-2.43E+00	2.68E-05
490051173	lyase	1.32E+01	3.12E+00	2.68E-05	-1.36E+00	2.83E-03	-4.48E+00	6.37E-06
497683136	RNA polymerase subunit sigma-24	1.51E+01	3.12E+00	1.16E-05	-1.43E+00	8.69E-04	-4.56E+00	3.24E-06
490057021	siderophore biosynthesis protein	1.24E+01	3.02E+00	2.69E-05	2.02E-01	5.05E-01	-2.82E+00	4.63E-05
490057339	N-acetyltransferase GCN5	1.26E+01	2.97E+00	1.30E-05	-9.18E-01	6.85E-03	-3.88E+00	5.20E-06
490053329	quinolinate synthetase	1.19E+01	2.94E+00	5.49E-06	-2.08E-01	3.26E-01	-3.15E+00	5.57E-06
497685194	5,10-methylenetetrahydrofolate reductase	1.33E+01	2.93E+00	1.57E-06	-2.36E+00	5.07E-06	-5.29E+00	2.01E-07
497681303	ribulose-phosphate 3-epimerase	1.19E+01	2.91E+00	1.80E-05	-1.09E+00	3.84E-03	-4.01E+00	5.57E-06
497681777	short-chain dehydrogenase	7.07E+00	2.88E+00	2.90E-05	-7.99E+00	1.12E-06	-1.09E+01	2.18E-07
497682256	hypothetical protein	1.26E+01	2.83E+00	2.14E-04	8.45E-02	8.45E-01	-2.74E+00	3.24E-04
497683951	LysR family transcriptional regulator	1.13E+01	2.81E+00	1.45E-05	-2.30E+00	5.62E-05	-5.11E+00	2.03E-06
490060082	polyketide cyclase	1.07E+01	2.81E+00	1.29E-03	-8.61E-01	1.67E-01	-3.67E+00	4.20E-04
490057955	ribokinase	1.24E+01	2.80E+00	4.85E-05	7.90E-03	9.80E-01	-2.79E+00	6.07E-05
490061074	Telomere-associated protein	1.07E+01	2.79E+00	3.03E-06	-7.39E-01	2.84E-03	-3.53E+00	2.03E-06
490058700	orotate phosphoribosyltransferase	1.17E+01	2.75E+00	4.75E-05	-1.89E+00	4.72E-04	-4.64E+00	5.44E-06
497682120	alanine glycine permease	1.19E+01	2.71E+00	4.08E-04	5.59E-01	2.38E-01	-2.15E+00	1.76E-03
497683221	aminotransferase AlaT	1.16E+01	2.71E+00	8.57E-05	4.46E-01	2.04E-01	-2.26E+00	2.72E-04
490052136	hydrolase	1.23E+01	2.69E+00	4.55E-04	2.00E-01	6.69E-01	-2.49E+00	9.00E-04
490052497	PTS sugar transporter	1.11E+01	2.69E+00	1.60E-05	1.61E-01	5.03E-01	-2.53E+00	2.62E-05
497681699	mechanosensitive ion channel protein	1.21E+01	2.68E+00	1.27E-05	1.75E+00	1.54E-04	-9.35E-01	3.36E-03
490051552	hypothetical protein	1.07E+01	2.63E+00	1.80E-05	-9.77E-01	4.10E-03	-3.61E+00	5.57E-06
497681050	hypothetical protein	9.85E+00	2.63E+00	1.11E-05	-1.66E+00	1.58E-04	-4.28E+00	2.32E-06
490059990	O-methyltransferase	1.01E+01	2.60E+00	7.18E-04	-5.87E-01	2.46E-01	-3.19E+00	3.24E-04
490058695	hydrolase	8.43E+00	2.59E+00	6.47E-06	4.75E-02	8.06E-01	-2.55E+00	8.90E-06
497681264	phosphoenolpyruvate-protein phosphotransferase	1.15E+01	2.54E+00	1.87E-06	-4.26E-01	1.19E-02	-2.97E+00	1.68E-06
490051466	TetR family transcriptional regulator	1.14E+01	2.53E+00	1.23E-04	-1.65E-01	6.28E-01	-2.69E+00	1.09E-04
490058520	molybdopterin biosynthesis protein MoeA	1.25E+01	2.52E+00	1.77E-05	-1.59E+00	2.55E-04	-4.11E+00	2.96E-06
490056354	hydroxylase	1.25E+01	2.51E+00	2.05E-05	-1.54E+00	3.52E-04	-4.05E+00	3.42E-06
490052447	integration host factor	1.04E+01	2.51E+00	9.24E-04	1.41E+00	2.00E-02	-1.09E+00	4.95E-02

497682686	nosiheptide resistance regulatory protein	1.43E+01	2.49E+00	2.68E-05	-2.35E-01	3.48E-01	-2.73E+00	2.14E-05
490056986	Putative dehydrogenase	1.23E+01	2.49E+00	6.27E-06	-7.40E-01	4.07E-03	-3.23E+00	3.06E-06
490057424	hypothetical protein	1.06E+01	2.49E+00	3.76E-05	1.66E+00	4.44E-04	-8.28E-01	1.24E-02
490057887	hypothetical protein	1.07E+01	2.46E+00	9.26E-06	-1.07E+00	9.06E-04	-3.52E+00	2.96E-06
490058381	beta-N-acetylhexosaminidase	1.17E+01	2.45E+00	4.01E-05	-1.56E+00	6.10E-04	-4.01E+00	5.44E-06
490058168	hypothetical protein	1.02E+01	2.43E+00	7.44E-05	-9.51E-01	1.18E-02	-3.38E+00	1.81E-05
490060456	hypothetical protein	1.50E+01	2.42E+00	1.44E-03	1.00E+00	8.17E-02	-1.42E+00	2.27E-02
490058227	RarC protein	9.15E+00	2.42E+00	1.78E-05	-2.02E+00	6.25E-05	-4.44E+00	2.23E-06
497682030	membrane protein	9.29E+00	2.39E+00	3.09E-05	-1.73E+00	2.38E-04	-4.13E+00	3.79E-06
497681796	glutamine synthetase	1.21E+01	2.38E+00	1.62E-03	-1.57E-01	7.69E-01	-2.53E+00	1.53E-03
490060766	ornithine cyclodeaminase	1.15E+01	2.37E+00	1.88E-05	-1.81E+00	1.06E-04	-4.18E+00	2.57E-06
490058512	acetyltransferase	1.32E+01	2.36E+00	2.48E-05	3.63E-01	1.39E-01	-2.00E+00	7.12E-05
497681999	hypothetical protein	1.24E+01	2.36E+00	1.50E-03	6.09E-02	9.09E-01	-2.30E+00	2.25E-03
490052924	fructose 1,6-bisphosphatase	1.42E+01	2.35E+00	2.21E-05	7.52E-01	9.99E-03	-1.60E+00	1.96E-04
497681053	glutamate racemase	1.07E+01	2.35E+00	1.19E-03	-3.97E-01	4.20E-01	-2.75E+00	6.96E-04
497681259	hypothetical protein	1.01E+01	2.34E+00	6.94E-06	4.22E+00	1.68E-06	1.88E+00	2.43E-05
490054808	whiD	1.25E+01	2.33E+00	5.26E-05	-1.09E+00	3.88E-03	-3.42E+00	1.04E-05
490059255	alanine racemase	1.25E+01	2.27E+00	3.36E-05	-6.48E-01	2.31E-02	-2.91E+00	1.27E-05
497681781	hypothetical protein	1.23E+01	2.26E+00	3.02E-04	-7.92E-01	5.39E-02	-3.06E+00	8.05E-05
490050763	methyltransferase type 11	1.34E+01	2.23E+00	1.23E-05	-1.16E-01	5.39E-01	-2.34E+00	1.20E-05
490054626	ferritin	1.52E+01	2.21E+00	1.21E-04	3.56E-01	2.42E-01	-1.85E+00	3.81E-04
490052787	cytochrome P450	1.36E+01	2.21E+00	8.10E-05	-7.51E-01	2.29E-02	-2.96E+00	2.29E-05
497683596	hypothetical protein	9.33E+00	2.20E+00	6.08E-06	-6.67E-01	3.50E-03	-2.87E+00	2.96E-06
497683664	iron ABC transporter substrate-binding protein	1.27E+01	2.20E+00	2.72E-05	-6.17E-01	2.10E-02	-2.81E+00	1.08E-05
490054146	50S ribosomal protein L16	1.28E+01	2.17E+00	7.81E-04	-9.06E-01	5.50E-02	-3.08E+00	1.63E-04
490055741	initiation factor 2B subunit alpha	1.25E+01	2.16E+00	5.31E-05	7.86E-01	1.23E-02	-1.38E+00	7.13E-04
490058655	Ion-transporting ATPase	1.05E+01	2.15E+00	9.62E-05	2.22E+00	1.19E-04	7.28E-02	7.89E-01
490054410	histidinol dehydrogenase	1.16E+01	2.14E+00	2.29E-05	6.79E-01	1.06E-02	-1.46E+00	2.00E-04
490059687	transcriptional regulator	1.33E+01	2.13E+00	1.16E-05	-9.34E-01	1.10E-03	-3.06E+00	3.40E-06
490058111	hypothetical protein	1.48E+01	2.12E+00	7.16E-06	-5.71E-01	7.47E-03	-2.69E+00	3.79E-06
497681486	alanine dehydrogenase	9.59E+00	2.12E+00	8.41E-03	8.00E-01	2.40E-01	-1.32E+00	6.85E-02
497682584	XRE family transcriptional regulator	1.16E+01	2.11E+00	1.14E-05	-1.74E+00	4.30E-05	-3.86E+00	1.73E-06

490054322	hypothetical protein	6.74E+00	2.11E+00	2.57E-04	-7.93E+00	1.68E-06	-1.00E+01	5.97E-07
497682591	Xaa-Pro aminopeptidase	1.15E+01	2.11E+00	1.12E-05	1.65E-01	3.48E-01	-1.95E+00	2.01E-05
490054057	lauroyl acyltransferase	1.33E+01	2.11E+00	4.79E-06	-5.42E-01	6.27E-03	-2.65E+00	2.94E-06
490055874	conserved hypothetical protein	1.42E+01	2.08E+00	4.44E-06	-5.58E-01	4.53E-03	-2.64E+00	2.57E-06
490057951	histidine kinase	9.33E+00	2.07E+00	4.21E-04	-8.46E-01	3.90E-02	-2.92E+00	9.01E-05
490052584	membrane protein	1.32E+01	2.07E+00	1.78E-05	-6.15E-01	1.11E-02	-2.69E+00	6.58E-06
490059708	methylmalonyl-CoA carboxyltransferase	1.31E+01	2.07E+00	3.11E-05	-5.51E-01	2.91E-02	-2.62E+00	1.27E-05
490059776	4-aminobutyrate aminotransferase	1.39E+01	2.06E+00	9.38E-05	-6.57E-01	3.26E-02	-2.72E+00	2.84E-05
490060239	XRE family transcriptional regulator	1.31E+01	2.06E+00	1.32E-03	7.31E-01	1.19E-01	-1.32E+00	1.43E-02
497683553	hypothetical protein	1.33E+01	2.05E+00	8.83E-06	-1.96E+00	1.81E-05	-4.02E+00	1.22E-06
497683102	NAD-dependent dehydratase	1.30E+01	2.04E+00	1.71E-04	-9.87E-01	9.52E-03	-3.03E+00	2.88E-05
490056432	HAD family hydrolase	1.12E+01	2.04E+00	8.00E-05	-2.44E+00	4.81E-05	-4.48E+00	3.04E-06
497684774	phosphohydrolase	1.21E+01	2.03E+00	1.01E-04	-9.35E-01	7.46E-03	-2.97E+00	1.90E-05
490051692	sugar kinase	1.15E+01	2.02E+00	2.32E-05	-5.08E-01	2.84E-02	-2.52E+00	1.02E-05
497681680	indole-3-glycerol-phosphate synthase	1.04E+01	2.02E+00	6.33E-06	-8.83E-02	5.51E-01	-2.10E+00	6.61E-06
490055271	nucleoside diphosphate kinase	1.46E+01	1.99E+00	4.32E-03	-5.99E-01	2.76E-01	-2.59E+00	1.54E-03
490059045	glyoxalase	1.31E+01	1.98E+00	2.42E-04	-2.58E+00	9.21E-05	-4.56E+00	5.57E-06
490056344	aspartate-semialdehyde dehydrogenase	1.26E+01	1.98E+00	1.46E-05	-5.06E-01	1.75E-02	-2.48E+00	6.40E-06
497682234	50S ribosomal protein L25	1.18E+01	1.97E+00	4.03E-06	-1.25E+00	4.81E-05	-3.23E+00	1.22E-06
490058570	pantothenate synthetase	9.22E+00	1.97E+00	9.56E-04	-1.94E+00	1.53E-03	-3.91E+00	3.52E-05
490052535	phosphoenolpyruvate carboxykinase	1.06E+01	1.96E+00	9.23E-05	-9.17E-01	6.36E-03	-2.88E+00	1.71E-05
490054002	ABC transporter	1.47E+01	1.94E+00	2.37E-05	-8.80E-01	2.02E-03	-2.82E+00	5.57E-06
490054091	transcription antitermination protein NusB	1.30E+01	1.93E+00	6.92E-04	-3.90E+00	3.07E-05	-5.84E+00	4.35E-06
490050516	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1.29E+01	1.93E+00	4.81E-05	-1.20E+00	8.20E-04	-3.14E+00	6.17E-06
490060764	peptide synthetase	1.39E+01	1.93E+00	7.26E-05	-1.53E+00	3.43E-04	-3.46E+00	5.70E-06
490060765	peptide synthetase	1.32E+01	1.92E+00	7.47E-06	-1.42E+00	4.86E-05	-3.34E+00	1.61E-06
490053321	cysteine desulfurase	1.14E+01	1.91E+00	7.82E-05	-6.49E-01	2.20E-02	-2.56E+00	2.21E-05
497681283	amidohydrolase	1.18E+01	1.90E+00	1.43E-04	1.17E+00	2.66E-03	-7.36E-01	1.99E-02
490052663	hypothetical protein	1.46E+01	1.90E+00	4.29E-03	-6.41E-01	2.28E-01	-2.54E+00	1.34E-03
497681623	tellurium resistance protein TerC	1.32E+01	1.89E+00	4.46E-05	-3.11E-01	1.56E-01	-2.20E+00	2.59E-05
490052231	ornithine carbamoyltransferase	1.29E+01	1.86E+00	1.57E-04	-1.35E+00	1.19E-03	-3.21E+00	1.28E-05
490050088	ATP synthase subunit C	2.07E+01	1.86E+00	4.60E-06	-1.96E-02	8.80E-01	-1.88E+00	5.79E-06

490058302	acetolactate synthase	1.01E+01	1.85E+00	3.19E-04	-1.80E+00	5.48E-04	-3.66E+00	1.32E-05
490058437	metal ABC transporter substrate-binding protein	7.89E+00	1.84E+00	1.16E-03	-9.60E+00	1.55E-06	-1.14E+01	6.01E-07
490061076	NUDIX hydrolase	1.25E+01	1.82E+00	4.69E-06	-5.09E-01	4.10E-03	-2.33E+00	2.62E-06
490057973	acetyltransferase	1.21E+01	1.82E+00	2.86E-03	-2.79E-01	5.37E-01	-2.10E+00	1.83E-03
490051665	arginine ABC transporter ATP-binding protein	1.44E+01	1.82E+00	2.44E-04	5.49E-01	7.51E-02	-1.27E+00	2.05E-03
490060648	LuxR family transcriptional regulator	9.47E+00	1.80E+00	9.31E-03	-1.80E+00	1.33E-02	-3.61E+00	3.88E-04
490054741	transcriptional regulator	1.33E+01	1.80E+00	4.34E-06	-4.35E-01	7.05E-03	-2.24E+00	2.62E-06
490057864	glutamate synthase	1.26E+01	1.79E+00	5.46E-06	-1.38E+00	2.94E-05	-3.17E+00	1.22E-06
497682123	ATP-dependent Clp protease ClpS	1.19E+01	1.79E+00	4.85E-05	-3.60E-01	9.66E-02	-2.15E+00	2.42E-05
497682576	NADPH-dependent FMN reductase	1.43E+01	1.78E+00	1.64E-03	8.61E-01	5.48E-02	-9.23E-01	4.04E-02
490050760	hydroxyurea phosphotransferase	1.10E+01	1.78E+00	2.59E-04	-2.33E+00	9.77E-05	-4.12E+00	5.70E-06
497684022	choline oxidase	1.63E+01	1.77E+00	6.17E-03	2.20E+00	3.17E-03	4.38E-01	3.99E-01
497683062	TetR family transcriptional regulator	1.45E+01	1.75E+00	6.19E-05	-8.82E-01	3.13E-03	-2.63E+00	1.08E-05
490058279	Aldolase	1.25E+01	1.75E+00	8.97E-04	6.56E-01	8.27E-02	-1.09E+00	1.17E-02
490050023	acetate kinase	1.22E+01	1.74E+00	8.11E-06	-6.62E-01	1.55E-03	-2.40E+00	3.04E-06
490054608	glutamate ABC transporter permease	1.00E+01	1.74E+00	1.81E-04	1.29E+00	1.24E-03	-4.45E-01	9.76E-02
490054228	DNA helicase	1.08E+01	1.73E+00	2.09E-05	-1.52E+00	5.92E-05	-3.25E+00	2.29E-06
490057554	50S ribosomal protein L20	1.03E+01	1.73E+00	2.00E-03	7.84E+00	3.04E-06	6.12E+00	5.23E-06
490052948	GTP-binding protein TypA	1.23E+01	1.72E+00	3.59E-04	-8.38E-01	1.75E-02	-2.56E+00	5.75E-05
490052483	nicotinate phosphoribosyltransferase	1.33E+01	1.72E+00	1.27E-04	-2.18E+00	5.55E-05	-3.90E+00	3.79E-06
497682119	peptidase	1.29E+01	1.71E+00	4.60E-06	-1.83E+00	6.44E-06	-3.54E+00	6.01E-07
490051736	3-oxoacyl-ACP synthase	1.20E+01	1.71E+00	9.70E-03	-1.06E+00	8.12E-02	-2.77E+00	1.25E-03
490056480	methyltransferase type 12	1.25E+01	1.70E+00	8.68E-05	-1.54E+00	2.12E-04	-3.24E+00	5.39E-06
490060430	Puromycin N-acetyltransferase	1.24E+01	1.70E+00	1.80E-05	-2.32E+00	7.52E-06	-4.01E+00	1.10E-06
497683551	(dimethylallyl)adenosine tRNA methylthiotransferase	1.15E+01	1.69E+00	3.61E-05	5.26E-01	1.72E-02	-1.17E+00	3.10E-04
490052493	beta-lactamase	1.22E+01	1.69E+00	3.67E-05	-8.66E-01	1.67E-03	-2.55E+00	6.53E-06
490057336	adenosylmethionine--8-amino-7-oxononanoate aminotransferase	9.92E+00	1.68E+00	1.14E-04	-1.54E+00	2.60E-04	-3.23E+00	6.17E-06
490057514	Putative uroporphyrin-III methyltransferase	1.21E+01	1.68E+00	3.12E-05	-2.24E+00	1.41E-05	-3.93E+00	1.63E-06
490058310	Nocardamine synthetase	1.17E+01	1.68E+00	1.21E-03	-1.64E+00	2.06E-03	-3.32E+00	4.51E-05
490057467	rRNA cytosine-C5-methyltransferase	1.07E+01	1.68E+00	5.15E-04	-1.99E+00	3.27E-04	-3.67E+00	1.28E-05
497682387	aminotransferase	9.53E+00	1.68E+00	6.45E-06	-2.91E+00	1.81E-06	-4.59E+00	2.18E-07
490054396	dienelactone hydrolase	1.15E+01	1.68E+00	2.04E-05	2.75E+00	5.01E-06	1.08E+00	2.39E-04

490055694	glutamine amidotransferase	1.12E+01	1.67E+00	7.31E-05	-2.95E-01	1.64E-01	-1.96E+00	3.92E-05
490060089	peptidase U61	9.01E+00	1.67E+00	3.67E-05	1.55E-01	3.82E-01	-1.51E+00	7.37E-05
490057777	hypothetical protein	1.37E+01	1.66E+00	4.55E-04	-8.61E-01	1.62E-02	-2.52E+00	6.59E-05
490059784	ribosome maturation protein RimP	1.22E+01	1.66E+00	4.30E-04	-6.54E-01	4.50E-02	-2.31E+00	9.71E-05
490059201	hypothetical protein	1.33E+01	1.64E+00	1.90E-05	-1.21E+00	1.28E-04	-2.84E+00	2.57E-06
490059501	sugar transporter	1.37E+01	1.64E+00	2.09E-05	-1.77E+00	2.32E-05	-3.41E+00	1.73E-06
490053064	magnesium or manganese-dependent protein phosphatase	1.35E+01	1.63E+00	1.58E-05	-3.52E-01	3.67E-02	-1.98E+00	7.91E-06
497681406	glycine/betaine ABC transporter ATP-binding protein	1.34E+01	1.61E+00	1.88E-04	-1.06E+00	2.48E-03	-2.67E+00	1.89E-05
490052451	ABC transporter substrate-binding protein	1.17E+01	1.61E+00	5.54E-04	-9.41E-01	1.14E-02	-2.55E+00	6.45E-05
490059961	glycogen debranching protein	8.50E+00	1.60E+00	4.90E-04	-5.59E-01	7.31E-02	-2.16E+00	1.31E-04
497681957	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	1.83E+01	1.60E+00	1.23E-04	-8.46E-01	4.65E-03	-2.44E+00	1.84E-05
490051483	UTP--glucose-1-phosphate uridylyltransferase	1.69E+01	1.58E+00	2.12E-05	-4.53E-01	1.57E-02	-2.04E+00	8.28E-06
490055606	3-oxoacyl-ACP reductase	1.26E+01	1.58E+00	1.61E-04	2.10E-01	3.51E-01	-1.37E+00	4.36E-04
490059344	betaine-aldehyde dehydrogenase	1.12E+01	1.57E+00	1.83E-04	-1.22E+00	1.03E-03	-2.79E+00	1.31E-05
490059014	XRE family transcriptional regulator	1.23E+01	1.57E+00	3.97E-04	-5.10E-01	8.01E-02	-2.08E+00	1.15E-04
490057536	isocitrate dehydrogenase	1.13E+01	1.57E+00	4.16E-05	-6.75E-01	4.57E-03	-2.24E+00	9.31E-06
490054221	single-stranded DNA-binding protein	1.23E+01	1.56E+00	4.63E-05	4.54E-01	2.75E-02	-1.11E+00	3.42E-04
490054116	50S ribosomal protein L17	1.10E+01	1.56E+00	1.45E-03	-5.79E-01	1.11E-01	-2.14E+00	3.69E-04
490058039	MFS transporter	1.36E+01	1.55E+00	6.12E-05	-2.92E-01	1.32E-01	-1.85E+00	3.24E-05
490052772	hypothetical protein	1.01E+01	1.55E+00	8.17E-05	4.04E-01	6.07E-02	-1.15E+00	4.97E-04
490057863	dihydropyrimidine dehydrogenase subunit A	1.23E+01	1.55E+00	1.35E-05	-2.08E+00	6.36E-06	-3.63E+00	8.24E-07
497681989	2-nitropropane dioxygenase	1.15E+01	1.54E+00	2.55E-04	-4.78E-01	7.11E-02	-2.02E+00	7.88E-05
497683271	sodium:proton antiporter	1.40E+01	1.54E+00	9.13E-06	6.72E-02	5.82E-01	-1.47E+00	1.38E-05
497682215	NADH dehydrogenase	1.37E+01	1.53E+00	2.32E-05	-9.46E-01	4.03E-04	-2.48E+00	3.82E-06
490053226	membrane protein	1.12E+01	1.53E+00	4.63E-05	-9.88E-01	6.47E-04	-2.52E+00	5.70E-06
490054802	molecular chaperone GroES	1.00E+01	1.52E+00	2.11E-05	-8.59E-01	5.67E-04	-2.38E+00	3.92E-06
490050525	methylmalonate-semialdehyde dehydrogenase	9.97E+00	1.51E+00	6.45E-03	-2.19E+00	1.55E-03	-3.71E+00	8.71E-05
490055866	acetyltransferase	1.33E+01	1.51E+00	3.19E-05	4.74E-02	7.65E-01	-1.46E+00	4.58E-05
490056459	hypothetical protein	1.25E+01	1.50E+00	2.40E-04	-1.39E+00	5.42E-04	-2.89E+00	1.17E-05
490059514	hypothetical protein	1.35E+01	1.49E+00	1.02E-05	-5.38E-01	2.58E-03	-2.03E+00	3.80E-06
497683179	beta-N-acetylglucosaminidase	1.48E+01	1.49E+00	2.04E-05	2.98E-01	5.81E-02	-1.19E+00	7.47E-05

490055605	enoyl-ACP reductase	1.32E+01	1.49E+00	5.09E-04	-5.60E-01	5.88E-02	-2.05E+00	1.23E-04
497682237	transcriptional regulator	1.18E+01	1.48E+00	1.64E-04	-6.86E-01	1.12E-02	-2.17E+00	2.97E-05
490060233	phytoene dehydrogenase	8.94E+00	1.47E+00	1.78E-03	-1.64E+00	1.53E-03	-3.11E+00	4.63E-05
497681888	membrane protein	1.41E+01	1.47E+00	1.43E-05	-2.69E-01	6.05E-02	-1.74E+00	8.07E-06
490052783	lipase	1.22E+01	1.47E+00	1.38E-05	-2.03E+00	5.79E-06	-3.50E+00	8.19E-07
497683163	phosphoribosylglycinamide formyltransferase	1.29E+01	1.46E+00	3.08E-04	-7.00E-01	1.63E-02	-2.16E+00	5.06E-05
497681420	recombinase RecB	1.15E+01	1.45E+00	4.58E-05	-1.17E+00	2.02E-04	-2.63E+00	4.05E-06
497682044	mechanosensitive ion channel MscS	1.27E+01	1.45E+00	3.22E-05	-1.65E-01	2.83E-01	-1.62E+00	2.38E-05
490055486	hypothetical protein	1.02E+01	1.45E+00	1.42E-03	-1.84E+00	6.09E-04	-3.29E+00	2.68E-05
490054251	cytochrome BD ubiquinol oxidase subunit I	1.28E+01	1.45E+00	7.98E-05	5.62E-01	1.29E-02	-8.84E-01	1.31E-03
490055240	alcohol dehydrogenase	1.10E+01	1.44E+00	3.36E-04	-9.28E-01	4.71E-03	-2.37E+00	3.31E-05
490058360	hypothetical protein	1.30E+01	1.44E+00	9.65E-04	-1.23E+00	3.22E-03	-2.67E+00	4.91E-05
490054891	ABC transporter substrate-binding protein	1.31E+01	1.43E+00	1.55E-04	-1.32E+00	3.49E-04	-2.76E+00	7.91E-06
497683296	hypothetical protein	1.20E+01	1.43E+00	2.47E-03	-6.66E-01	7.95E-02	-2.10E+00	4.55E-04
490051184	hypothetical protein	1.54E+01	1.42E+00	1.52E-02	-3.25E-01	5.25E-01	-1.75E+00	8.15E-03
497682384	phosphoadenosine phosphosulfate reductase	1.39E+01	1.42E+00	2.64E-04	-3.58E-01	1.29E-01	-1.78E+00	1.04E-04
490056442	amino acid ABC transporter permease	1.44E+01	1.42E+00	3.13E-05	2.02E+00	1.00E-05	6.06E-01	3.21E-03
490057952	cysteine desulfurase	1.47E+01	1.42E+00	2.52E-03	-1.19E-01	7.32E-01	-1.53E+00	2.20E-03
490051647	DeoR family transcriptional regulator	1.14E+01	1.41E+00	4.00E-05	-1.96E+00	1.46E-05	-3.37E+00	1.73E-06
490060762	phosphoribosylglycinamide synthetase	1.46E+01	1.41E+00	1.94E-04	-1.75E+00	9.57E-05	-3.16E+00	5.34E-06
490057740	phosphate transporter	8.50E+00	1.41E+00	8.49E-03	-7.60E-01	1.09E-01	-2.17E+00	1.37E-03
497681070	putative electron transfer flavoprotein beta subunit, partial	8.92E+00	1.40E+00	6.92E-04	-1.76E+00	3.16E-04	-3.15E+00	1.43E-05
490054854	glycine dehydrogenase subunit 1	1.29E+01	1.39E+00	1.37E-04	-7.51E-02	6.96E-01	-1.47E+00	1.29E-04
490058303	guanidinobutyrase	1.54E+01	1.39E+00	4.82E-04	-1.13E-01	6.45E-01	-1.51E+00	4.22E-04
490059673	membrane protein	1.55E+01	1.39E+00	4.77E-05	-3.27E-01	6.02E-02	-1.72E+00	2.10E-05
497680874	hypothetical protein	1.16E+01	1.39E+00	1.45E-03	-2.48E+00	1.09E-04	-3.87E+00	1.06E-05
490054363	plant-type carbonic anhydrase	1.58E+01	1.38E+00	1.24E-04	3.52E-01	8.31E-02	-1.03E+00	7.28E-04
490058535	REX family transcriptional regulator	1.26E+01	1.38E+00	4.17E-04	-8.76E-01	6.13E-03	-2.26E+00	4.11E-05
497682165	XRE family transcriptional regulator	1.04E+01	1.38E+00	5.22E-03	-2.96E+00	1.61E-04	-4.34E+00	2.01E-05
490055042	potassium transporter TrkA	1.04E+01	1.37E+00	1.30E-03	-1.43E+00	1.58E-03	-2.80E+00	4.10E-05
497685090	hypothetical protein	1.63E+01	1.37E+00	1.55E-04	-1.07E+00	8.38E-04	-2.44E+00	1.12E-05
490055961	chitinase	1.80E+01	1.37E+00	1.76E-04	2.67E-01	1.93E-01	-1.10E+00	7.00E-04

497683518	riboflavin kinase	1.44E+01	1.37E+00	1.22E-04	-1.41E+00	1.53E-04	-2.77E+00	5.43E-06
490059729	ATP-dependent DNA helicase RecG	1.14E+01	1.36E+00	6.14E-05	-5.56E-01	8.47E-03	-1.92E+00	1.44E-05
490054261	ABC transporter permease	1.13E+01	1.36E+00	1.90E-04	-1.01E+00	1.36E-03	-2.37E+00	1.49E-05
497682479	tryptophan 2,3-dioxygenase	1.21E+01	1.36E+00	2.79E-04	6.27E-02	7.73E-01	-1.30E+00	4.64E-04
490055313	50S ribosomal protein L28	1.22E+01	1.36E+00	1.60E-02	-1.10E+00	5.01E-02	-2.46E+00	1.28E-03
490050335	capsular polysaccharide biosynthesis protein CapB	1.33E+01	1.36E+00	1.19E-04	-1.31E+00	2.10E-04	-2.67E+00	5.80E-06
497685127	threonine dehydratase	1.35E+01	1.36E+00	3.71E-04	-2.24E+00	4.41E-05	-3.59E+00	4.56E-06
490052615	ABC transporter substrate-binding protein	9.33E+00	1.36E+00	4.81E-03	-3.95E-01	3.02E-01	-1.75E+00	1.80E-03
497682317	dihydropteroate synthase	1.24E+01	1.35E+00	2.09E-04	-1.72E+00	9.17E-05	-3.07E+00	5.37E-06
490059268	inosine 5'-monophosphate dehydrogenase	1.22E+01	1.35E+00	1.30E-04	-9.29E-01	1.30E-03	-2.28E+00	1.20E-05
497683414	ABC transporter	1.31E+01	1.35E+00	1.37E-04	7.09E-01	5.32E-03	-6.37E-01	7.87E-03
497683929	serine/threonine protein kinase	1.02E+01	1.34E+00	8.24E-04	-2.46E-01	3.52E-01	-1.59E+00	4.51E-04
490055201	hypothetical protein	1.26E+01	1.34E+00	1.50E-05	-2.36E-01	7.10E-02	-1.58E+00	8.67E-06
497681024	nitrilase	1.07E+01	1.34E+00	1.81E-03	-2.80E+00	6.12E-05	-4.14E+00	8.03E-06
490053904	hypothetical protein	1.23E+01	1.33E+00	2.22E-04	2.98E-01	1.59E-01	-1.04E+00	1.09E-03
490054073	GTP pyrophosphokinase	1.24E+01	1.33E+00	8.82E-04	-1.35E-01	6.05E-01	-1.46E+00	7.02E-04
490058944	phosphoribosylglycinamide synthetase	1.18E+01	1.33E+00	7.69E-04	-2.13E+00	1.00E-04	-3.46E+00	8.14E-06
490053239	dUTPase	1.36E+01	1.32E+00	3.09E-03	-5.30E-01	1.36E-01	-1.85E+00	7.42E-04
490051507	porphobilinogen deaminase	1.44E+01	1.32E+00	2.87E-04	-3.15E+00	7.36E-06	-4.48E+00	2.02E-06
490056083	ABC transporter substrate-binding protein	1.44E+01	1.32E+00	6.04E-05	-1.72E-01	2.77E-01	-1.49E+00	4.02E-05
490051158	phosphoglyceromutase	1.22E+01	1.32E+00	6.35E-03	-1.20E+00	1.40E-02	-2.52E+00	3.16E-04
490058550	hypothetical protein	1.22E+01	1.32E+00	4.86E-04	-1.16E+00	1.43E-03	-2.47E+00	2.46E-05
490057574	5'-3' exonuclease	1.42E+01	1.31E+00	3.76E-05	-8.28E-01	5.86E-04	-2.14E+00	5.23E-06
490051253	hypothetical protein	1.47E+01	1.31E+00	2.66E-05	-1.31E-01	3.19E-01	-1.44E+00	2.10E-05
490051180	hypothetical protein	1.40E+01	1.30E+00	2.10E-04	-1.44E+00	1.88E-04	-2.74E+00	6.86E-06
497683263	N-succinyldiaminopimelate aminotransferase	1.40E+01	1.30E+00	5.80E-05	-1.59E+00	3.33E-05	-2.89E+00	2.57E-06
497681739	hypothetical protein	1.30E+01	1.30E+00	9.99E-03	8.21E-01	7.78E-02	-4.77E-01	2.68E-01
490055041	DNA-binding protein	1.33E+01	1.30E+00	2.15E-04	-6.71E-01	8.73E-03	-1.97E+00	3.24E-05
490059197	hypothetical protein	1.22E+01	1.29E+00	9.54E-04	-9.37E-01	6.95E-03	-2.23E+00	7.13E-05
490057591	ferredoxin	1.23E+01	1.29E+00	1.48E-03	-1.33E+00	1.88E-03	-2.62E+00	4.72E-05
490050602	hypothetical protein	1.45E+01	1.29E+00	3.02E-03	1.10E+00	9.51E-03	-1.93E-01	5.50E-01
490054831	ATP-dependent DNA helicase PcrA	1.14E+01	1.29E+00	1.87E-03	-1.82E+00	4.74E-04	-3.10E+00	2.61E-05

490058819	histidine kinase	1.38E+01	1.29E+00	1.23E-04	-1.94E-01	2.71E-01	-1.48E+00	7.30E-05
490051537	hypothetical protein	1.37E+01	1.28E+00	4.42E-03	2.18E-02	9.52E-01	-1.26E+00	6.41E-03
497681016	glucosamine-6-phosphate deaminase	8.64E+00	1.28E+00	2.08E-03	-1.09E+00	6.76E-03	-2.37E+00	1.09E-04
497683012	hypothetical protein	1.58E+01	1.28E+00	3.61E-03	5.02E-01	1.53E-01	-7.74E-01	4.06E-02
490058897	branched-chain alpha-keto acid dehydrogenase subunit E2	1.22E+01	1.28E+00	3.68E-04	-2.74E+00	1.42E-05	-4.02E+00	2.57E-06
490059740	acetyltransferase	1.29E+01	1.27E+00	1.63E-03	-1.44E+00	1.30E-03	-2.71E+00	4.14E-05
490057607	cysteine--1-D-myo-inosityl 2-amino-2-deoxy-alpha-D-glucopyranoside ligase	1.31E+01	1.26E+00	4.77E-05	-5.71E-01	4.10E-03	-1.83E+00	9.82E-06
497682938	putative guanyltransferase	1.17E+01	1.26E+00	5.87E-04	-1.13E+00	1.53E-03	-2.39E+00	2.78E-05
490057293	ABC transporter permease	1.22E+01	1.25E+00	9.54E-04	-2.49E+00	4.28E-05	-3.75E+00	5.57E-06
490057478	shikimate kinase	1.51E+01	1.25E+00	1.39E-04	-2.86E+00	5.40E-06	-4.11E+00	1.55E-06
490052229	aspartate decarboxylase	1.43E+01	1.25E+00	1.22E-03	-1.29E+00	1.53E-03	-2.54E+00	3.96E-05
497683476	acylphosphatase	1.54E+01	1.25E+00	7.16E-05	-5.94E-01	4.64E-03	-1.84E+00	1.29E-05
490052778	fructose-bisphosphate aldolase	1.01E+01	1.24E+00	3.03E-04	-2.99E-01	1.53E-01	-1.54E+00	1.25E-04
490056752	RNA polymerase subunit sigma24	1.23E+01	1.23E+00	2.64E-04	-1.34E+00	2.51E-04	-2.57E+00	8.67E-06
490056909	polyketide synthase	1.62E+01	1.23E+00	8.12E-05	-3.66E-01	3.81E-02	-1.59E+00	2.70E-05
497683636	DNA polymerase III subunit epsilon	1.20E+01	1.22E+00	4.52E-05	4.71E-01	8.29E-03	-7.54E-01	7.10E-04
490059709	hypothetical protein	7.67E+00	1.22E+00	3.81E-04	1.18E-01	5.66E-01	-1.11E+00	8.50E-04
490058538	glycerol acyltransferase	1.58E+01	1.22E+00	6.42E-05	-1.12E+00	1.53E-04	-2.34E+00	4.22E-06
497683144	FAD-dependent oxidoreductase	1.44E+01	1.22E+00	5.63E-04	-6.20E-01	2.10E-02	-1.84E+00	8.53E-05
490056621	polyisoprenoid-binding protein	1.24E+01	1.22E+00	4.20E-03	-7.19E-01	5.35E-02	-1.94E+00	5.30E-04
490051149	pyridoxamine 5'-phosphate oxidase	1.43E+01	1.22E+00	2.86E-03	6.09E-01	7.07E-02	-6.12E-01	6.60E-02
490054076	peptidylprolyl isomerase	1.32E+01	1.21E+00	2.67E-03	-2.25E-02	9.42E-01	-1.24E+00	3.19E-03
490054698	glyceraldehyde-3-phosphate dehydrogenase	1.05E+01	1.21E+00	8.41E-05	-1.18E+00	1.39E-04	-2.39E+00	4.56E-06
490060358	3-oxoacyl-ACP reductase	1.33E+01	1.21E+00	3.36E-04	-1.53E+00	1.45E-04	-2.74E+00	7.44E-06
490061540	ABC-type Fe3+-hydroxamate transport system, solute-binding protein	1.06E+01	1.20E+00	2.68E-04	-2.31E+00	1.80E-05	-3.52E+00	2.61E-06
490054113	ABC transporter	1.15E+01	1.20E+00	9.57E-05	-8.38E-01	9.13E-04	-2.04E+00	8.94E-06
490057041	endoribonuclease L-PSP	9.68E+00	1.20E+00	8.60E-03	4.13E-01	2.84E-01	-7.89E-01	5.86E-02

[a] Identification is based on annotation by NCBI. **[b]** Description is based on NCBI annotation of protein similarity by BLAST. **[c]** Average normalized expression in the WT strain. **[d]** Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain.

[e]Adjusted P-value in *ΔbldG* as compared to the WT strain. [f] Normalized log_2 fold change in *ΔbldA* as compared to the WT strain. [g] Adjusted P-value in *ΔbldA* as compared to the WT strain. [h] Normalized log_2 fold change in *ΔbldA* as compared to the *ΔbldG* strain and [i] Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Table A.1.2: Proteins determined to be significantly (P=0.01) under-expressed in the *ΔbldG* compared to the WT strain of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G -WT[e]	logFC A -WT[f]	adj.P.Val A-WT[g]	logFC A -G[h]	adj.P.Val A -G[i]
497682057	hypothetical protein	1.28E+01	-1.06E+01	1.04E-02	-3.58E+00	3.11E-01	7.00E+00	6.63E-02
490060465	cytochrome P450	7.00E+00	-9.14E+00	1.86E-03	-3.42E+00	1.23E-01	5.71E+00	2.14E-02
490058756	CRISPR-associated protein Cas2	5.73E+00	-9.07E+00	9.69E-08	2.69E-01	1.52E-01	9.34E+00	4.46E-08
497684074	hypothetical protein, partial	4.02E+00	-7.64E+00	7.44E-05	-3.00E+00	1.14E-02	4.63E+00	1.26E-03
490050597	thioredoxin	1.50E+01	-5.61E+00	1.16E-06	-1.01E+00	2.72E-03	4.60E+00	2.25E-06
490051386	anti-sigma B factor antagonist	1.54E+01	-5.23E+00	2.60E-06	-3.00E+00	4.11E-05	2.23E+00	1.49E-04
490051454	conserved hypothetical protein	1.23E+01	-5.21E+00	6.60E-05	-3.32E-01	5.94E-01	4.87E+00	1.13E-04
490052896	hypothetical protein	1.20E+01	-5.05E+00	1.15E-06	-2.30E+00	2.11E-05	2.75E+00	7.02E-06
490055111	hypothetical protein	1.36E+01	-4.95E+00	1.16E-06	-2.39E+00	2.04E-05	2.57E+00	1.11E-05
490059803	hypothetical protein	1.41E+01	-4.79E+00	1.15E-06	-1.96E+00	3.07E-05	2.83E+00	4.97E-06
490050805	aminotransferase class III	9.69E+00	-4.65E+00	3.42E-06	-4.09E+00	9.05E-06	5.57E-01	7.58E-02
490053893	NADH:ubiquinone oxidoreductase subunit N	1.42E+01	-4.63E+00	3.76E-06	-1.11E+00	5.65E-03	3.52E+00	1.46E-05
490059696	short-chain dehydrogenase	1.37E+01	-4.53E+00	2.02E-05	-3.60E+00	9.28E-05	9.29E-01	4.95E-02
490050315	methyltransferase	1.38E+01	-4.45E+00	2.52E-06	-2.09E+00	1.05E-04	2.36E+00	4.57E-05
490056213	isochorismatase	1.29E+01	-4.40E+00	1.15E-06	-4.31E+00	1.55E-06	9.56E-02	5.75E-01
490053550	acyl-CoA dehydrogenase	1.51E+01	-4.36E+00	1.57E-06	-4.18E+00	2.70E-06	1.86E-01	3.57E-01
490052844	lectin PVL	1.47E+01	-4.36E+00	1.87E-06	-2.00E+00	7.92E-05	2.36E+00	2.91E-05
497681423	peptide-binding protein	1.27E+01	-4.29E+00	3.74E-05	-1.75E+00	5.35E-03	2.54E+00	7.23E-04
490053554	flavoprotein	1.21E+01	-4.27E+00	3.03E-06	-3.22E+00	1.64E-05	1.05E+00	3.51E-03
497685434	plasmid stabilization protein	1.04E+01	-4.26E+00	1.75E-05	-2.25E+00	6.37E-04	2.01E+00	1.02E-03
490052684	nucleoside-diphosphate kinase	1.36E+01	-4.26E+00	1.15E-06	-8.32E-01	1.62E-03	3.43E+00	2.23E-06
490051568	reductase	1.04E+01	-4.26E+00	1.87E-06	-6.06E-02	7.83E-01	4.20E+00	2.49E-06
490055022	hypothetical protein	1.49E+01	-4.21E+00	1.63E-04	-2.61E+00	2.84E-03	1.60E+00	2.35E-02
490053425	saicar synthetase	1.38E+01	-4.20E+00	1.67E-06	-3.44E+00	5.07E-06	7.61E-01	5.44E-03
497684432	hypothetical protein	1.13E+01	-4.16E+00	1.15E-06	-5.15E+00	4.81E-07	-9.89E-01	2.57E-04
497682856	hypothetical protein	1.35E+01	-4.12E+00	1.99E-06	-5.46E+00	1.64E-06	-1.35E+00	4.45E-04
497684454	hypothetical protein	1.14E+01	-4.10E+00	2.19E-06	-5.07E+00	2.14E-06	-9.77E-01	2.56E-03

490050391	3-beta hydroxysteroid dehydrogenase	1.36E+01	-4.09E+00	3.93E-06	-1.66E+00	4.28E-04	2.43E+00	5.08E-05
490053549	N-acetyltransferase GCN5	1.29E+01	-4.08E+00	3.02E-06	-3.49E+00	8.97E-06	5.92E-01	3.54E-02
490061051	protein kinase	1.24E+01	-4.02E+00	3.11E-04	-2.59E+00	4.41E-03	1.43E+00	4.86E-02
490050172	conserved hypothetical protein	1.37E+01	-4.01E+00	5.20E-06	-3.28E+00	2.19E-05	7.28E-01	2.75E-02
490054628	competence damage-inducible protein A	1.39E+01	-4.00E+00	3.29E-06	-1.88E+00	1.57E-04	2.12E+00	7.12E-05
490059144	D-alanine--D-alanine ligase	1.22E+01	-3.96E+00	9.13E-06	-5.20E+00	5.40E-06	-1.24E+00	4.06E-03
497685016	hypothetical protein	1.44E+01	-3.95E+00	3.03E-06	-9.89E-02	6.81E-01	3.85E+00	4.31E-06
490060440	hypothetical protein	1.46E+01	-3.91E+00	2.89E-06	-9.81E-01	3.40E-03	2.93E+00	1.16E-05
490060539	calcium-binding protein	1.48E+01	-3.90E+00	7.40E-06	-4.96E-01	1.18E-01	3.41E+00	1.76E-05
497683080	hypothetical protein	1.08E+01	-3.90E+00	2.83E-03	7.42E-01	4.46E-01	4.64E+00	1.55E-03
497685206	hypothetical protein	1.49E+01	-3.85E+00	2.94E-06	-2.12E+00	6.14E-05	1.73E+00	1.48E-04
490050161	conserved hypothetical protein	1.20E+01	-3.85E+00	2.59E-06	-2.66E+00	1.82E-05	1.18E+00	8.44E-04
490056704	dynein regulation protein LC7	9.64E+00	-3.82E+00	1.15E-06	-3.91E+00	1.12E-06	-8.40E-02	5.53E-01
490052035	short-chain dehydrogenase	1.36E+01	-3.82E+00	1.87E-06	-6.99E-01	7.34E-03	3.12E+00	4.39E-06
490050350	hypothetical protein	1.14E+01	-3.82E+00	3.33E-06	-2.18E+00	6.09E-05	1.64E+00	2.18E-04
490055024	geranylgeranyl pyrophosphate synthase	1.05E+01	-3.81E+00	1.35E-03	-2.11E+00	2.92E-02	1.70E+00	5.90E-02
497684393	CRISPR-associated Cse1 family protein	1.34E+01	-3.81E+00	6.08E-06	-2.91E+00	3.30E-05	9.05E-01	9.88E-03
497682409	pilus biosynthesis protein TadE	1.41E+01	-3.81E+00	1.16E-03	-5.05E-01	5.25E-01	3.31E+00	3.10E-03
490061049	alkanal monooxygenase	1.33E+01	-3.81E+00	2.09E-05	-2.33E+00	3.72E-04	1.48E+00	3.36E-03
490059108	cytochrome P450	1.34E+01	-3.79E+00	1.15E-06	-2.71E+00	2.89E-06	1.08E+00	1.02E-04
497685001	hypothetical protein	1.25E+01	-3.78E+00	9.66E-06	-3.85E+00	1.49E-05	-7.18E-02	8.10E-01
490061142	amidohydrolase	1.20E+01	-3.75E+00	1.50E-05	-5.07E-01	1.45E-01	3.24E+00	3.71E-05
497683836	thioredoxin reductase	1.40E+01	-3.73E+00	2.02E-06	-3.93E+00	3.04E-06	-2.01E-01	3.23E-01
490057366	hypothetical protein	9.29E+00	-3.71E+00	1.67E-06	-3.20E+00	4.33E-06	5.13E-01	1.76E-02
497684462	DSBA oxidoreductase	1.26E+01	-3.70E+00	1.15E-06	-3.09E+00	2.70E-06	6.15E-01	3.03E-03
490059562	Clavaminate synthase 2	1.25E+01	-3.70E+00	1.02E-05	-2.74E+00	6.44E-05	9.61E-01	1.10E-02
497684269	cobyrinic acid a,c-diamide synthase	1.18E+01	-3.68E+00	3.70E-06	-3.48E+00	7.36E-06	1.93E-01	4.10E-01
497684923	hypothetical protein	1.14E+01	-3.67E+00	3.63E-06	-4.91E+00	2.63E-06	-1.24E+00	8.68E-04
490050150	3'-hydroxymethylcephem carbamoyltransferase	1.18E+01	-3.67E+00	4.48E-06	-3.69E+00	7.67E-06	-2.35E-02	9.25E-01
490053433	hypothetical protein	1.24E+01	-3.66E+00	1.67E-06	-3.41E+00	3.04E-06	2.52E-01	1.65E-01
497685225	beta-lactamase	1.23E+01	-3.65E+00	1.15E-06	-1.12E+00	1.53E-04	2.53E+00	3.34E-06
497683069	permease	1.36E+01	-3.63E+00	1.15E-06	-6.14E-01	3.38E-03	3.01E+00	2.03E-06

490050798	tellurium resistance protein	1.31E+01	-3.62E+00	1.48E-06	8.52E-01	1.09E-03	4.47E+00	8.19E-07
490054446	conserved hypothetical protein	1.22E+01	-3.59E+00	2.48E-05	-7.67E-01	5.42E-02	2.82E+00	1.04E-04
490050170	beta-lactamase	1.26E+01	-3.59E+00	1.32E-06	-2.33E+00	7.16E-06	1.26E+00	9.42E-05
490055747	membrane protein	1.24E+01	-3.58E+00	1.02E-05	-2.08E+00	2.19E-04	1.50E+00	1.04E-03
490056624	peptide synthetase	1.37E+01	-3.54E+00	2.69E-05	-3.11E+00	7.75E-05	4.33E-01	2.31E-01
490060520	cell surface protein	1.37E+01	-3.50E+00	9.66E-06	-1.71E+00	5.11E-04	1.79E+00	3.43E-04
497680886	ABC transporter	1.27E+01	-3.48E+00	1.04E-04	-2.98E+00	3.41E-04	5.03E-01	2.73E-01
490060020	serine/threonine protein kinase	1.19E+01	-3.48E+00	2.61E-06	-3.28E+00	5.46E-06	1.94E-01	3.34E-01
497683148	hypothetical protein	1.44E+01	-3.44E+00	1.87E-06	-1.57E+00	6.97E-05	1.86E+00	2.55E-05
490060096	glyoxalase	1.25E+01	-3.43E+00	2.65E-04	1.32E-01	8.07E-01	3.56E+00	2.82E-04
490058537	RNA polymerase subunit sigma-24	1.13E+01	-3.42E+00	3.40E-06	-6.56E-01	1.41E-02	2.77E+00	9.80E-06
490051126	cold-shock protein	1.48E+01	-3.41E+00	8.11E-06	-1.37E+00	1.19E-03	2.04E+00	1.25E-04
490052383	hypothetical protein	1.25E+01	-3.40E+00	1.15E-06	-3.37E+00	1.09E-06	3.31E-02	7.70E-01
490058900	pirin	1.13E+01	-3.40E+00	2.88E-06	-3.50E+00	5.07E-06	-1.05E-01	6.00E-01
490056196	transcriptional regulator	1.42E+01	-3.38E+00	8.89E-05	1.07E+00	3.26E-02	4.45E+00	2.73E-05
490055080	endonuclease VII	1.27E+01	-3.38E+00	2.57E-04	-2.44E+00	2.07E-03	9.41E-01	9.43E-02
490051865	hypothetical protein	1.25E+01	-3.37E+00	1.70E-06	-1.78E+00	3.19E-05	1.60E+00	4.25E-05
490050147	conserved hypothetical protein	1.26E+01	-3.36E+00	4.11E-06	-2.80E+00	1.52E-05	5.59E-01	2.97E-02
490053555	oxidoreductase	1.13E+01	-3.36E+00	4.65E-05	-3.66E+00	4.59E-05	-2.99E-01	4.26E-01
490060463	sugar-binding protein	1.19E+01	-3.34E+00	1.48E-06	-1.38E+00	5.93E-05	1.96E+00	9.29E-06
490056077	acetyltransferase	1.21E+01	-3.33E+00	1.11E-05	-2.42E+00	7.59E-05	9.05E-01	9.64E-03
490055825	hypothetical protein	1.34E+01	-3.32E+00	4.79E-06	-8.26E-01	7.27E-03	2.49E+00	2.29E-05
497685041	calcium-binding protein	1.18E+01	-3.32E+00	2.41E-06	-2.39E+00	1.46E-05	9.29E-01	1.26E-03
490060049	putative secreted FAD-linked oxidase	1.35E+01	-3.29E+00	2.79E-06	3.97E-01	6.54E-02	3.69E+00	2.57E-06
497685168	hypothetical protein	1.35E+01	-3.28E+00	1.68E-06	-2.55E+00	6.07E-06	7.36E-01	2.00E-03
497685018	hypothetical protein	1.42E+01	-3.27E+00	1.87E-06	2.49E-01	1.60E-01	3.52E+00	2.03E-06
497683835	peptide synthetase	1.21E+01	-3.27E+00	2.19E-06	-2.79E+00	6.51E-06	4.79E-01	2.39E-02
497683343	L-lysine aminotransferase	1.39E+01	-3.27E+00	4.09E-06	-2.85E+00	1.25E-05	4.16E-01	7.40E-02
490053551	hypothetical protein	1.26E+01	-3.23E+00	3.93E-06	-3.56E+00	5.07E-06	-3.32E-01	1.30E-01
490061303	histidine decarboxylase	1.34E+01	-3.22E+00	3.20E-04	1.54E-01	7.71E-01	3.38E+00	3.26E-04
490060518	hypothetical protein	1.28E+01	-3.22E+00	1.69E-06	-3.25E+00	2.82E-06	-3.32E-02	8.32E-01
490059489	catalase	1.40E+01	-3.22E+00	1.40E-06	-1.55E+00	2.72E-05	1.67E+00	1.47E-05

490060264	glucose-methanol-choline oxidoreductase	1.24E+01	-3.21E+00	1.14E-05	-3.36E+00	1.58E-05	-1.46E-01	5.82E-01
490059212	NADH:ubiquinone oxidoreductase subunit J	1.34E+01	-3.20E+00	4.16E-06	-3.61E-01	1.13E-01	2.84E+00	8.68E-06
497683966	O-acetylhomoserine aminocarboxypropyltransferase	1.16E+01	-3.20E+00	1.48E-06	-1.74E+00	1.84E-05	1.46E+00	3.12E-05
497683145	serine/threonine protein kinase	1.19E+01	-3.20E+00	8.16E-03	-3.04E+00	1.47E-02	1.62E-01	8.67E-01
497684150	hypothetical protein	1.35E+01	-3.20E+00	4.69E-06	-1.34E-01	5.44E-01	3.06E+00	7.39E-06
497683456	thioester reductase	1.23E+01	-3.20E+00	7.43E-06	-3.11E+00	1.47E-05	8.22E-02	7.34E-01
490050319	glutamine synthetase	1.55E+01	-3.19E+00	1.87E-06	-6.18E-02	7.09E-01	3.13E+00	2.57E-06
497680944	phosphotransferase	1.10E+01	-3.18E+00	5.46E-06	-1.51E+00	3.13E-04	1.66E+00	1.61E-04
490061297	cytochrome P450	1.12E+01	-3.17E+00	1.57E-06	-4.51E+00	8.46E-07	-1.35E+00	4.78E-05
490050711	type 11 methyltransferase	1.40E+01	-3.16E+00	1.87E-06	-2.69E+00	5.79E-06	4.73E-01	1.80E-02
497682154	sugar ABC transporter substrate-binding protein	1.14E+01	-3.16E+00	6.33E-06	-2.57E-01	2.78E-01	2.91E+00	1.18E-05
490056623	acyl carrier protein	1.15E+01	-3.16E+00	1.71E-05	-4.12E+00	8.33E-06	-9.60E-01	8.74E-03
490060448	MFS transporter	1.41E+01	-3.16E+00	1.67E-06	-1.97E+00	1.49E-05	1.19E+00	1.28E-04
497681787	regulator	1.49E+01	-3.15E+00	1.46E-04	7.25E-01	1.22E-01	3.88E+00	6.24E-05
490050165	conserved hypothetical protein	1.30E+01	-3.14E+00	1.15E-06	-2.11E+00	4.11E-06	1.03E+00	6.22E-05
490051445	hypothetical protein	1.33E+01	-3.14E+00	1.90E-06	-8.65E-01	1.15E-03	2.27E+00	7.86E-06
497683074	XRE family transcriptional regulator	1.34E+01	-3.13E+00	4.47E-03	-1.98E+00	4.41E-02	1.16E+00	1.90E-01
497685015	hypothetical protein	1.09E+01	-3.13E+00	4.43E-06	-1.66E+00	1.32E-04	1.46E+00	2.21E-04
497684140	hypothetical protein	1.29E+01	-3.13E+00	3.42E-06	-1.45E+00	1.81E-04	1.68E+00	7.22E-05
490061383	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1.02E+01	-3.12E+00	4.03E-06	-3.98E+00	3.04E-06	-8.59E-01	2.93E-03
490055141	DNA-binding protein	1.45E+01	-3.10E+00	1.30E-05	-1.41E+00	1.02E-03	1.69E+00	3.37E-04
497683341	decarboxylase	1.10E+01	-3.08E+00	1.49E-05	-3.88E+00	8.55E-06	-8.00E-01	1.55E-02
490054600	hypothetical protein	1.43E+01	-3.07E+00	2.66E-05	-1.13E+00	6.27E-03	1.94E+00	3.54E-04
490054316	amino acid ABC transporter ATPase	1.35E+01	-3.07E+00	5.52E-05	-1.74E+00	1.53E-03	1.32E+00	5.32E-03
490051661	superoxide dismutase	1.46E+01	-3.05E+00	4.07E-03	5.43E-01	5.08E-01	3.59E+00	2.39E-03
497685044	hypothetical protein	1.30E+01	-3.05E+00	1.87E-06	-2.51E+00	6.07E-06	5.39E-01	8.46E-03
497685442	acetyltransferase	1.19E+01	-3.04E+00	3.68E-05	-1.47E+00	2.30E-03	1.57E+00	1.42E-03
490059556	ABC-type dipeptide transport system, solute-binding protein	1.28E+01	-3.03E+00	4.04E-06	-2.35E+00	2.02E-05	6.82E-01	8.05E-03
497683348	isopenicillin N-epimerase	1.12E+01	-3.03E+00	4.47E-06	-1.75E+00	9.22E-05	1.29E+00	3.84E-04
490058785	membrane protein	1.29E+01	-3.02E+00	5.74E-05	1.52E-01	6.64E-01	3.18E+00	5.47E-05
497682291	hypothetical protein	1.26E+01	-3.01E+00	1.09E-02	2.07E+00	6.40E-02	5.08E+00	1.16E-03
490056746	hypothetical protein	1.22E+01	-3.00E+00	1.87E-06	-2.89E+00	3.94E-06	1.08E-01	4.93E-01

490052474	glyoxalase/bleomycin resistance protein/dioxygenase	1.35E+01	-2.99E+00	1.54E-04	-3.03E+00	2.13E-04	-3.80E-02	9.28E-01
490059210	NADH dehydrogenase subunit F	1.43E+01	-2.99E+00	2.69E-06	-5.54E-01	1.18E-02	2.43E+00	6.85E-06
490050055	hypothetical protein	1.37E+01	-2.97E+00	6.94E-06	-2.37E-01	2.95E-01	2.73E+00	1.28E-05
497682610	transcriptional regulator	1.27E+01	-2.96E+00	1.09E-04	-9.56E-01	3.47E-02	2.01E+00	1.05E-03
490055006	oxidoreductase	1.43E+01	-2.95E+00	2.63E-06	-3.26E+00	3.17E-06	-3.03E-01	9.45E-02
490052906	alkyl hydroperoxide reductase	1.42E+01	-2.95E+00	2.79E-06	-2.22E+00	1.49E-05	7.31E-01	3.03E-03
490050156	N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase	1.25E+01	-2.94E+00	1.32E-06	-2.12E+00	5.07E-06	8.18E-01	3.09E-04
490053887	NADH:ubiquinone oxidoreductase subunit H	1.43E+01	-2.94E+00	6.71E-04	-2.33E+00	3.32E-03	6.12E-01	2.73E-01
490051270	aldehyde dehydrogenase	1.32E+01	-2.92E+00	1.57E-04	-1.04E+00	3.19E-02	1.88E+00	1.98E-03
490060320	hypothetical protein	1.21E+01	-2.92E+00	4.44E-06	-2.03E+00	3.73E-05	8.94E-01	2.05E-03
497684412	hypothetical protein	1.49E+01	-2.92E+00	1.78E-05	-4.25E+00	5.83E-06	-1.33E+00	1.27E-03
490055025	hypothetical protein	1.27E+01	-2.92E+00	8.11E-06	-1.71E+00	1.66E-04	1.20E+00	9.07E-04
490054479	ATP-binding protein	1.34E+01	-2.91E+00	8.85E-04	1.07E+00	8.70E-02	3.98E+00	2.23E-04
497684722	translation initiation factor 2	1.33E+01	-2.91E+00	3.40E-06	-2.37E+00	1.34E-05	5.42E-01	1.46E-02
490050309	hypothetical protein	1.04E+01	-2.91E+00	1.57E-05	-3.64E+00	9.05E-06	-7.38E-01	1.80E-02
490050168	cytochrome P450	1.35E+01	-2.90E+00	2.71E-06	-2.08E+00	1.73E-05	8.24E-01	1.40E-03
497685451	hydrolase	1.47E+01	-2.90E+00	6.56E-06	-1.85E+00	8.76E-05	1.05E+00	1.38E-03
497683335	biotin carboxylase	1.18E+01	-2.89E+00	2.69E-06	-2.84E+00	5.07E-06	4.93E-02	7.67E-01
497684483	cysteine desulfurase, SufS subfamily protein	1.18E+01	-2.89E+00	6.06E-04	-4.23E+00	1.27E-04	-1.34E+00	2.95E-02
497682512	ABC transporter substrate-binding protein	1.11E+01	-2.89E+00	2.17E-05	-2.24E+00	1.16E-04	6.50E-01	3.86E-02
490059927	ABC transporter substrate-binding protein	1.31E+01	-2.88E+00	4.69E-06	-4.33E-02	8.31E-01	2.84E+00	6.51E-06
490050986	monooxygenase	1.03E+01	-2.88E+00	1.78E-05	-2.95E+00	2.49E-05	-7.16E-02	7.84E-01
490057028	Germacradienol/germacrene D synthase	1.24E+01	-2.87E+00	2.11E-05	-1.96E+00	2.13E-04	9.11E-01	8.95E-03
490050956	short-chain dehydrogenase	1.44E+01	-2.86E+00	1.14E-05	-1.64E+00	2.71E-04	1.23E+00	1.08E-03
490057622	phenoxazinone synthase	1.16E+01	-2.82E+00	2.70E-05	-1.77E+00	4.41E-04	1.06E+00	5.39E-03
490060252	histidine kinase	9.56E+00	-2.82E+00	5.67E-04	-2.41E+00	1.90E-03	4.05E-01	4.29E-01
490059168	ABC transporter ATP-binding protein	1.13E+01	-2.81E+00	4.44E-06	-1.24E-01	5.15E-01	2.69E+00	6.66E-06
497685222	DNA-binding protein	1.24E+01	-2.80E+00	1.67E-06	-3.28E+00	1.68E-06	-4.73E-01	7.42E-03
490059697	FAD-dependent monooxygenase	1.23E+01	-2.80E+00	4.69E-06	-3.31E+00	5.07E-06	-5.08E-01	2.52E-02
490059531	histidine kinase	1.38E+01	-2.79E+00	4.63E-05	6.83E-01	5.19E-02	3.48E+00	1.98E-05
497684897	hypothetical protein	1.16E+01	-2.79E+00	4.03E-06	-3.17E+00	5.07E-06	-3.78E-01	5.94E-02
490051359	conserved hypothetical protein	1.25E+01	-2.79E+00	3.56E-05	-2.96E+00	4.05E-05	-1.71E-01	5.57E-01

490058506	histidyl-tRNA synthetase	1.31E+01	-2.78E+00	2.69E-05	-8.07E-01	1.81E-02	1.98E+00	1.94E-04
490057367	ATP-binding protein	1.51E+01	-2.77E+00	1.02E-05	-3.35E-01	1.57E-01	2.44E+00	2.27E-05
490050677	short-chain dehydrogenase	1.16E+01	-2.77E+00	6.10E-06	-1.81E+00	6.86E-05	9.59E-01	1.58E-03
497681233	histidine kinase	1.31E+01	-2.76E+00	4.53E-06	-1.41E+00	1.74E-04	1.35E+00	1.84E-04
490060439	hypothetical protein	1.37E+01	-2.75E+00	1.30E-04	-2.21E+00	5.83E-04	5.36E-01	1.66E-01
490050174	hypothetical protein	1.40E+01	-2.74E+00	1.67E-06	-1.35E+00	3.92E-05	1.39E+00	2.78E-05
490057416	histidine kinase	1.30E+01	-2.72E+00	1.87E-06	-4.57E-01	1.16E-02	2.26E+00	4.39E-06
490057652	ATP/GTP-binding protein	1.41E+01	-2.72E+00	6.93E-06	-3.25E+00	5.83E-06	-5.35E-01	2.53E-02
497682964	chorismate mutase	1.25E+01	-2.72E+00	1.14E-05	-1.62E+00	2.19E-04	1.10E+00	1.41E-03
490053886	NADH dehydrogenase subunit G	1.30E+01	-2.71E+00	2.35E-06	-2.20E+00	8.24E-06	5.16E-01	8.32E-03
490052939	hypothetical protein	1.44E+01	-2.71E+00	1.86E-06	-5.77E-01	3.36E-03	2.13E+00	4.84E-06
490057877	tryptophan synthase subunit alpha	1.45E+01	-2.71E+00	6.82E-05	-2.56E+00	1.34E-04	1.48E-01	6.46E-01
497682597	XRE family transcriptional regulator	1.22E+01	-2.70E+00	2.76E-05	-1.00E+00	6.34E-03	1.70E+00	3.87E-04
490057051	Biotin carboxylase	1.32E+01	-2.70E+00	2.11E-05	-2.81E+00	2.77E-05	-1.06E-01	6.78E-01
490050167	oxidoreductase	1.35E+01	-2.70E+00	3.01E-05	-2.60E+00	5.53E-05	1.02E-01	7.10E-01
497683559	TerD-family protein	1.39E+01	-2.67E+00	1.17E-05	-2.17E+00	4.81E-05	5.04E-01	4.50E-02
490057035	alpha/beta hydrolase	1.40E+01	-2.67E+00	4.16E-06	-2.43E+00	1.04E-05	2.35E-01	1.96E-01
490050882	endoribonuclease	1.36E+01	-2.66E+00	3.93E-06	-2.93E+00	5.07E-06	-2.72E-01	1.32E-01
490058590	XRE family transcriptional regulator	1.26E+01	-2.65E+00	1.06E-03	-7.51E-01	1.83E-01	1.90E+00	7.20E-03
497683347	putative regulatory protein (AfsR-like protein)	1.52E+01	-2.64E+00	8.11E-06	-2.57E+00	1.59E-05	7.25E-02	7.22E-01
490050756	flavodoxin	1.26E+01	-2.63E+00	4.09E-06	-1.95E+00	2.49E-05	6.86E-01	4.04E-03
497685343	hypothetical protein	1.54E+01	-2.63E+00	1.99E-06	-7.17E-01	1.28E-03	1.91E+00	8.05E-06
490050764	conserved hypothetical protein	1.41E+01	-2.63E+00	4.60E-06	-5.89E-01	1.09E-02	2.04E+00	1.89E-05
490054137	50S ribosomal protein L18	1.40E+01	-2.62E+00	2.52E-03	-1.79E+00	2.07E-02	8.30E-01	2.03E-01
490056851	hypothetical protein	1.36E+01	-2.59E+00	1.67E-06	-1.92E+00	7.21E-06	6.77E-01	8.95E-04
490050989	diadenosine tetraphosphatase	1.26E+01	-2.59E+00	1.42E-03	-1.50E+00	2.52E-02	1.09E+00	7.38E-02
490061312	alkylhydroperoxidase	1.06E+01	-2.58E+00	2.79E-06	-3.56E+00	1.81E-06	-9.83E-01	3.26E-04
490059693	cytochrome P450	1.26E+01	-2.57E+00	1.67E-06	-2.94E+00	1.81E-06	-3.69E-01	1.59E-02
490052686	hypothetical protein	1.51E+01	-2.57E+00	1.33E-04	-1.16E+00	1.03E-02	1.41E+00	3.79E-03
490050881	cytochrome P450	1.31E+01	-2.57E+00	3.03E-03	-1.96E+00	1.53E-02	6.11E-01	3.50E-01
490060513	terpene synthase	1.25E+01	-2.57E+00	4.16E-06	-1.65E+00	4.76E-05	9.13E-01	8.62E-04
490060901	hypothetical protein	1.20E+01	-2.56E+00	1.99E-06	-2.65E+00	3.17E-06	-8.39E-02	5.40E-01

490060633	hypothetical protein	1.51E+01	-2.55E+00	4.16E-06	-6.50E-01	5.31E-03	1.90E+00	1.95E-05
497682943	hydrolase	1.43E+01	-2.54E+00	1.47E-03	-2.37E+00	3.10E-03	1.64E-01	7.67E-01
490058852	Hypothetical protein	1.35E+01	-2.54E+00	7.44E-05	1.99E+00	3.79E-04	4.53E+00	5.94E-06
490053438	adenine phosphoribosyltransferase	1.22E+01	-2.53E+00	3.86E-06	-3.19E+00	3.04E-06	-6.53E-01	3.70E-03
490060205	oxidoreductase	1.35E+01	-2.53E+00	4.16E-06	-2.54E+00	7.16E-06	-1.48E-02	9.29E-01
490052722	ornithine cyclodeaminase	1.33E+01	-2.52E+00	2.04E-05	-1.62E+00	2.85E-04	9.07E-01	4.84E-03
490050159	PbsX family transcriptional regulator	1.38E+01	-2.52E+00	3.03E-06	-2.45E+00	5.79E-06	7.16E-02	6.35E-01
490052605	RNA polymerase sigma70 factor	1.16E+01	-2.48E+00	2.19E-06	-1.70E-01	2.28E-01	2.31E+00	3.74E-06
490055938	hypothetical protein	1.15E+01	-2.48E+00	4.40E-05	-8.16E-01	1.58E-02	1.66E+00	4.38E-04
490057023	regulatory protein	1.28E+01	-2.47E+00	1.39E-05	-2.75E-01	2.15E-01	2.20E+00	2.98E-05
490060062	3-oxoadipate enol-lactonase	1.25E+01	-2.47E+00	1.91E-04	-1.10E+00	1.52E-02	1.37E+00	5.07E-03
497681148	hypothetical protein	1.47E+01	-2.47E+00	2.28E-05	-7.68E-01	1.15E-02	1.70E+00	1.88E-04
497681010	dihydroxyacetone kinase subunit K	1.31E+01	-2.46E+00	1.87E-06	5.22E-01	4.17E-03	2.98E+00	1.58E-06
490054981	aldehyde dehydrogenase	1.17E+01	-2.46E+00	7.43E-06	-1.33E+00	2.26E-04	1.13E+00	4.76E-04
490057118	N-acetyltransferase GCN5	1.45E+01	-2.45E+00	9.38E-06	-1.43E+00	2.00E-04	1.02E+00	9.85E-04
490060508	nitroreductase	1.36E+01	-2.44E+00	7.55E-04	1.18E-02	9.80E-01	2.46E+00	9.77E-04
490058329	amidase	1.27E+01	-2.43E+00	2.24E-04	7.21E-01	7.58E-02	3.15E+00	7.35E-05
497685110	5,10-methylenetetrahydromethanopterin reductase	1.32E+01	-2.43E+00	6.27E-06	-2.51E+00	9.05E-06	-8.16E-02	6.44E-01
497685093	1,4-dihydropyridine enantioselective esterase	1.04E+01	-2.43E+00	6.60E-04	-4.31E+00	5.24E-05	-1.89E+00	3.13E-03
490059211	(4Fe-4S)-binding protein	1.35E+01	-2.43E+00	1.35E-05	-2.51E+00	1.85E-05	-8.81E-02	6.71E-01
497682747	hypothetical protein	1.34E+01	-2.42E+00	2.79E-06	-1.02E+00	2.17E-04	1.40E+00	3.66E-05
490060435	hypothetical protein	1.16E+01	-2.42E+00	2.44E-04	-1.38E+00	6.28E-03	1.04E+00	1.96E-02
490059700	amidase	1.27E+01	-2.42E+00	4.03E-03	-1.98E+00	1.45E-02	4.36E-01	4.98E-01
497684135	hypothetical protein	1.32E+01	-2.41E+00	8.11E-06	-1.79E+00	5.11E-05	6.22E-01	9.10E-03
497682392	hypothetical protein	1.37E+01	-2.40E+00	1.90E-06	-4.05E-01	1.23E-02	2.00E+00	4.72E-06
490050778	lipid hydroperoxide peroxidase	1.26E+01	-2.40E+00	6.46E-04	-3.75E+00	9.70E-05	-1.35E+00	1.39E-02
497684051	carbon starvation protein CstA	1.44E+01	-2.40E+00	3.93E-06	-2.69E-01	1.08E-01	2.13E+00	7.86E-06
490051946	hypothetical protein	1.07E+01	-2.40E+00	1.20E-04	-2.73E+00	9.04E-05	-3.31E-01	3.05E-01
490060317	glucose-methanol-choline oxidoreductase	1.41E+01	-2.39E+00	6.08E-06	-1.98E+00	2.34E-05	4.15E-01	3.61E-02
490052143	cytochrome P450	1.13E+01	-2.39E+00	3.93E-06	-4.08E+00	1.24E-06	-1.69E+00	2.13E-05
490055290	hypothetical protein	1.49E+01	-2.39E+00	5.12E-06	1.16E-01	4.91E-01	2.50E+00	5.57E-06
490058978	phosphate ABC transporter ATP-binding protein	1.25E+01	-2.38E+00	2.71E-06	-4.70E-01	9.27E-03	1.91E+00	7.63E-06

497682848	TetR family transcriptional regulator	1.27E+01	-2.37E+00	1.13E-03	-2.72E+00	8.42E-04	-3.44E-01	4.81E-01
497681172	putative ferrodoxin oxidoreductase alpha subunit, partial	1.38E+01	-2.37E+00	4.41E-04	-4.68E+00	2.30E-05	-2.31E+00	6.57E-04
497685139	peptidoglycan-binding protein	1.34E+01	-2.36E+00	2.83E-06	-1.32E+00	5.57E-05	1.05E+00	1.48E-04
490059171	N5,N10-methylenetetrahydromethanopterin reductase	9.09E+00	-2.36E+00	7.64E-05	-1.65E+00	7.10E-04	7.12E-01	3.25E-02
490055074	peptidase dimerization protein	1.09E+01	-2.36E+00	6.86E-04	-1.22E+00	2.28E-02	1.14E+00	2.74E-02
497684117	hypothetical protein	1.31E+01	-2.36E+00	3.93E-06	-2.33E+00	7.10E-06	2.95E-02	8.44E-01
490059698	lipase	1.30E+01	-2.35E+00	3.46E-03	-2.06E+00	9.42E-03	2.91E-01	6.32E-01
490059209	NADH dehydrogenase subunit D	1.20E+01	-2.35E+00	3.62E-04	1.90E-01	6.26E-01	2.54E+00	3.11E-04
490056066	N-acetylglutamate synthase	1.27E+01	-2.35E+00	1.14E-05	-2.44E+00	1.64E-05	-9.23E-02	6.34E-01
490059675	membrane protein	1.28E+01	-2.35E+00	1.83E-04	3.50E-01	3.12E-01	2.70E+00	1.11E-04
490057355	hypothetical protein	1.30E+01	-2.34E+00	4.60E-06	-2.11E+00	1.29E-05	2.31E-01	1.64E-01
497683661	hypothetical protein	1.36E+01	-2.34E+00	3.76E-06	-2.77E+00	3.75E-06	-4.31E-01	1.70E-02
490052942	magnesium or manganese-dependent protein phosphatase	1.21E+01	-2.34E+00	8.83E-06	-2.46E+00	1.23E-05	-1.17E-01	5.24E-01
490053882	NADH dehydrogenase subunit C	1.48E+01	-2.33E+00	8.00E-05	-6.73E-01	4.22E-02	1.66E+00	5.95E-04
490051696	ABC transporter permease	1.14E+01	-2.33E+00	6.15E-06	-2.90E+00	5.07E-06	-5.72E-01	8.66E-03
497683989	SAM-dependent methyltransferase	1.31E+01	-2.32E+00	1.08E-05	-3.08E+00	5.79E-06	-7.53E-01	4.12E-03
490059601	glycosyltransferase family 1	1.48E+01	-2.32E+00	2.28E-05	-2.54E+00	2.39E-05	-2.15E-01	3.40E-01
490057052	Arginase/agmatinase/formiminoglutamase	1.33E+01	-2.32E+00	3.33E-06	-1.67E+00	2.13E-05	6.45E-01	2.12E-03
490050721	hypothetical protein	1.79E+01	-2.31E+00	2.43E-05	2.04E-01	3.71E-01	2.52E+00	2.04E-05
490051932	hypothetical protein	9.85E+00	-2.31E+00	6.85E-03	-1.89E+00	2.32E-02	4.20E-01	5.42E-01
490057070	histidine kinase	1.25E+01	-2.31E+00	2.95E-05	3.18E-01	1.92E-01	2.63E+00	2.00E-05
497684912	aminotransferase	1.30E+01	-2.30E+00	6.14E-06	-3.04E+00	4.11E-06	-7.39E-01	2.35E-03
490055964	septum formation initiator	1.08E+01	-2.30E+00	7.89E-04	-4.77E-01	2.92E-01	1.83E+00	3.38E-03
490059323	transferase	1.48E+01	-2.30E+00	1.37E-04	-2.37E+00	1.74E-04	-6.96E-02	8.23E-01
497683312	dimethylallyltranstransferase	1.13E+01	-2.27E+00	2.91E-04	1.08E+00	1.59E-02	3.36E+00	4.82E-05
490057169	hypothetical protein	1.02E+01	-2.27E+00	9.65E-05	-2.75E+00	5.41E-05	-4.83E-01	1.16E-01
490055968	secretion protein	1.31E+01	-2.27E+00	6.36E-06	-5.08E-01	1.49E-02	1.76E+00	2.61E-05
497681151	hypothetical protein	1.13E+01	-2.26E+00	4.34E-06	5.46E-01	7.13E-03	2.81E+00	2.62E-06
490060065	gamma-glutamyltransferase	1.40E+01	-2.25E+00	1.21E-03	-1.28E+00	2.43E-02	9.73E-01	6.07E-02
497682033	putative gamma-aminobutyrate permease	1.43E+01	-2.25E+00	4.76E-03	2.18E+00	8.07E-03	4.42E+00	1.94E-04
490052842	hypothetical protein	1.24E+01	-2.25E+00	2.33E-04	-4.06E-01	2.47E-01	1.84E+00	8.63E-04
490059695	short-chain dehydrogenase	1.26E+01	-2.24E+00	4.21E-06	-1.71E+00	2.28E-05	5.27E-01	7.01E-03

497684011	GDP-mannose 6-dehydrogenase	1.23E+01	-2.24E+00	7.36E-05	-3.13E+00	2.27E-05	-8.92E-01	9.80E-03
497685398	hypothetical protein	1.59E+01	-2.24E+00	4.21E-05	-2.01E+00	1.07E-04	2.22E-01	3.64E-01
497681011	dihydroxyacetone kinase subunit DhaL	1.05E+01	-2.22E+00	1.70E-04	-3.90E-01	2.34E-01	1.83E+00	5.96E-04
497685105	amidohydrolase	1.39E+01	-2.22E+00	3.74E-05	-7.06E-01	1.62E-02	1.51E+00	3.42E-04
490051269	hypothetical protein	1.03E+01	-2.22E+00	3.93E-06	5.59E-01	4.75E-03	2.78E+00	2.49E-06
490054247	membrane protein	1.36E+01	-2.22E+00	2.17E-05	1.39E+00	3.49E-04	3.60E+00	3.58E-06
490053891	NADH:ubiquinone oxidoreductase subunit L	1.22E+01	-2.21E+00	2.92E-03	-2.26E+00	3.96E-03	-4.74E-02	9.31E-01
490050162	proclavaminate amidinohydrolase	9.99E+00	-2.20E+00	2.66E-04	-6.01E-01	1.06E-01	1.60E+00	1.82E-03
490059534	ATP/GTP-binding protein	1.20E+01	-2.20E+00	1.48E-04	-1.36E+00	2.62E-03	8.40E-01	2.15E-02
497683462	histidine kinase	1.34E+01	-2.20E+00	4.60E-06	-2.55E+00	5.07E-06	-3.46E-01	4.23E-02
490059408	L-glyceraldehyde 3-phosphate reductase	1.50E+01	-2.20E+00	3.93E-06	-3.76E-01	2.70E-02	1.82E+00	1.08E-05
497682104	ATP-dependent helicase	1.30E+01	-2.20E+00	3.97E-05	-2.37E+00	4.17E-05	-1.72E-01	4.68E-01
490059942	hypothetical protein	1.23E+01	-2.19E+00	2.43E-05	-2.78E+00	1.39E-05	-5.96E-01	1.99E-02
490051231	membrane protein	1.36E+01	-2.19E+00	3.74E-05	-6.18E-01	2.63E-02	1.57E+00	2.61E-04
490054320	branched-chain amino acid ABC transporter substrate-binding protein	1.19E+01	-2.18E+00	2.56E-05	-1.51E+00	2.46E-04	6.71E-01	1.25E-02
490052490	molybdenum cofactor biosynthesis protein MoaD	1.34E+01	-2.17E+00	5.51E-04	-4.38E+00	2.49E-05	-2.22E+00	6.42E-04
490052791	transcriptional regulator	1.40E+01	-2.16E+00	1.90E-05	-1.87E+00	5.82E-05	2.97E-01	1.54E-01
490061466	hypothetical protein	1.48E+01	-2.15E+00	7.44E-05	-2.93E-01	2.74E-01	1.86E+00	1.96E-04
490053291	ABC transporter substrate-binding protein	1.30E+01	-2.15E+00	3.10E-03	-1.87E+00	8.92E-03	2.82E-01	6.03E-01
490057875	membrane protein	1.37E+01	-2.13E+00	4.38E-03	2.45E+00	3.37E-03	4.58E+00	1.11E-04
490058912	amidohydrolase	1.38E+01	-2.12E+00	1.39E-05	-1.74E+00	5.43E-05	3.85E-01	5.75E-02
497683687	ATP-binding protein	9.36E+00	-2.11E+00	1.30E-05	-6.39E-01	7.62E-03	1.47E+00	9.39E-05
497683124	Fis family transcriptional regulator	1.30E+01	-2.11E+00	1.70E-05	-1.48E+00	1.42E-04	6.27E-01	9.53E-03
490059888	hypothetical protein	1.29E+01	-2.10E+00	4.46E-05	-2.65E+00	2.31E-05	-5.43E-01	3.89E-02
490059603	radical SAM protein	1.31E+01	-2.10E+00	4.23E-04	-3.26E+00	6.61E-05	-1.16E+00	1.04E-02
490054344	pseudouridine-5'-phosphate glycosidase	1.35E+01	-2.10E+00	2.79E-06	-5.82E-01	1.88E-03	1.52E+00	1.27E-05
497685291	methyltransferase	1.20E+01	-2.09E+00	1.55E-04	-1.58E+00	9.71E-04	5.07E-01	1.05E-01
497683391	hypothetical protein	1.17E+01	-2.08E+00	4.44E-06	-8.56E-01	5.17E-04	1.23E+00	6.68E-05
490050164	glutamate N-acetyltransferase 2	1.34E+01	-2.08E+00	7.08E-06	-3.80E-01	3.67E-02	1.70E+00	2.27E-05
490060995	F420-dependent oxidoreductase	1.25E+01	-2.07E+00	1.77E-04	-1.98E+00	3.35E-04	9.34E-02	7.54E-01
490057888	cytochrome P450	1.11E+01	-2.05E+00	3.68E-05	-1.71E+00	1.39E-04	3.47E-01	1.30E-01
497685457	hypothetical protein	1.54E+01	-2.05E+00	1.33E-04	-8.45E-02	7.67E-01	1.97E+00	2.07E-04

490054846	membrane protein	1.49E+01	-2.04E+00	1.09E-02	-1.95E+00	1.89E-02	8.97E-02	8.93E-01
490051901	hypothetical protein	1.49E+01	-2.03E+00	7.60E-05	-7.84E-01	1.27E-02	1.25E+00	1.23E-03
490054419	chemotaxis protein CheY	1.34E+01	-2.03E+00	6.63E-05	-2.92E-01	2.40E-01	1.74E+00	1.84E-04
490059955	beta-glucosidase	1.47E+01	-2.03E+00	1.08E-05	3.95E-01	3.97E-02	2.42E+00	6.05E-06
490060509	hypothetical protein	1.15E+01	-2.03E+00	4.93E-05	-1.77E+00	1.44E-04	2.53E-01	2.75E-01
490051909	deaminase reductase	1.35E+01	-2.02E+00	3.11E-05	-3.58E+00	5.07E-06	-1.55E+00	1.48E-04
490058834	penicillin-binding protein	1.30E+01	-2.01E+00	4.08E-04	-1.14E+00	1.01E-02	8.76E-01	2.81E-02
490056694	GntR family transcriptional regulator	1.35E+01	-2.01E+00	1.28E-03	-3.04E+00	2.22E-04	-1.03E+00	3.40E-02
490056047	O-methyltransferase	1.43E+01	-2.00E+00	3.30E-05	-3.53E+00	5.07E-06	-1.53E+00	1.65E-04
490056409	hypothetical protein	1.37E+01	-2.00E+00	1.91E-04	-5.64E-01	8.01E-02	1.44E+00	1.40E-03
490060993	esterase	1.49E+01	-2.00E+00	3.36E-05	-7.32E-01	8.00E-03	1.27E+00	4.54E-04
490057319	1-acyl-sn-glycerol-3-phosphate acyltransferase	1.51E+01	-2.00E+00	1.20E-04	-4.83E-01	9.42E-02	1.51E+00	6.43E-04
497681584	DNA-binding protein	1.42E+01	-1.99E+00	1.14E-05	-4.00E-01	3.74E-02	1.59E+00	4.05E-05
490051891	hypothetical protein	1.47E+01	-1.98E+00	6.92E-06	-1.28E+00	8.61E-05	7.06E-01	1.60E-03
490059527	Lon protease	1.30E+01	-1.98E+00	5.73E-05	-2.78E+00	1.84E-05	-7.96E-01	7.67E-03
497683809	glutamine amidotransferase	1.30E+01	-1.98E+00	7.15E-04	-2.30E+00	4.90E-04	-3.20E-01	3.97E-01
497681088	UDP-N-acetylglucosamine 2-epimerase	1.30E+01	-1.97E+00	2.00E-05	-3.07E+00	5.34E-06	-1.10E+00	4.95E-04
490057075	antibiotic resistance macrolide glycosyltransferase	1.42E+01	-1.97E+00	8.11E-06	-1.52E+00	4.30E-05	4.53E-01	1.54E-02
490058790	IclR family transcriptional regulator	1.23E+01	-1.97E+00	1.35E-03	-1.82E+00	2.95E-03	1.43E-01	7.33E-01
490059102	glycosyl transferase	1.32E+01	-1.96E+00	1.23E-04	-1.16E+00	2.72E-03	8.02E-01	1.38E-02
490055729	glutamine amidotransferase	1.35E+01	-1.96E+00	6.01E-05	2.60E-01	2.67E-01	2.22E+00	3.96E-05
490053097	conserved hypothetical protein	1.25E+01	-1.96E+00	1.08E-03	-1.97E+00	1.53E-03	-1.64E-02	9.67E-01
490057490	heme peroxidase	1.32E+01	-1.95E+00	2.68E-04	-1.74E+00	7.28E-04	2.11E-01	4.91E-01
490055317	AsnC family transcriptional regulator	1.37E+01	-1.94E+00	1.49E-05	-1.48E+00	8.36E-05	4.68E-01	2.14E-02
497685273	hypothetical protein	1.35E+01	-1.94E+00	5.45E-05	3.32E-01	1.58E-01	2.28E+00	3.12E-05
490052367	cold-shock protein	1.27E+01	-1.94E+00	7.81E-04	-3.80E+00	3.84E-05	-1.87E+00	1.26E-03
490056027	hypothetical protein	1.27E+01	-1.93E+00	1.89E-04	-2.49E+00	7.70E-05	-5.59E-01	6.96E-02
497682770	hypothetical protein	1.13E+01	-1.93E+00	1.92E-05	1.19E+00	3.22E-04	3.12E+00	3.24E-06
497682129	IclR family transcriptional regulator	1.52E+01	-1.93E+00	3.86E-05	-1.86E+00	6.86E-05	6.58E-02	7.49E-01
490054317	branched-chain amino acid ABC transporter ATP-binding protein	1.23E+01	-1.93E+00	7.67E-04	-1.93E+00	1.15E-03	-2.31E-04	9.99E-01
490058239	hypothetical protein	1.22E+01	-1.93E+00	1.02E-05	-1.76E+00	2.44E-05	1.64E-01	2.98E-01
490059034	diguanylate cyclase	1.10E+01	-1.93E+00	8.86E-06	-1.50E+00	4.39E-05	4.28E-01	1.91E-02

490050995	hypothetical protein	1.31E+01	-1.92E+00	2.17E-05	9.49E-02	6.05E-01	2.02E+00	2.14E-05
490051281	maltose O-acetyltransferase	1.39E+01	-1.92E+00	2.32E-05	8.89E-01	1.77E-03	2.81E+00	5.46E-06
497684131	hypothetical protein	1.33E+01	-1.92E+00	1.54E-05	-3.56E+00	2.70E-06	-1.64E+00	3.96E-05
490059933	3'-5' exonuclease	1.22E+01	-1.91E+00	4.80E-05	-2.50E+00	2.13E-05	-5.91E-01	2.08E-02
497682351	protein-L-isoaspartate O-methyltransferase	1.28E+01	-1.90E+00	2.68E-04	-3.06E+00	3.74E-05	-1.16E+00	4.57E-03
490061125	precorrin 6A synthase	1.45E+01	-1.90E+00	2.29E-05	-3.42E-01	8.72E-02	1.56E+00	7.62E-05
490058396	hypothetical protein	1.50E+01	-1.89E+00	2.32E-05	-1.10E+00	5.38E-04	7.88E-01	2.67E-03
490058078	Putative integral membrane protein	1.77E+01	-1.89E+00	2.11E-05	-1.50E+00	9.91E-05	3.87E-01	5.20E-02
490050149	deacetoxycephalosporin C hydroxylase	1.36E+01	-1.89E+00	3.14E-04	-1.60E+00	1.10E-03	2.84E-01	3.55E-01
490050729	peptidoglycan bridge formation protein FemAB	1.03E+01	-1.88E+00	1.02E-05	-1.68E+00	2.66E-05	1.99E-01	2.03E-01
490055475	methionyl-tRNA formyltransferase	1.18E+01	-1.88E+00	5.01E-05	-6.58E-01	1.38E-02	1.22E+00	5.97E-04
490057415	dynein regulation protein LC7	1.34E+01	-1.88E+00	2.55E-04	-3.05E+00	3.37E-05	-1.18E+00	3.69E-03
490050636	conserved hypothetical protein	9.29E+00	-1.88E+00	1.28E-04	-3.00E+00	2.05E-05	-1.12E+00	2.32E-03
490050890	hypothetical protein	1.13E+01	-1.86E+00	4.25E-03	-2.72E+00	9.41E-04	-8.63E-01	1.06E-01
490046206	whiK	1.45E+01	-1.86E+00	2.04E-05	2.27E+00	1.39E-05	4.13E+00	1.57E-06
490051916	hypothetical protein	1.23E+01	-1.84E+00	5.02E-05	-1.05E+00	1.33E-03	7.89E-01	5.03E-03
497681807	alpha-N-acetylglucosaminidase	1.45E+01	-1.84E+00	5.24E-05	1.82E-01	3.86E-01	2.02E+00	4.02E-05
490053431	oxidoreductase	1.41E+01	-1.83E+00	3.10E-05	-2.17E+00	2.28E-05	-3.31E-01	9.94E-02
497683955	Galactose oxidase	1.37E+01	-1.83E+00	4.82E-05	-2.22E+00	2.91E-05	-3.92E-01	7.75E-02
490059039	aldehyde dehydrogenase	1.27E+01	-1.82E+00	1.71E-05	-5.00E-01	1.49E-02	1.32E+00	1.02E-04
490061208	acetyltransferase	1.47E+01	-1.82E+00	2.57E-04	-1.60E+00	7.45E-04	2.18E-01	4.42E-01
490056114	cytidylate kinase	1.36E+01	-1.82E+00	2.57E-04	-2.34E+00	1.06E-04	-5.20E-01	8.68E-02
490058973	membrane protein	1.53E+01	-1.81E+00	6.18E-06	3.41E-01	2.92E-02	2.16E+00	4.06E-06
490051924	hypothetical protein	1.26E+01	-1.81E+00	1.87E-05	-2.30E-01	1.85E-01	1.58E+00	4.38E-05
490051830	conserved hypothetical protein	1.44E+01	-1.81E+00	4.93E-04	-8.64E-01	2.44E-02	9.47E-01	1.55E-02
497685246	hypothetical protein	1.39E+01	-1.80E+00	1.31E-04	-2.67E+00	2.83E-05	-8.71E-01	6.86E-03
490054938	peptidase C45	1.32E+01	-1.79E+00	6.95E-06	-2.32E+00	5.07E-06	-5.28E-01	4.29E-03
490061238	3-ketoacyl-ACP reductase	1.34E+01	-1.79E+00	5.02E-05	-1.16E+00	7.08E-04	6.35E-01	1.21E-02
490056384	LuxR family transcriptional regulator	1.50E+01	-1.79E+00	5.87E-03	-3.24E+00	4.38E-04	-1.45E+00	1.94E-02
490054000	AMP-dependent synthetase	1.36E+01	-1.78E+00	1.80E-05	1.56E-01	3.45E-01	1.94E+00	1.49E-05
490058755	CRISPR-associated protein Cse4	1.46E+01	-1.78E+00	1.56E-04	-8.91E-01	7.49E-03	8.85E-01	6.99E-03
490055338	dynein regulation protein LC7	1.31E+01	-1.77E+00	1.49E-04	-2.69E+00	2.88E-05	-9.19E-01	5.58E-03

490055173	LuxR family transcriptional regulator	1.36E+01	-1.77E+00	9.21E-05	-1.59E+00	2.32E-04	1.79E-01	4.27E-01
490059598	nucleotide pyrophosphatase	1.34E+01	-1.77E+00	1.35E-05	1.57E-01	3.10E-01	1.93E+00	1.12E-05
490052798	hypothetical protein	1.43E+01	-1.77E+00	2.68E-05	-1.95E+00	2.66E-05	-1.81E-01	3.10E-01
490059075	membrane protein	1.41E+01	-1.77E+00	4.29E-05	-1.52E+00	1.35E-04	2.47E-01	2.12E-01
490056340	DSBA oxidoreductase	1.52E+01	-1.76E+00	5.08E-05	-8.45E-01	3.30E-03	9.18E-01	1.92E-03
497684177	hypothetical protein	1.38E+01	-1.75E+00	2.85E-05	-1.74E+00	4.43E-05	6.74E-03	9.69E-01
490056701	cytochrome P450	1.25E+01	-1.75E+00	1.33E-04	2.82E-01	2.49E-01	2.03E+00	7.53E-05
490052575	septum formation protein Maf	1.03E+01	-1.75E+00	2.21E-03	-4.92E+00	1.96E-05	-3.17E+00	1.29E-04
490057927	transcriptional regulator	1.51E+01	-1.74E+00	1.66E-04	-2.32E+00	5.72E-05	-5.80E-01	3.91E-02
490050144	deacetoxycephalosporin C synthetase	1.07E+01	-1.71E+00	3.30E-05	-2.92E+00	5.50E-06	-1.21E+00	2.50E-04
490052127	carbonate dehydratase	1.32E+01	-1.71E+00	2.72E-05	1.83E+00	3.10E-05	3.53E+00	2.03E-06
497681987	peptidase S41	1.32E+01	-1.70E+00	5.32E-04	-1.85E+00	5.09E-04	-1.54E-01	6.11E-01
490060251	ATP-binding protein	1.21E+01	-1.70E+00	6.12E-05	-1.10E+00	8.55E-04	5.96E-01	1.48E-02
490051122	alpha,alpha-trehalose-phosphate synthase	1.22E+01	-1.70E+00	9.66E-06	-1.49E+00	2.73E-05	2.05E-01	1.48E-01
490053246	FAD-linked oxidoreductase	1.43E+01	-1.69E+00	2.86E-05	-1.25E+00	2.05E-04	4.46E-01	2.62E-02
490061352	UDP-glucose 4-epimerase	1.22E+01	-1.69E+00	7.81E-06	7.37E-01	7.35E-04	2.43E+00	2.57E-06
490059032	sugar isomerase	1.24E+01	-1.69E+00	6.23E-03	-3.57E+00	2.12E-04	-1.88E+00	4.97E-03
490060889	luciferase	1.03E+01	-1.68E+00	1.21E-04	-3.18E+00	9.05E-06	-1.50E+00	2.72E-04
490055030	methyltransferase	1.38E+01	-1.67E+00	1.40E-05	-6.03E-01	3.51E-03	1.06E+00	1.61E-04
497684176	dihydrouridine synthase	1.42E+01	-1.66E+00	1.58E-05	-4.12E+00	1.11E-06	-2.46E+00	3.82E-06
490060104	alcohol dehydrogenase	1.28E+01	-1.65E+00	2.82E-04	-1.34E+00	1.24E-03	3.11E-01	2.45E-01
497683403	ATP-dependent DNA helicase	1.35E+01	-1.65E+00	1.77E-05	-2.08E-01	1.84E-01	1.45E+00	4.07E-05
497682751	hypothetical protein	1.44E+01	-1.65E+00	1.30E-04	-1.84E-02	9.38E-01	1.63E+00	1.71E-04
490054860	oxidoreductase	1.39E+01	-1.65E+00	1.09E-04	-2.29E+00	3.20E-05	-6.37E-01	1.57E-02
490050142	aldehyde dehydrogenase	8.97E+00	-1.65E+00	2.60E-05	-1.88E+00	2.27E-05	-2.34E-01	1.66E-01
490054198	thioredoxin	1.32E+01	-1.63E+00	1.87E-04	-2.45E+00	3.68E-05	-8.20E-01	7.91E-03
490057012	cation-binding protein	1.24E+01	-1.63E+00	2.96E-04	2.60E-01	3.23E-01	1.89E+00	1.75E-04
497685265	LuxR family transcriptional regulator	1.04E+01	-1.61E+00	2.70E-05	-2.69E+00	5.34E-06	-1.08E+00	2.72E-04
497683853	amidohydrolase	1.41E+01	-1.61E+00	1.77E-05	-1.37E+00	5.74E-05	2.42E-01	1.17E-01
497685350	oxidoreductase	1.36E+01	-1.61E+00	2.05E-04	-2.74E+00	2.30E-05	-1.13E+00	1.66E-03
490056765	conserved hypothetical protein	1.37E+01	-1.61E+00	1.50E-05	-2.77E+00	3.04E-06	-1.16E+00	9.03E-05
490050047	cellulose-binding protein	1.39E+01	-1.60E+00	1.55E-05	-7.45E-01	1.10E-03	8.58E-01	4.61E-04

490059388	hypothetical protein	1.43E+01	-1.58E+00	2.13E-04	-1.30E+00	8.81E-04	2.81E-01	2.47E-01
497685301	salicylate hydroxylase	1.41E+01	-1.57E+00	1.78E-05	-1.29E+00	6.94E-05	2.87E-01	6.72E-02
490059876	integral membrane protein	1.52E+01	-1.57E+00	4.69E-06	-7.58E-01	2.50E-04	8.11E-01	1.48E-04
490056065	N-acetyl-gamma-glutamyl-phosphate reductase	1.22E+01	-1.56E+00	1.40E-03	-4.83E-01	1.70E-01	1.08E+00	1.10E-02
497684029	2-amino-3-ketobutyrate CoA ligase	1.39E+01	-1.55E+00	6.22E-05	-1.96E+00	3.07E-05	-4.09E-01	4.62E-02
490058055	molecular chaperone GroES	1.31E+01	-1.54E+00	1.88E-04	-1.88E-01	4.05E-01	1.35E+00	4.78E-04
490051367	hypothetical protein	1.27E+01	-1.53E+00	1.48E-04	-1.44E+00	3.02E-04	9.25E-02	6.63E-01
497680901	cytochrome P450	1.27E+01	-1.53E+00	2.07E-03	1.00E-01	7.81E-01	1.63E+00	1.97E-03
497681909	hypothetical protein	1.35E+01	-1.53E+00	1.11E-05	-2.73E-01	5.46E-02	1.25E+00	3.44E-05
490054110	30S ribosomal protein S9	1.51E+01	-1.52E+00	5.63E-04	-4.80E-01	1.05E-01	1.04E+00	5.10E-03
497684175	hypothetical protein	1.40E+01	-1.52E+00	4.62E-04	-3.01E+00	2.37E-05	-1.49E+00	6.73E-04
490058075	antibiotic biosynthesis monooxygenase	1.47E+01	-1.51E+00	7.05E-03	-1.61E+00	7.88E-03	-9.16E-02	8.39E-01
490052166	apolipoprotein acyltransferase	1.23E+01	-1.51E+00	1.18E-04	1.52E-01	4.50E-01	1.67E+00	8.77E-05
490056214	hypothetical protein	1.49E+01	-1.51E+00	7.23E-04	-2.10E+00	2.01E-04	-5.84E-01	6.35E-02
490055439	adenosine deaminase	1.30E+01	-1.51E+00	2.42E-04	-9.45E-01	3.99E-03	5.65E-01	3.40E-02
497683449	hypothetical protein	1.23E+01	-1.50E+00	6.49E-04	-3.27E-01	2.51E-01	1.17E+00	3.00E-03
497683521	hypothetical protein	1.45E+01	-1.50E+00	5.28E-03	-3.21E-01	4.50E-01	1.18E+00	2.03E-02
490050212	alanine-phosphoribitol ligase	1.28E+01	-1.49E+00	5.16E-04	-2.07E+00	1.40E-04	-5.85E-01	4.84E-02
490057278	histidine kinase	1.24E+01	-1.48E+00	3.69E-05	-5.77E-01	6.63E-03	9.08E-01	5.97E-04
497685208	hypothetical protein	1.18E+01	-1.48E+00	1.96E-04	-7.61E-01	8.29E-03	7.20E-01	9.65E-03
490056091	hypothetical protein	1.03E+01	-1.47E+00	6.54E-04	-2.77E+00	4.04E-05	-1.29E+00	1.68E-03
490054313	hypothetical protein	1.45E+01	-1.47E+00	2.00E-05	-3.30E-01	3.82E-02	1.14E+00	8.65E-05
490051366	DNA mismatch repair protein	1.34E+01	-1.47E+00	2.11E-05	-1.51E+00	2.91E-05	-3.86E-02	7.80E-01
490056569	hypothetical protein	1.47E+01	-1.47E+00	4.73E-03	-5.70E-01	1.78E-01	8.98E-01	4.80E-02
490051113	fructose-bisphosphate aldolase	1.32E+01	-1.46E+00	9.24E-05	-7.59E-01	3.94E-03	7.05E-01	5.02E-03
490054101	guanylate kinase	1.51E+01	-1.46E+00	6.46E-04	-3.12E+00	2.28E-05	-1.66E+00	4.40E-04
490054966	membrane protein	1.56E+01	-1.46E+00	8.63E-05	-4.18E+00	2.02E-06	-2.72E+00	5.70E-06
490051447	hypothetical protein	1.39E+01	-1.46E+00	6.83E-04	-8.44E-01	1.43E-02	6.18E-01	4.51E-02
490050139	D-alanyl-D-alanine carboxypeptidase	1.22E+01	-1.46E+00	9.76E-05	-1.99E+00	3.20E-05	-5.28E-01	1.93E-02
497684079	hypothetical protein	1.41E+01	-1.46E+00	2.69E-05	-1.30E+00	7.13E-05	1.58E-01	2.84E-01
490057423	GntR family transcriptional regulator	1.54E+01	-1.45E+00	2.39E-04	-1.61E+00	2.10E-04	-1.59E-01	4.75E-01
490059462	ATP-binding protein	1.47E+01	-1.45E+00	3.94E-04	-3.11E+00	1.49E-05	-1.66E+00	2.49E-04

490052137	IclR family transcriptional regulator	1.43E+01	-1.44E+00	2.44E-05	-8.78E-02	5.35E-01	1.36E+00	4.10E-05
490056448	peptidase M48	1.41E+01	-1.44E+00	2.41E-03	-1.83E+00	1.06E-03	-3.91E-01	2.67E-01
490051727	NADP-dependent oxidoreductase	1.23E+01	-1.44E+00	1.30E-05	-2.03E+00	5.40E-06	-5.96E-01	1.44E-03
490051883	hypothetical protein	9.96E+00	-1.44E+00	1.19E-03	1.86E-01	5.35E-01	1.62E+00	8.37E-04
497682482	aminotransferase	1.49E+01	-1.43E+00	1.80E-05	-6.71E-01	1.23E-03	7.58E-01	5.75E-04
490051214	phosphate ABC transporter substrate-binding protein	1.38E+01	-1.43E+00	5.40E-05	-6.32E-01	5.20E-03	7.97E-01	1.43E-03
490053036	NAD(P)H quinone oxidoreductase	1.43E+01	-1.42E+00	1.11E-03	-2.69E+00	6.14E-05	-1.27E+00	2.50E-03
490050509	carotenoid oxygenase	1.10E+01	-1.42E+00	9.00E-04	-1.49E+00	1.04E-03	-7.29E-02	7.93E-01
497682011	hypothetical protein	1.31E+01	-1.41E+00	4.89E-04	-1.23E-01	6.20E-01	1.29E+00	1.05E-03
497682216	hypothetical protein	1.15E+01	-1.41E+00	7.41E-04	1.57E+00	6.52E-04	2.98E+00	2.10E-05
490059124	pyridoxamine 5'-phosphate oxidase	1.13E+01	-1.41E+00	1.27E-04	-2.82E+00	7.74E-06	-1.40E+00	1.61E-04
497684188	hypothetical protein	1.17E+01	-1.41E+00	2.87E-03	-1.33E+00	5.73E-03	8.36E-02	8.10E-01
490060086	peptide ABC transporter substrate-binding protein	1.39E+01	-1.41E+00	1.70E-03	-2.92E-01	3.59E-01	1.12E+00	7.03E-03
490059532	hypothetical protein	1.26E+01	-1.41E+00	1.26E-04	-8.32E-02	6.62E-01	1.32E+00	2.15E-04
497683513	acetyltransferase	1.37E+01	-1.41E+00	7.86E-05	-1.89E+00	2.80E-05	-4.83E-01	1.97E-02
490056993	cytochrome P450	1.46E+01	-1.40E+00	1.13E-04	-8.82E-01	1.80E-03	5.19E-01	1.94E-02
490060507	UDP-glucose 4-epimerase	1.53E+01	-1.40E+00	5.26E-05	-9.33E-02	5.59E-01	1.31E+00	9.26E-05
490058131	ferredoxin	1.31E+01	-1.40E+00	9.97E-05	-7.14E-01	4.56E-03	6.83E-01	5.03E-03
490053985	aminoglycoside phosphotransferase	1.26E+01	-1.40E+00	1.82E-04	-2.13E+00	3.32E-05	-7.36E-01	6.16E-03
490054708	oxppcycle protein	1.41E+01	-1.39E+00	3.29E-04	-2.37E+00	3.39E-05	-9.81E-01	2.57E-03
497681972	Fur family transcriptional regulator	1.37E+01	-1.38E+00	2.36E-03	-4.25E+00	1.46E-05	-2.87E+00	6.96E-05
490061073	RNA polymerase subunit sigma-70	1.45E+01	-1.38E+00	3.19E-05	-1.57E+00	2.73E-05	-1.87E-01	2.03E-01
497681756	ubiquinol-cytochrome C reductase	1.29E+01	-1.38E+00	5.04E-04	-1.19E+00	1.63E-03	1.89E-01	4.39E-01
490055036	histidinol-phosphatase	1.39E+01	-1.37E+00	2.87E-04	3.47E-01	1.32E-01	1.71E+00	1.11E-04
490059189	transcriptional antiterminator	9.78E+00	-1.36E+00	9.79E-05	-1.05E+00	5.41E-04	3.08E-01	9.84E-02
490054350	export associated protein	1.36E+01	-1.36E+00	1.43E-04	-1.54E+00	1.12E-04	-1.82E-01	3.40E-01
497681415	ATPase AAA	1.42E+01	-1.36E+00	1.77E-04	-7.41E-01	5.72E-03	6.20E-01	1.17E-02
497681741	cholesterol oxidase	1.35E+01	-1.36E+00	4.23E-04	-4.11E-01	1.02E-01	9.50E-01	3.48E-03
490056673	50S ribosomal protein L19	1.35E+01	-1.35E+00	1.40E-04	-1.86E+00	4.25E-05	-5.06E-01	2.24E-02
497685167	hypothetical protein	1.12E+01	-1.35E+00	6.05E-04	-1.84E+00	1.82E-04	-4.90E-01	6.91E-02
490058412	hypothetical protein	1.53E+01	-1.34E+00	5.15E-04	-1.15E-01	6.29E-01	1.23E+00	1.09E-03
497683465	histidine kinase	1.39E+01	-1.34E+00	1.30E-05	-9.06E-01	1.29E-04	4.34E-01	4.97E-03

490055057	acetyltransferase	1.03E+01	-1.34E+00	4.72E-04	1.74E-02	9.42E-01	1.35E+00	5.79E-04
497683819	hypothetical protein	1.21E+01	-1.33E+00	5.13E-03	-4.78E+00	1.49E-05	-3.45E+00	5.06E-05
497683410	hypothetical protein	1.33E+01	-1.33E+00	7.73E-05	6.12E-01	5.99E-03	1.95E+00	1.48E-05
490052111	hypothetical protein	1.30E+01	-1.33E+00	1.21E-03	-1.25E+00	2.48E-03	8.10E-02	7.70E-01
497683211	cystathionine gamma-synthase	1.11E+01	-1.33E+00	9.50E-04	-2.54E+00	5.22E-05	-1.21E+00	2.05E-03
490053914	LuxR family transcriptional regulator	1.37E+01	-1.33E+00	1.36E-04	-2.22E+00	1.81E-05	-8.91E-01	1.40E-03
497680879	hypothetical protein	1.36E+01	-1.33E+00	1.96E-04	-1.90E+00	4.90E-05	-5.67E-01	1.73E-02
497685356	PBS lyase	1.62E+01	-1.33E+00	2.54E-03	-2.15E+00	3.22E-04	-8.23E-01	2.87E-02
490055714	proteasome component	1.44E+01	-1.33E+00	1.28E-04	-1.59E-01	3.78E-01	1.17E+00	3.15E-04
490058782	magnesium transporter CorA	1.30E+01	-1.33E+00	1.79E-04	-6.38E-01	1.01E-02	6.88E-01	6.54E-03
490051986	hypothetical protein	1.92E+01	-1.33E+00	3.46E-03	-1.55E+00	2.41E-03	-2.24E-01	5.14E-01
490053420	6-phosphogluconate dehydrogenase	1.37E+01	-1.33E+00	5.36E-05	-1.70E+00	2.49E-05	-3.76E-01	3.20E-02
490058041	XRE family transcriptional regulator	1.05E+01	-1.32E+00	1.75E-04	-2.26E+00	1.96E-05	-9.43E-01	1.30E-03
490059100	hypothetical protein	1.58E+01	-1.32E+00	2.88E-05	-5.20E-01	4.99E-03	7.99E-01	4.90E-04
490052943	fumarate reductase	1.24E+01	-1.32E+00	4.41E-03	2.14E+00	5.69E-04	3.46E+00	4.06E-05
497685232	short-chain dehydrogenase	8.76E+00	-1.32E+00	2.82E-03	-2.31E+00	2.37E-04	-9.93E-01	1.39E-02
490055136	membrane protein	8.75E+00	-1.31E+00	2.83E-03	-2.61E+00	1.25E-04	-1.30E+00	3.98E-03
497682206	cystathionine beta-synthase	1.24E+01	-1.31E+00	2.17E-04	-4.18E-01	5.88E-02	8.90E-01	2.08E-03
490050318	cytochrome P450	9.47E+00	-1.30E+00	2.33E-05	-7.54E-01	5.69E-04	5.51E-01	2.51E-03
490054018	2-hydroxyacid dehydrogenase	1.62E+01	-1.29E+00	1.30E-04	-4.25E-01	3.73E-02	8.66E-01	1.33E-03
490054144	30S ribosomal protein S17	1.40E+01	-1.29E+00	1.26E-04	-1.42E+00	1.10E-04	-1.37E-01	4.31E-01
497681663	hypothetical protein	1.49E+01	-1.29E+00	7.88E-04	-2.17E-01	3.84E-01	1.07E+00	2.66E-03
497682455	cytochrome P450	1.38E+01	-1.28E+00	4.45E-04	-1.06E+00	1.77E-03	2.22E-01	3.22E-01
497681558	hypothetical protein	1.19E+01	-1.28E+00	2.49E-03	1.88E+00	5.34E-04	3.16E+00	3.14E-05
490059415	Magnesium or manganese-dependent protein phosphatase	1.46E+01	-1.28E+00	3.10E-05	-9.77E-01	1.81E-04	3.01E-01	4.22E-02
490055572	hypothetical protein	1.29E+01	-1.27E+00	1.09E-02	-1.63E+00	5.31E-03	-3.53E-01	4.07E-01
497684950	terpene synthase	1.39E+01	-1.27E+00	9.53E-05	-1.03E+00	4.14E-04	2.44E-01	1.49E-01
490053474	von Willebrand factor A	1.46E+01	-1.27E+00	9.55E-05	-5.48E-01	9.51E-03	7.24E-01	2.23E-03
497682603	short-chain dehydrogenase	1.53E+01	-1.27E+00	1.09E-04	-3.62E-01	5.42E-02	9.08E-01	7.92E-04
497681341	membrane protein	1.34E+01	-1.27E+00	1.35E-03	-5.69E-01	6.12E-02	6.99E-01	2.77E-02
490054052	membrane protein	1.38E+01	-1.26E+00	1.80E-04	-7.08E-03	9.69E-01	1.26E+00	2.35E-04
490055879	AraC family transcriptional regulator	1.36E+01	-1.26E+00	8.85E-05	-2.52E+00	5.93E-06	-1.26E+00	1.09E-04

490060245	TetR family transcriptional regulator	1.54E+01	-1.26E+00	6.86E-05	-3.74E-01	3.43E-02	8.84E-01	5.42E-04
490051893	hypothetical protein	1.33E+01	-1.26E+00	1.13E-04	1.07E-01	5.21E-01	1.36E+00	9.05E-05
490054135	50S ribosomal protein L30	1.54E+01	-1.25E+00	5.57E-03	-1.64E+00	2.21E-03	-3.88E-01	2.83E-01
490051029	DtxR family transcriptional regulator	1.42E+01	-1.25E+00	4.95E-04	-2.53E+00	2.28E-05	-1.29E+00	5.52E-04
490060208	L-carnitine dehydratase	1.34E+01	-1.25E+00	1.42E-04	-2.85E+00	5.40E-06	-1.61E+00	4.68E-05
490055876	response regulator	1.44E+01	-1.24E+00	2.76E-05	-1.10E+00	7.59E-05	1.40E-01	2.68E-01
490058194	dihydrofolate synthase	1.34E+01	-1.24E+00	3.49E-04	-3.44E+00	5.07E-06	-2.20E+00	2.31E-05
497683042	transcriptional regulator	1.36E+01	-1.24E+00	2.64E-04	3.94E-01	6.69E-02	1.63E+00	7.95E-05
497683342	isopenicillin N synthase	1.23E+01	-1.24E+00	7.17E-04	-2.63E+00	2.49E-05	-1.39E+00	5.05E-04
490051928	hypothetical protein	1.44E+01	-1.23E+00	9.76E-05	-1.64E+00	3.55E-05	-4.08E-01	2.72E-02
490055478	DNA-binding protein	1.26E+01	-1.23E+00	5.29E-05	6.14E-01	2.77E-03	1.84E+00	9.37E-06
497683380	UDP-glucose 4-epimerase	1.30E+01	-1.23E+00	1.69E-04	-3.07E-02	8.64E-01	1.20E+00	2.44E-04
497682198	diaminopimelate decarboxylase	1.61E+01	-1.21E+00	3.58E-05	-1.56E+00	1.81E-05	-3.50E-01	2.15E-02
490054314	pyruvate kinase	1.24E+01	-1.21E+00	2.37E-04	-3.80E-01	6.52E-02	8.31E-01	2.16E-03
490051458	oxidoreductase	1.44E+01	-1.21E+00	1.88E-04	-1.08E+00	4.95E-04	1.27E-01	4.73E-01
490056068	acetylglutamate kinase	1.45E+01	-1.20E+00	5.82E-04	-2.25E+00	3.73E-05	-1.05E+00	1.58E-03
497683554	hypothetical protein	1.05E+01	-1.20E+00	1.43E-03	7.87E-01	1.50E-02	1.98E+00	1.31E-04
490057587	proteasome subunit beta	1.40E+01	-1.19E+00	3.43E-04	-3.71E+00	3.42E-06	-2.52E+00	1.06E-05
490059357	membrane protein	1.49E+01	-1.19E+00	1.49E-03	-4.79E-01	9.10E-02	7.14E-01	2.16E-02
490061010	monooxygenase	1.47E+01	-1.19E+00	7.78E-05	-1.69E+00	2.27E-05	-4.96E-01	8.46E-03
490057299	glutathione peroxidase	1.29E+01	-1.18E+00	3.29E-03	-7.26E-01	3.87E-02	4.56E-01	1.49E-01
497681752	hypothetical protein	1.50E+01	-1.18E+00	7.88E-04	-3.37E+00	7.74E-06	-2.19E+00	4.08E-05
497681630	hypothetical protein	1.36E+01	-1.18E+00	5.76E-05	-1.28E-01	3.55E-01	1.05E+00	1.29E-04
497682714	3-hydroxyacyl-CoA dehydrogenase	1.37E+01	-1.18E+00	4.04E-04	-1.22E-01	5.40E-01	1.06E+00	9.36E-04
490060425	hypothetical protein	1.43E+01	-1.17E+00	7.68E-03	1.09E+00	1.52E-02	2.26E+00	3.77E-04
490050197	DNA-binding protein	9.67E+00	-1.17E+00	9.20E-04	-2.34E+00	4.11E-05	-1.17E+00	1.24E-03
490060516	hypothetical protein	1.20E+01	-1.17E+00	3.36E-04	-2.69E+00	9.26E-06	-1.52E+00	1.09E-04
490055920	metallophosphoesterase	1.44E+01	-1.17E+00	4.05E-03	-1.15E+00	6.49E-03	1.91E-02	9.51E-01
490060580	dynein regulation protein LC7	1.32E+01	-1.16E+00	7.37E-03	-1.72E+00	1.61E-03	-5.60E-01	1.31E-01
490058291	beta-N-acetylhexosaminidase	1.18E+01	-1.16E+00	4.71E-04	-2.47E-01	2.37E-01	9.12E-01	2.12E-03
497683313	hypothetical protein	1.34E+01	-1.16E+00	9.54E-04	-3.64E-01	1.38E-01	7.93E-01	8.10E-03
490052433	cell division protein FtsE	1.29E+01	-1.16E+00	7.11E-03	-2.44E+00	2.51E-04	-1.28E+00	5.86E-03

497683965	phosphohydrolase	1.38E+01	-1.15E+00	6.76E-05	-2.36E-01	1.10E-01	9.12E-01	2.79E-04
497683812	isopentenyl-diphosphate delta-isomerase	1.04E+01	-1.14E+00	7.41E-04	-2.33E+00	3.09E-05	-1.19E+00	8.00E-04
497683252	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	1.46E+01	-1.14E+00	5.91E-04	-2.07E+00	4.28E-05	-9.28E-01	2.20E-03
490055281	ATP-dependent Clp protease proteolytic subunit	1.20E+01	-1.14E+00	1.22E-03	-7.59E-01	1.23E-02	3.77E-01	1.32E-01
490058344	methionine ABC transporter ATP-binding protein	1.45E+01	-1.14E+00	3.06E-04	-2.92E+00	5.83E-06	-1.78E+00	3.87E-05
490046282	30S ribosomal protein S10	1.29E+01	-1.13E+00	9.35E-03	-1.94E+00	1.02E-03	-8.08E-01	4.74E-02
497680988	hypothetical protein	1.44E+01	-1.13E+00	7.04E-03	-2.05E+00	5.48E-04	-9.17E-01	2.33E-02
497682612	serine/threonine protein kinase	1.44E+01	-1.13E+00	4.09E-05	-1.22E+00	4.25E-05	-9.05E-02	4.61E-01
497681764	hypothetical protein	1.63E+01	-1.13E+00	2.35E-03	-1.55E+00	6.82E-04	-4.25E-01	1.34E-01
490057830	ATP-grasp superfamily enzyme	1.21E+01	-1.13E+00	1.19E-04	-3.14E+00	2.70E-06	-2.01E+00	8.58E-06
497682197	imidazolonepropionase	1.43E+01	-1.13E+00	4.04E-05	-4.12E-01	9.41E-03	7.13E-01	5.43E-04
497681849	DNA primase	1.16E+01	-1.12E+00	5.81E-04	-8.87E-01	2.89E-03	2.34E-01	2.60E-01
490059837	LexA repressor	1.16E+01	-1.12E+00	6.18E-03	1.87E+00	7.01E-04	2.99E+00	5.16E-05
490057565	short-chain dehydrogenase	1.45E+01	-1.12E+00	6.94E-04	-1.11E+00	1.09E-03	1.01E-02	9.61E-01
490059366	membrane protein	1.24E+01	-1.12E+00	5.36E-03	5.86E-02	8.57E-01	1.18E+00	5.59E-03
490054993	glutamate-1-semialdehyde 2,1-aminomutase	1.18E+01	-1.11E+00	1.55E-04	-1.66E+00	3.15E-05	-5.51E-01	7.11E-03
497681714	ATPase	9.79E+00	-1.11E+00	1.33E-03	-3.15E+00	1.24E-05	-2.04E+00	7.03E-05
497681029	alpha-mannosidase	1.44E+01	-1.10E+00	6.21E-05	8.30E-01	3.99E-04	1.93E+00	5.70E-06
497682486	nitrilase	1.56E+01	-1.10E+00	2.20E-03	-6.67E-01	2.97E-02	4.33E-01	1.15E-01
490061145	hypothetical protein	1.33E+01	-1.10E+00	1.77E-04	-8.84E-01	8.15E-04	2.15E-01	1.90E-01
497683088	hypothetical protein	1.36E+01	-1.10E+00	2.11E-04	-2.70E+00	5.46E-06	-1.61E+00	3.80E-05
490058118	acyl-CoA synthetase	1.41E+01	-1.10E+00	4.63E-05	-4.68E-01	5.29E-03	6.30E-01	1.06E-03
490053926	preprotein translocase SecA	1.48E+01	-1.10E+00	1.87E-04	-1.72E+00	3.07E-05	-6.19E-01	4.59E-03
490055176	sulfurtransferase	1.51E+01	-1.10E+00	4.28E-03	-1.29E-01	6.64E-01	9.66E-01	1.02E-02
490050709	hypothetical protein	1.33E+01	-1.09E+00	4.24E-04	-8.16E-01	2.86E-03	2.78E-01	1.54E-01
490052661	phosphoribosylformylglycinamidine synthase	1.48E+01	-1.09E+00	3.67E-04	-1.03E+00	7.41E-04	6.11E-02	7.35E-01
490056180	methionine synthase	1.31E+01	-1.09E+00	2.56E-03	-1.11E+00	3.48E-03	-2.13E-02	9.35E-01
497683500	hypothetical protein	1.34E+01	-1.09E+00	1.06E-03	-7.64E-01	8.75E-03	3.25E-01	1.59E-01
490059637	sporulation protein	1.34E+01	-1.09E+00	7.98E-05	1.45E+00	2.94E-05	2.54E+00	2.57E-06
490055925	dihydrodipicolinate synthase	1.34E+01	-1.08E+00	4.55E-03	1.03E-01	7.32E-01	1.18E+00	3.90E-03
490051040	acetyl-CoA carboxylase	9.43E+00	-1.08E+00	4.55E-04	-1.08E+00	6.87E-04	2.48E-03	9.89E-01
490056473	membrane protein	1.26E+01	-1.08E+00	1.67E-03	-6.84E-01	2.00E-02	3.95E-01	1.20E-01

490058342	membrane protein	1.33E+01	-1.08E+00	2.12E-04	9.30E-01	6.72E-04	2.01E+00	1.20E-05
497682945	threonine synthase	1.20E+01	-1.08E+00	1.59E-04	-2.19E+00	8.55E-06	-1.11E+00	1.71E-04
490056110	glycosyl transferase	1.30E+01	-1.08E+00	4.18E-04	-1.90E+00	3.56E-05	-8.25E-01	2.13E-03
490051384	potassium transporter	1.37E+01	-1.07E+00	9.27E-04	1.63E+00	1.60E-04	2.70E+00	1.12E-05
490061463	calcium-binding protein	1.37E+01	-1.07E+00	1.20E-04	1.20E+00	9.84E-05	2.27E+00	4.52E-06
490061373	hypothetical protein	1.22E+01	-1.07E+00	8.28E-04	-3.98E-01	8.19E-02	6.73E-01	1.06E-02
497681565	IclR family transcriptional regulator	1.34E+01	-1.07E+00	1.77E-04	-1.06E+00	2.75E-04	1.05E-02	9.45E-01
490057267	transcriptional activator	1.45E+01	-1.07E+00	3.96E-03	9.80E-01	8.66E-03	2.05E+00	1.82E-04
490051786	HAD family hydrolase	1.15E+01	-1.07E+00	8.28E-03	1.17E+00	7.86E-03	2.24E+00	2.61E-04
490054231	MarR family transcriptional regulator	1.37E+01	-1.06E+00	3.31E-03	-1.42E+00	1.12E-03	-3.65E-01	1.92E-01
490057557	50S ribosomal protein L35	1.42E+01	-1.06E+00	2.14E-04	-1.03E+00	3.67E-04	2.66E-02	8.64E-01
497683691	hypothetical protein	1.55E+01	-1.06E+00	7.07E-04	-1.68E+00	9.75E-05	-6.23E-01	1.23E-02
490056177	cytochrome C	1.21E+01	-1.05E+00	1.70E-04	-1.83E-01	2.39E-01	8.70E-01	5.90E-04
490052517	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	1.32E+01	-1.05E+00	1.24E-03	-1.36E+00	4.76E-04	-3.13E-01	1.71E-01
490059057	heat-shock protein Hsp90	1.24E+01	-1.05E+00	1.12E-03	-1.06E+00	1.61E-03	-6.01E-03	9.77E-01
490051254	GTP cyclohydrolase	1.27E+01	-1.05E+00	9.41E-04	-3.36E+00	5.79E-06	-2.31E+00	2.11E-05
490052118	GCN5 family N-acetyltransferase	1.45E+01	-1.05E+00	1.41E-03	-1.26E+00	8.33E-04	-2.09E-01	3.58E-01
490057935	LuxR family transcriptional regulator	1.51E+01	-1.05E+00	6.12E-05	-6.00E-01	1.61E-03	4.47E-01	6.15E-03
490061374	beta-lactamase	1.28E+01	-1.04E+00	4.62E-04	-1.62E+00	7.30E-05	-5.72E-01	1.19E-02
490051541	hypothetical protein	1.31E+01	-1.04E+00	3.28E-04	4.60E-01	2.41E-02	1.50E+00	6.23E-05
490055544	metallophosphoesterase	1.57E+01	-1.04E+00	1.39E-04	2.89E-01	6.80E-02	1.33E+00	4.78E-05
490057610	phosphoglycerate mutase	1.59E+01	-1.03E+00	1.53E-04	-1.51E-01	3.04E-01	8.80E-01	4.46E-04
497683434	hypothetical protein	1.37E+01	-1.03E+00	3.06E-04	-4.37E-01	2.65E-02	5.89E-01	6.70E-03
490060489	hypothetical protein	1.39E+01	-1.02E+00	3.19E-04	-5.66E-01	9.10E-03	4.58E-01	2.08E-02
497681120	cold-shock protein	1.35E+01	-1.02E+00	4.35E-03	-8.61E-01	1.40E-02	1.63E-01	5.55E-01
490054173	MaoC family dehydratase	1.35E+01	-1.02E+00	1.15E-04	-2.50E+00	3.93E-06	-1.47E+00	2.25E-05
490050100	transcription termination factor Rho	1.44E+01	-1.02E+00	9.43E-05	-9.37E-01	2.12E-04	8.19E-02	5.27E-01
497682739	hypothetical protein	1.41E+01	-1.02E+00	9.92E-05	6.50E-01	1.48E-03	1.67E+00	1.10E-05
497683807	RNA-binding protein	1.34E+01	-1.02E+00	1.33E-03	-1.27E+00	6.20E-04	-2.55E-01	2.49E-01
490055263	metal-binding protein	1.34E+01	-1.02E+00	2.42E-04	-4.55E-01	1.79E-02	5.62E-01	6.44E-03
490061267	beta-lactamase	1.29E+01	-1.01E+00	7.98E-05	-2.36E-01	8.29E-02	7.73E-01	4.03E-04
497682315	hypothetical protein	1.39E+01	-1.01E+00	1.41E-04	-5.69E-01	3.94E-03	4.40E-01	1.17E-02

490060987	hypothetical protein	1.44E+01	-1.01E+00	1.16E-04	-1.54E-01	2.60E-01	8.54E-01	3.44E-04
490053516	hypothetical protein	1.43E+01	-1.01E+00	7.00E-04	-6.32E-01	1.01E-02	3.76E-01	6.95E-02
490057908	laccase	1.21E+01	-1.01E+00	1.57E-03	1.47E-01	5.10E-01	1.15E+00	1.04E-03
497683549	arginine ABC transporter ATP-binding protein	1.35E+01	-1.01E+00	4.76E-04	-3.04E-01	1.09E-01	7.03E-01	3.95E-03
490060088	acyl-peptide hydrolase	1.26E+01	-1.01E+00	1.53E-03	-3.17E+00	8.60E-06	-2.16E+00	3.79E-05
497684181	diaminopimelate epimerase, partial	1.56E+01	-1.00E+00	1.12E-03	-8.11E-01	4.76E-03	1.90E-01	3.60E-01
497682262	esterase	1.37E+01	-9.98E-01	1.43E-04	-1.92E+00	9.86E-06	-9.21E-01	2.73E-04
497682159	chemotaxis protein CheY	1.46E+01	-9.94E-01	8.43E-04	-1.83E+00	5.53E-05	-8.37E-01	2.66E-03
490051187	hypothetical protein	1.34E+01	-9.94E-01	2.81E-04	-4.14E-01	2.71E-02	5.80E-01	5.74E-03
490058353	hypothetical protein	1.39E+01	-9.86E-01	1.38E-03	-2.05E-01	3.40E-01	7.81E-01	5.75E-03
490050423	folylpolyglutamate synthase	1.12E+01	-9.85E-01	1.94E-04	1.26E+00	8.29E-05	2.24E+00	5.05E-06
490059902	membrane protein	1.50E+01	-9.82E-01	3.93E-04	-6.00E-01	6.93E-03	3.83E-01	4.12E-02
497681509	ABC transporter ATPase	1.39E+01	-9.81E-01	8.76E-04	-1.92E-01	3.25E-01	7.89E-01	3.47E-03
490058320	membrane protein	1.45E+01	-9.81E-01	4.94E-04	-9.15E-01	1.07E-03	6.64E-02	7.00E-01
490052578	DeoR family transcripitonal regulator	8.23E+00	-9.72E-01	1.87E-03	-2.11E+00	5.35E-05	-1.14E+00	1.11E-03
490059367	GlcNAc-PI de-N-acetylase	1.35E+01	-9.65E-01	1.43E-04	-2.02E+00	7.21E-06	-1.06E+00	1.11E-04
497682588	protease	1.39E+01	-9.62E-01	2.96E-04	-5.96E-01	5.07E-03	3.66E-01	3.71E-02
490057772	1-aminocyclopropane-1-carboxylate deaminase	1.51E+01	-9.60E-01	5.95E-03	-2.28E+00	1.11E-04	-1.32E+00	1.63E-03
490054882	uracil-DNA glycosylase	1.55E+01	-9.52E-01	4.32E-04	-1.00E+00	4.98E-04	-4.84E-02	7.67E-01
497683061	NmrA family protein	1.21E+01	-9.51E-01	1.66E-03	-2.76E+00	1.39E-05	-1.81E+00	7.54E-05
490051193	LacI family transcriptional regulator	1.35E+01	-9.46E-01	2.79E-03	-2.84E+00	1.84E-05	-1.89E+00	1.00E-04
497682009	gamma-glutamyl phosphate reductase	1.27E+01	-9.36E-01	3.94E-03	-2.00E+00	1.24E-04	-1.06E+00	2.79E-03
490053875	acetyltransferase	1.39E+01	-9.34E-01	7.68E-04	-8.26E-01	2.16E-03	1.09E-01	5.42E-01
497684047	hypothetical protein	1.26E+01	-9.34E-01	6.89E-03	-2.56E+00	6.40E-05	-1.62E+00	5.71E-04
490058757	CRISPR-associated protein Cas1	1.29E+01	-9.33E-01	1.12E-03	5.04E-01	2.77E-02	1.44E+00	1.50E-04
490052594	transcriptional regulator	1.52E+01	-9.31E-01	1.57E-04	-1.04E+00	1.34E-04	-1.05E-01	4.26E-01
497683461	dynein regulation protein LC7	1.68E+01	-9.29E-01	1.66E-03	-2.13E+00	3.74E-05	-1.20E+00	5.90E-04
490061480	hypothetical protein	1.35E+01	-9.28E-01	1.12E-04	-2.65E-02	8.31E-01	9.02E-01	1.60E-04
490055896	acetyl-CoA carboxylase subunit beta	1.14E+01	-9.25E-01	9.24E-03	-4.87E-01	1.22E-01	4.38E-01	1.55E-01
497681801	reductase	1.34E+01	-9.25E-01	1.29E-03	-2.35E+00	1.93E-05	-1.42E+00	1.77E-04
490060991	acetyltransferase	1.27E+01	-9.25E-01	3.01E-03	-1.74E+00	1.81E-04	-8.12E-01	7.46E-03
490054220	30S ribosomal protein S6	1.15E+01	-9.17E-01	2.99E-03	-4.13E+00	4.33E-06	-3.21E+00	7.28E-06

490056425	membrane protein	1.13E+01	-9.14E-01	4.99E-03	1.31E+00	1.23E-03	2.23E+00	6.70E-05
490054309	methionine aminopeptidase	1.59E+01	-9.12E-01	1.44E-03	-4.78E-01	3.78E-02	4.35E-01	4.93E-02
490059976	glyoxalase	1.20E+01	-9.10E-01	2.00E-03	9.40E-01	2.55E-03	1.85E+00	6.45E-05
490052491	cysteine synthase	1.35E+01	-9.02E-01	3.58E-03	-2.20E+00	5.74E-05	-1.30E+00	7.49E-04
490059733	ribonuclease III	1.41E+01	-8.98E-01	2.57E-04	-1.15E+00	1.09E-04	-2.51E-01	9.29E-02
490051871	phosphatase	1.19E+01	-8.98E-01	1.94E-03	-7.94E-01	5.31E-03	1.04E-01	6.12E-01
490055033	aminotransferase	1.40E+01	-8.98E-01	1.68E-03	1.28E+00	4.00E-04	2.18E+00	2.27E-05
490058199	ATP-dependent Clp protease ClpP	1.27E+01	-8.96E-01	3.43E-03	-1.44E+00	4.61E-04	-5.42E-01	3.94E-02
497682274	penicillin amidase	1.42E+01	-8.94E-01	2.35E-03	-8.00E-01	5.96E-03	9.37E-02	6.59E-01
490054484	acetyl-CoA synthetase	1.32E+01	-8.87E-01	3.12E-03	-1.15E+00	1.24E-03	-2.68E-01	2.44E-01
490054541	DNA-binding protein	1.52E+01	-8.79E-01	3.19E-04	1.02E+00	2.20E-04	1.90E+00	8.76E-06
490059245	50S ribosomal protein L23	1.38E+01	-8.76E-01	1.18E-03	-1.66E+00	6.67E-05	-7.80E-01	2.75E-03
490054041	glyceraldehyde-3-phosphate dehydrogenase	1.14E+01	-8.74E-01	2.04E-03	-2.28E+00	2.49E-05	-1.40E+00	2.30E-04
497683561	hypothetical protein	1.31E+01	-8.74E-01	5.37E-03	-7.01E-02	7.80E-01	8.04E-01	1.04E-02
490055279	ATP-dependent protease	1.30E+01	-8.66E-01	1.56E-03	-1.51E+00	1.32E-04	-6.44E-01	8.65E-03
490053065	aspartyl-tRNA synthetase	1.32E+01	-8.64E-01	8.71E-03	-1.42E+00	1.15E-03	-5.56E-01	6.33E-02
490051939	hypothetical protein	1.44E+01	-8.64E-01	5.55E-04	-1.89E+00	1.84E-05	-1.03E+00	2.96E-04
490055708	membrane protein	1.31E+01	-8.63E-01	3.81E-04	-7.44E-01	1.22E-03	1.19E-01	4.13E-01
497683802	acetyl-CoA acetyltransferase	1.20E+01	-8.62E-01	6.23E-04	-4.15E+00	1.31E-06	-3.29E+00	2.03E-06
490061357	Moenomycin biosynthesis protein MoeN5	1.08E+01	-8.52E-01	4.07E-03	-1.06E+00	2.04E-03	-2.10E-01	3.59E-01
490053814	protease	1.32E+01	-8.50E-01	1.16E-03	-2.00E+00	2.40E-05	-1.15E+00	3.11E-04
490051790	hypothetical protein	1.26E+01	-8.45E-01	4.30E-04	-2.49E+00	5.07E-06	-1.64E+00	1.89E-05
490057429	ankyrin	1.30E+01	-8.43E-01	1.60E-03	-2.48E+00	1.25E-05	-1.64E+00	6.45E-05
490059196	FAD-dependent oxidoreductase	1.32E+01	-8.39E-01	8.29E-03	-8.95E-01	8.94E-03	-5.66E-02	8.26E-01
490053540	aspartyl/glutamyl-tRNA amidotransferase subunit B	1.45E+01	-8.39E-01	3.00E-04	-7.48E-01	8.21E-04	9.08E-02	4.98E-01
497683785	isochorismatase	1.28E+01	-8.36E-01	3.92E-03	-8.90E-01	4.35E-03	-5.40E-02	8.06E-01
490057306	TetR family transcriptional regulator	1.15E+01	-8.32E-01	1.18E-03	-2.64E+00	7.11E-06	-1.81E+00	2.78E-05
490055587	hypothetical protein	1.40E+01	-8.28E-01	3.55E-04	-1.76E-01	2.13E-01	6.52E-01	1.60E-03
490056901	hypothetical protein	1.30E+01	-8.24E-01	2.97E-03	-1.35E+00	3.58E-04	-5.26E-01	2.89E-02
490050087	F0F1 ATP synthase subunit B	1.34E+01	-8.24E-01	2.23E-03	-1.24E+00	3.99E-04	-4.20E-01	5.22E-02
490054845	mannose-1-phosphate guanyltransferase	1.33E+01	-8.22E-01	2.07E-03	-1.32E+00	2.73E-04	-4.95E-01	2.71E-02
490059021	restriction endonuclease	1.11E+01	-8.20E-01	3.55E-03	-7.41E-01	8.48E-03	7.93E-02	7.10E-01

490059602	GCN5 family acetyltransferase	8.99E+00	-8.18E-01	3.49E-03	2.15E-01	3.18E-01	1.03E+00	1.44E-03
497683590	hypothetical protein	1.39E+01	-8.14E-01	6.20E-04	-1.59E+00	3.21E-05	-7.75E-01	1.06E-03
497680947	hypothetical protein	1.36E+01	-8.12E-01	2.94E-03	-4.41E+00	2.50E-06	-3.59E+00	3.08E-06
497683045	hypothetical protein	1.33E+01	-8.02E-01	7.81E-04	-3.91E-01	3.16E-02	4.11E-01	2.43E-02
490050095	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	1.43E+01	-8.02E-01	5.46E-03	2.68E-01	2.52E-01	1.07E+00	1.74E-03
497682087	LuxAB-like protein (oxygenase)	1.21E+01	-8.00E-01	4.89E-04	-1.62E+00	2.29E-05	-8.18E-01	5.73E-04

[a] Identification is based on annotation by NCBI. **[b]** Description is based on NCBI annotation of protein similarity by BLAST. **[c]** Average normalized expression in the WT strain. **[d]** Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. **[e]**Adjusted P-value in *ΔbldG* as compared to the WT strain. **[f]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. **[g]** Adjusted P-value in *ΔbldA* as compared to the WT strain. **[h]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and **[i]** Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Table A.1.3: Proteins determined to be significantly (P = 0.01) over-expressed in the *ΔbldA* compared to the WT strain of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G -WT[e]	logFC A -WT[f]	adj.P.Val A-WT[g]	logFC A -G[h]	adj.P.Val A -G[i]
490054719	spermidine/putrescine ABC transporter ATP-binding protein	9.14E+00	2.20E+00	1.92E-02	8.96E+00	3.07E-05	6.76E+00	9.98E-05
490057554	50S ribosomal protein L20	1.03E+01	1.73E+00	2.00E-03	7.84E+00	3.04E-06	6.12E+00	5.23E-06
490053262	cell division protein SepF	9.78E+00	1.07E+00	9.94E-04	7.08E+00	6.87E-07	6.00E+00	8.19E-07
490050666	endoribonuclease L-PSP	1.36E+01	-7.85E-01	5.23E-02	4.94E+00	1.49E-05	5.73E+00	5.81E-06
497681259	hypothetical protein	1.01E+01	2.34E+00	6.94E-06	4.22E+00	1.68E-06	1.88E+00	2.43E-05
490059845	GntR family transcriptional regulator	1.37E+01	-2.52E-01	7.66E-01	3.85E+00	2.66E-03	4.10E+00	1.68E-03
490059429	succinate dehydrogenase	1.39E+01	-5.60E-01	2.01E-01	3.44E+00	1.73E-04	4.00E+00	6.58E-05
497684987	hypothetical protein	1.08E+01	-9.87E-01	8.85E-02	3.32E+00	6.75E-04	4.31E+00	1.48E-04
490055426	peptidase M4	1.28E+01	-9.57E-01	1.16E-01	2.92E+00	1.82E-03	3.88E+00	3.65E-04
490059937	flavoprotein oxidoreductase	1.01E+01	-1.48E-02	9.68E-01	2.92E+00	5.22E-05	2.93E+00	4.11E-05
497681271	hypothetical protein, partial	1.25E+01	3.41E-02	9.16E-01	2.87E+00	5.82E-05	2.84E+00	5.01E-05
490053784	ATP-dependent helicase	1.16E+01	-8.05E-01	5.90E-02	2.84E+00	2.71E-04	3.65E+00	6.26E-05
490050062	3-hydroxybutyryl-CoA dehydrogenase	8.99E+00	4.18E-01	1.32E-02	2.83E+00	3.04E-06	2.41E+00	3.85E-06
497683991	polyketide synthase	1.25E+01	-7.41E-01	2.45E-02	2.79E+00	5.81E-05	3.54E+00	1.54E-05
490054396	dienelactone hydrolase	1.15E+01	1.68E+00	2.04E-05	2.75E+00	5.01E-06	1.08E+00	2.39E-04
497683200	pyridine nucleotide-disulfide oxidoreductase	1.05E+01	4.04E-01	4.04E-02	2.54E+00	1.09E-05	2.13E+00	1.79E-05
490057875	membrane protein	1.37E+01	-2.13E+00	4.38E-03	2.45E+00	3.37E-03	4.58E+00	1.11E-04
490053447	CRISPR-associated protein	1.69E+01	8.38E-03	9.73E-01	2.41E+00	2.73E-05	2.40E+00	2.17E-05
490059920	endoribonuclease	1.19E+01	9.60E-02	6.81E-01	2.34E+00	5.15E-05	2.25E+00	5.08E-05
490052167	aminotransferase class III	9.70E+00	-6.58E-01	1.75E-01	2.33E+00	2.09E-03	2.99E+00	5.05E-04
490052448	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	9.98E+00	3.75E+00	1.80E-04	2.28E+00	3.45E-03	-1.47E+00	2.24E-02
490046206	whiK	1.45E+01	-1.86E+00	2.04E-05	2.27E+00	1.39E-05	4.13E+00	1.57E-06
490058655	Ion-transporting ATPase	1.05E+01	2.15E+00	9.62E-05	2.22E+00	1.19E-04	7.28E-02	7.89E-01
497684022	choline oxidase	1.63E+01	1.77E+00	6.17E-03	2.20E+00	3.17E-03	4.38E-01	3.99E-01
497682033	putative gamma-aminobutyrate permease	1.43E+01	-2.25E+00	4.76E-03	2.18E+00	8.07E-03	4.42E+00	1.94E-04
497681093	hypothetical protein	1.23E+01	-8.52E-01	3.06E-02	2.17E+00	5.75E-04	3.02E+00	8.78E-05

490054507	conserved hypothetical protein	1.20E+01	1.00E+00	3.49E-03	2.16E+00	1.03E-04	1.16E+00	2.20E-03
490052943	fumarate reductase	1.24E+01	-1.32E+00	4.41E-03	2.14E+00	5.69E-04	3.46E+00	4.06E-05
490056442	amino acid ABC transporter permease	1.44E+01	1.42E+00	3.13E-05	2.02E+00	1.00E-05	6.06E-01	3.21E-03
490058852	Hypothetical protein	1.35E+01	-2.54E+00	7.44E-05	1.99E+00	3.79E-04	4.53E+00	5.94E-06
490056767	PTS glucose transporter subunit IIA	9.90E+00	3.86E+00	1.67E-06	1.96E+00	3.03E-05	-1.91E+00	2.71E-05
490057727	oxidoreductase	1.40E+01	-1.51E-02	9.46E-01	1.92E+00	5.02E-05	1.94E+00	3.96E-05
497681558	hypothetical protein	1.19E+01	-1.28E+00	2.49E-03	1.88E+00	5.34E-04	3.16E+00	3.14E-05
490059837	LexA repressor	1.16E+01	-1.12E+00	6.18E-03	1.87E+00	7.01E-04	2.99E+00	5.16E-05
490052127	carbonate dehydratase	1.32E+01	-1.71E+00	2.72E-05	1.83E+00	3.10E-05	3.53E+00	2.03E-06
497684179	diaminopimelate epimerase	1.06E+01	-4.33E-01	1.23E-01	1.79E+00	4.29E-04	2.22E+00	1.17E-04
490054440	DNA-binding protein	1.21E+01	1.93E-01	7.22E-01	1.77E+00	1.34E-02	1.57E+00	2.01E-02
490060397	cytochrome P450	1.73E+01	4.76E-01	1.44E-01	1.76E+00	1.06E-03	1.28E+00	4.64E-03
497681699	mechanosensitive ion channel protein	1.21E+01	2.68E+00	1.27E-05	1.75E+00	1.54E-04	-9.35E-01	3.36E-03
490057424	hypothetical protein	1.06E+01	2.49E+00	3.76E-05	1.66E+00	4.44E-04	-8.28E-01	1.24E-02
490051384	potassium transporter	1.37E+01	-1.07E+00	9.27E-04	1.63E+00	1.60E-04	2.70E+00	1.12E-05
490052557	membrane protein	1.39E+01	3.30E-01	6.19E-02	1.62E+00	5.50E-05	1.29E+00	1.44E-04
490057150	aldolase	1.06E+01	1.11E-02	9.69E-01	1.59E+00	3.49E-04	1.58E+00	3.12E-04
497682216	hypothetical protein	1.15E+01	-1.41E+00	7.41E-04	1.57E+00	6.52E-04	2.98E+00	2.10E-05
497681532	stress protein	1.39E+01	3.37E+00	1.55E-05	1.47E+00	1.54E-03	-1.90E+00	3.51E-04
490054803	molecular chaperone GroEL	1.06E+01	-1.80E-02	9.52E-01	1.46E+00	8.66E-04	1.48E+00	7.10E-04
490059637	sporulation protein	1.34E+01	-1.09E+00	7.98E-05	1.45E+00	2.94E-05	2.54E+00	2.57E-06
490061097	DNA primase	1.14E+01	-6.96E-01	3.92E-03	1.40E+00	1.67E-04	2.10E+00	1.89E-05
490054247	membrane protein	1.36E+01	-2.22E+00	2.17E-05	1.39E+00	3.49E-04	3.60E+00	3.58E-06
497681947	multidrug ABC transporter ATP-binding protein	1.20E+01	1.19E+00	6.65E-03	1.36E+00	5.30E-03	1.68E-01	6.33E-01
490056425	membrane protein	1.13E+01	-9.14E-01	4.99E-03	1.31E+00	1.23E-03	2.23E+00	6.70E-05
490054608	glutamate ABC transporter permease	1.00E+01	1.74E+00	1.81E-04	1.29E+00	1.24E-03	-4.45E-01	9.76E-02
490055033	aminotransferase	1.40E+01	-8.98E-01	1.68E-03	1.28E+00	4.00E-04	2.18E+00	2.27E-05
490057132	membrane protein	1.32E+01	7.47E-01	8.49E-04	1.27E+00	8.25E-05	5.24E-01	6.63E-03
490050423	folylpolyglutamate synthase	1.12E+01	-9.85E-01	1.94E-04	1.26E+00	8.29E-05	2.24E+00	5.05E-06
490051030	hypothetical protein	1.47E+01	6.22E-01	2.41E-03	1.25E+00	1.01E-04	6.26E-01	3.04E-03
490061463	calcium-binding protein	1.37E+01	-1.07E+00	1.20E-04	1.20E+00	9.84E-05	2.27E+00	4.52E-06

[a] Identification is based on annotation by NCBI. [b] Description is based on NCBI annotation of protein similarity by BLAST. [c] Average normalized expression in the WT strain. [d] Normalized log_2 fold change in *ΔbldG* as compared to the WT strain. [e]Adjusted P-value in *ΔbldG* as compared to the WT strain. [f] Normalized log_2 fold change in *ΔbldA* as compared to the WT strain. [g] Adjusted P-value in *ΔbldA* as compared to the WT strain. [h] Normalized log_2 fold change in *ΔbldA* as compared to the *ΔbldG* strain and [i] Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Table A.1.4: Proteins determined to be significantly (P = 0.01) under-expressed in the *ΔbldA* compared to the WT strain of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G-WT[e]	logFC A-WT[f]	adj.P.Val A-WT[g]	logFC A-G[h]	adj.P.Val A-G[i]
497683181	RNA polymerase	1.24E+01	6.61E-01	3.95E-01	-1.62E+01	3.04E-06	-1.68E+01	2.23E-06
490056771	acetoacetyl-CoA synthetase	8.45E+00	-1.06E-01	6.65E-01	-1.13E+01	1.47E-07	-1.12E+01	1.05E-07
490059712	hypothetical protein	8.12E+00	8.38E-01	3.35E-03	-1.04E+01	1.03E-07	-1.12E+01	4.46E-08
490055894	hydroxymethylglutaryl-CoA lyase	7.27E+00	-9.31E-01	2.62E-02	-1.02E+01	1.24E-06	-9.22E+00	1.48E-06
490058414	F420-0--gamma-glutamyl ligase	7.74E+00	4.03E-01	4.93E-02	-1.01E+01	9.52E-08	-1.05E+01	4.46E-08
490056716	cold-shock protein	1.12E+01	-6.54E-01	7.78E-01	-9.61E+00	4.18E-03	-8.96E+00	5.25E-03
490058437	metal ABC transporter substrate-binding protein	7.89E+00	1.84E+00	1.16E-03	-9.60E+00	1.55E-06	-1.14E+01	6.01E-07
490053513	glycine cleavage system protein T	7.26E+00	8.88E-01	3.04E-03	-9.24E+00	1.87E-07	-1.01E+01	9.76E-08
490056217	hypothetical protein	5.31E+00	-3.43E+00	1.75E-01	-8.80E+00	9.64E-03	-5.37E+00	6.18E-02
490056026	hypothetical protein	5.83E+00	-1.64E+00	1.14E-02	-8.59E+00	6.44E-06	-6.95E+00	1.14E-05
490059370	hypothetical protein	7.41E+00	2.60E+00	2.22E-01	-8.58E+00	5.30E-03	-1.12E+01	1.25E-03
490051788	hypothetical protein	6.33E+00	3.35E-01	2.49E-02	-8.27E+00	5.94E-08	-8.60E+00	4.46E-08
490058300	putative integral membrane protein	9.02E+00	-1.98E+00	3.15E-01	-8.08E+00	5.19E-03	-6.09E+00	1.67E-02
497681777	short-chain dehydrogenase	7.07E+00	2.88E+00	2.90E-05	-7.99E+00	1.12E-06	-1.09E+01	2.18E-07
490054322	hypothetical protein	6.74E+00	2.11E+00	2.57E-04	-7.93E+00	1.68E-06	-1.00E+01	5.97E-07
490050623	short-chain dehydrogenase	6.89E+00	-1.34E+00	1.49E-01	-7.67E+00	1.20E-04	-6.33E+00	2.75E-04
497683463	hypothetical protein	8.65E+00	-8.05E-01	6.61E-01	-7.34E+00	5.57E-03	-6.53E+00	8.60E-03
490058410	hypothetical protein	7.26E+00	5.63E-01	5.53E-01	-7.33E+00	2.10E-04	-7.89E+00	1.20E-04
490050134	hypothetical protein	8.93E+00	-5.53E-01	8.02E-01	-6.92E+00	1.41E-02	-6.36E+00	1.85E-02
490053713	carbonic anhydrase	9.46E+00	-1.70E+00	8.27E-02	-6.92E+00	2.25E-04	-5.22E+00	8.59E-04
490058488	trans-aconitate 2-methyltransferase	6.45E+00	5.05E+00	8.06E-04	-6.08E+00	4.59E-04	-1.11E+01	1.87E-05
497682856	hypothetical protein	1.35E+01	-4.12E+00	1.99E-06	-5.46E+00	1.64E-06	-1.35E+00	4.45E-04
497683354	HAD-superfamily hydrolase	5.38E+00	3.57E+00	2.17E-03	-5.39E+00	3.89E-04	-8.95E+00	2.46E-05
490059144	D-alanine--D-alanine ligase	1.22E+01	-3.96E+00	9.13E-06	-5.20E+00	5.40E-06	-1.24E+00	4.06E-03
497684432	hypothetical protein	1.13E+01	-4.16E+00	1.15E-06	-5.15E+00	4.81E-07	-9.89E-01	2.57E-04
497684454	hypothetical protein	1.14E+01	-4.10E+00	2.19E-06	-5.07E+00	2.14E-06	-9.77E-01	2.56E-03
490052575	septum formation protein Maf	1.03E+01	-1.75E+00	2.21E-03	-4.92E+00	1.96E-05	-3.17E+00	1.29E-04

497684923	hypothetical protein	1.14E+01	-3.67E+00	3.63E-06	-4.91E+00	2.63E-06	-1.24E+00	8.68E-04
497683819	hypothetical protein	1.21E+01	-1.33E+00	5.13E-03	-4.78E+00	1.49E-05	-3.45E+00	5.06E-05
490057931	thiamine biosynthesis protein ThiS	1.29E+01	9.19E-01	9.99E-02	-4.70E+00	9.73E-05	-5.62E+00	3.29E-05
497681172	putative ferrodoxin oxidoreductase alpha subunit, partial	1.38E+01	-2.37E+00	4.41E-04	-4.68E+00	2.30E-05	-2.31E+00	6.57E-04
490061297	cytochrome P450	1.12E+01	-3.17E+00	1.57E-06	-4.51E+00	8.46E-07	-1.35E+00	4.78E-05
490057878	tryptophan synthase subunit beta	1.09E+01	-4.71E-01	1.69E-01	-4.45E+00	1.57E-05	-3.98E+00	1.92E-05
497680947	hypothetical protein	1.36E+01	-8.12E-01	2.94E-03	-4.41E+00	2.50E-06	-3.59E+00	3.08E-06
490052490	molybdenum cofactor biosynthesis protein MoaD	1.34E+01	-2.17E+00	5.51E-04	-4.38E+00	2.49E-05	-2.22E+00	6.42E-04
497685093	1,4-dihydropyridine enantioselective esterase	1.04E+01	-2.43E+00	6.60E-04	-4.31E+00	5.24E-05	-1.89E+00	3.13E-03
490056213	isochorismatase	1.29E+01	-4.40E+00	1.15E-06	-4.31E+00	1.55E-06	9.56E-02	5.75E-01
497681972	Fur family transcriptional regulator	1.37E+01	-1.38E+00	2.36E-03	-4.25E+00	1.46E-05	-2.87E+00	6.96E-05
497684412	hypothetical protein	1.49E+01	-2.92E+00	1.78E-05	-4.25E+00	5.83E-06	-1.33E+00	1.27E-03
497684483	cysteine desulfurase, SufS subfamily protein	1.18E+01	-2.89E+00	6.06E-04	-4.23E+00	1.27E-04	-1.34E+00	2.95E-02
497682231	cellulose-binding protein	1.37E+01	-1.40E-01	3.20E-01	-4.23E+00	1.11E-06	-4.09E+00	8.19E-07
490054966	membrane protein	1.56E+01	-1.46E+00	8.63E-05	-4.18E+00	2.02E-06	-2.72E+00	5.70E-06
490053550	acyl-CoA dehydrogenase	1.51E+01	-4.36E+00	1.57E-06	-4.18E+00	2.70E-06	1.86E-01	3.57E-01
490050011	histidine kinase	4.27E+00	3.04E+00	3.60E-02	-4.17E+00	1.43E-02	-7.21E+00	9.14E-04
497683802	acetyl-CoA acetyltransferase	1.20E+01	-8.62E-01	6.23E-04	-4.15E+00	1.31E-06	-3.29E+00	2.03E-06
490054220	30S ribosomal protein S6	1.15E+01	-9.17E-01	2.99E-03	-4.13E+00	4.33E-06	-3.21E+00	7.28E-06
490056623	acyl carrier protein	1.15E+01	-3.16E+00	1.71E-05	-4.12E+00	8.33E-06	-9.60E-01	8.74E-03
497684176	dihydrouridine synthase	1.42E+01	-1.66E+00	1.58E-05	-4.12E+00	1.11E-06	-2.46E+00	3.82E-06
490051238	MarR family transcriptional regulator	1.17E+01	6.92E-01	1.12E-03	-4.10E+00	1.11E-06	-4.79E+00	4.00E-07
490050805	aminotransferase class III	9.69E+00	-4.65E+00	3.42E-06	-4.09E+00	9.05E-06	5.57E-01	7.58E-02
490052143	cytochrome P450	1.13E+01	-2.39E+00	3.93E-06	-4.08E+00	1.24E-06	-1.69E+00	2.13E-05
490061383	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1.02E+01	-3.12E+00	4.03E-06	-3.98E+00	3.04E-06	-8.59E-01	2.93E-03
490050625	alpha/beta hydrolase	1.40E+01	4.34E-01	2.12E-01	-3.95E+00	2.92E-05	-4.38E+00	1.42E-05
497683836	thioredoxin reductase	1.40E+01	-3.73E+00	2.02E-06	-3.93E+00	3.04E-06	-2.01E-01	3.23E-01
490056704	dynein regulation protein LC7	9.64E+00	-3.82E+00	1.15E-06	-3.91E+00	1.12E-06	-8.40E-02	5.53E-01
490054091	transcription antitermination protein NusB	1.30E+01	1.93E+00	6.92E-04	-3.90E+00	3.07E-05	-5.84E+00	4.35E-06
497683341	decarboxylase	1.10E+01	-3.08E+00	1.49E-05	-3.88E+00	8.55E-06	-8.00E-01	1.55E-02

497681632	dephospho-CoA kinase	1.27E+01	-8.85E-02	7.88E-01	-3.88E+00	2.22E-05	-3.79E+00	1.89E-05
490060039	hypothetical protein	1.39E+01	-7.06E-01	1.84E-02	-3.86E+00	8.15E-06	-3.16E+00	1.48E-05
497685001	hypothetical protein	1.25E+01	-3.78E+00	9.66E-06	-3.85E+00	1.49E-05	-7.18E-02	8.10E-01
490052367	cold-shock protein	1.27E+01	-1.94E+00	7.81E-04	-3.80E+00	3.84E-05	-1.87E+00	1.26E-03
490050778	lipid hydroperoxide peroxidase	1.26E+01	-2.40E+00	6.46E-04	-3.75E+00	9.70E-05	-1.35E+00	1.39E-02
490057710	peptidase	1.32E+01	-4.84E-01	4.42E-01	-3.72E+00	8.77E-04	-3.23E+00	1.57E-03
490057587	proteasome subunit beta	1.40E+01	-1.19E+00	3.43E-04	-3.71E+00	3.42E-06	-2.52E+00	1.06E-05
490051435	hypothetical protein	1.50E+01	7.95E-01	2.06E-02	-3.70E+00	1.86E-05	-4.50E+00	5.98E-06
490057009	hypothetical protein	1.40E+01	-1.06E-01	4.92E-01	-3.70E+00	2.23E-06	-3.59E+00	1.88E-06
490050150	3'-hydroxymethylcephem carbamoyltransferase	1.18E+01	-3.67E+00	4.48E-06	-3.69E+00	7.67E-06	-2.35E-02	9.25E-01
490053555	oxidoreductase	1.13E+01	-3.36E+00	4.65E-05	-3.66E+00	4.59E-05	-2.99E-01	4.26E-01
490050309	hypothetical protein	1.04E+01	-2.91E+00	1.57E-05	-3.64E+00	9.05E-06	-7.38E-01	1.80E-02
490058786	N5,N10-methylene tetrahydromethanopterin reductase	1.08E+01	6.75E-01	2.49E-02	-3.61E+00	1.29E-05	-4.29E+00	4.77E-06
490059696	short-chain dehydrogenase	1.37E+01	-4.53E+00	2.02E-05	-3.60E+00	9.28E-05	9.29E-01	4.95E-02
490051870	acetyltransferase	1.26E+01	-4.74E-01	3.72E-02	-3.59E+00	5.08E-06	-3.12E+00	5.98E-06
490053054	hypothetical protein	1.14E+01	-6.56E-01	1.85E-01	-3.59E+00	2.51E-04	-2.94E+00	6.22E-04
490051909	deaminase reductase	1.35E+01	-2.02E+00	3.11E-05	-3.58E+00	5.07E-06	-1.55E+00	1.48E-04
497681625	export associated protein	1.27E+01	-1.16E+00	2.56E-01	-3.58E+00	1.01E-02	-2.42E+00	4.50E-02
490059032	sugar isomerase	1.24E+01	-1.69E+00	6.23E-03	-3.57E+00	2.12E-04	-1.88E+00	4.97E-03
490053523	peptide ABC transporter ATPase	1.03E+01	-1.35E+00	8.01E-02	-3.56E+00	1.99E-03	-2.21E+00	1.69E-02
490053551	hypothetical protein	1.26E+01	-3.23E+00	3.93E-06	-3.56E+00	5.07E-06	-3.32E-01	1.30E-01
490061312	alkylhydroperoxidase	1.06E+01	-2.58E+00	2.79E-06	-3.56E+00	1.81E-06	-9.83E-01	3.26E-04
497684131	hypothetical protein	1.33E+01	-1.92E+00	1.54E-05	-3.56E+00	2.70E-06	-1.64E+00	3.96E-05
490056047	O-methyltransferase	1.43E+01	-2.00E+00	3.30E-05	-3.53E+00	5.07E-06	-1.53E+00	1.65E-04
490057723	DNA polymerase III subunit epsilon	3.92E+00	3.41E+00	1.47E-03	-3.53E+00	1.85E-03	-6.93E+00	4.66E-05
490058900	pirin	1.13E+01	-3.40E+00	2.88E-06	-3.50E+00	5.07E-06	-1.05E-01	6.00E-01
490051139	hydroxyurea phosphotransferase	1.17E+01	-2.02E-01	7.34E-01	-3.50E+00	7.48E-04	-3.30E+00	9.00E-04
490053549	N-acetyltransferase GCN5	1.29E+01	-4.08E+00	3.02E-06	-3.49E+00	8.97E-06	5.92E-01	3.54E-02
497684269	cobyrinic acid a,c-diamide synthase	1.18E+01	-3.68E+00	3.70E-06	-3.48E+00	7.36E-06	1.93E-01	4.10E-01
490055902	thiazole synthase	1.42E+01	-1.24E+00	1.34E-02	-3.45E+00	1.26E-04	-2.21E+00	1.11E-03

490058194	dihydrofolate synthase	1.34E+01	-1.24E+00	3.49E-04	-3.44E+00	5.07E-06	-2.20E+00	2.31E-05
490053425	saicar synthetase	1.38E+01	-4.20E+00	1.67E-06	-3.44E+00	5.07E-06	7.61E-01	5.44E-03
497681361	DSBA oxidoreductase	1.28E+01	1.35E-01	3.64E-01	-3.43E+00	2.50E-06	-3.56E+00	1.65E-06
490059435	N-acetyl-1-D-myo-inosityl-2-amino-2	1.17E+01	9.01E-01	2.56E-04	-3.42E+00	1.68E-06	-4.32E+00	5.97E-07
490053387	arsenate reductase	1.07E+01	7.35E-02	8.04E-01	-3.41E+00	2.44E-05	-3.49E+00	1.72E-05
490053433	hypothetical protein	1.24E+01	-3.66E+00	1.67E-06	-3.41E+00	3.04E-06	2.52E-01	1.65E-01
490051245	amino acid ABC transporter substrate-binding protein	1.35E+01	9.67E-02	6.29E-01	-3.38E+00	5.79E-06	-3.48E+00	3.92E-06
497681752	hypothetical protein	1.50E+01	-1.18E+00	7.88E-04	-3.37E+00	7.74E-06	-2.19E+00	4.08E-05
497681908	hypothetical protein	1.32E+01	6.21E-01	8.13E-04	-3.37E+00	1.11E-06	-3.99E+00	4.00E-07
490052383	hypothetical protein	1.25E+01	-3.40E+00	1.15E-06	-3.37E+00	1.09E-06	3.31E-02	7.70E-01
490060264	glucose-methanol-choline oxidoreductase	1.24E+01	-3.21E+00	1.14E-05	-3.36E+00	1.58E-05	-1.46E-01	5.82E-01
490051254	GTP cyclohydrolase	1.27E+01	-1.05E+00	9.41E-04	-3.36E+00	5.79E-06	-2.31E+00	2.11E-05
490055841	hypothetical protein	1.30E+01	-7.87E-01	1.51E-03	-3.35E+00	3.04E-06	-2.56E+00	5.70E-06
490054178	hypothetical protein	1.27E+01	-5.44E-01	1.03E-01	-3.32E+00	4.30E-05	-2.77E+00	8.74E-05
490059697	FAD-dependent monooxygenase	1.23E+01	-2.80E+00	4.69E-06	-3.31E+00	5.07E-06	-5.08E-01	2.52E-02
490050172	conserved hypothetical protein	1.37E+01	-4.01E+00	5.20E-06	-3.28E+00	2.19E-05	7.28E-01	2.75E-02
490060020	serine/threonine protein kinase	1.19E+01	-3.48E+00	2.61E-06	-3.28E+00	5.46E-06	1.94E-01	3.34E-01
497685222	DNA-binding protein	1.24E+01	-2.80E+00	1.67E-06	-3.28E+00	1.68E-06	-4.73E-01	7.42E-03
490055301	50S ribosomal protein L32	1.64E+01	-8.57E-01	1.21E-01	-3.27E+00	6.22E-04	-2.41E+00	2.61E-03
490059603	radical SAM protein	1.31E+01	-2.10E+00	4.23E-04	-3.26E+00	6.61E-05	-1.16E+00	1.04E-02
497683724	lipoate-protein ligase A	1.17E+01	6.95E-01	1.91E-02	-3.26E+00	1.73E-05	-3.95E+00	5.57E-06
490055006	oxidoreductase	1.43E+01	-2.95E+00	2.63E-06	-3.26E+00	3.17E-06	-3.03E-01	9.45E-02
490056814	acetyltransferase	1.22E+01	-5.06E-01	9.66E-03	-3.25E+00	3.04E-06	-2.75E+00	3.79E-06
490057652	ATP/GTP-binding protein	1.41E+01	-2.72E+00	6.93E-06	-3.25E+00	5.83E-06	-5.35E-01	2.53E-02
490060518	hypothetical protein	1.28E+01	-3.22E+00	1.69E-06	-3.25E+00	2.82E-06	-3.32E-02	8.32E-01
490056384	LuxR family transcriptional regulator	1.50E+01	-1.79E+00	5.87E-03	-3.24E+00	4.38E-04	-1.45E+00	1.94E-02
490055162	signal peptide protein	1.12E+01	-1.79E-01	4.87E-01	-3.23E+00	2.18E-05	-3.05E+00	2.14E-05
490052171	inositol monophosphatase	1.03E+01	1.03E+00	5.87E-04	-3.22E+00	5.07E-06	-4.26E+00	1.64E-06
490050094	hypothetical protein	1.42E+01	4.75E-01	1.09E-02	-3.22E+00	2.82E-06	-3.69E+00	1.57E-06
497682498	hypothetical protein	1.07E+01	3.47E-02	8.21E-01	-3.22E+00	2.75E-06	-3.25E+00	2.03E-06
490053554	flavoprotein	1.21E+01	-4.27E+00	3.03E-06	-3.22E+00	1.64E-05	1.05E+00	3.51E-03

490057366	hypothetical protein	9.29E+00	-3.71E+00	1.67E-06	-3.20E+00	4.33E-06	5.13E-01	1.76E-02
497683433	short-chain dehydrogenase	9.44E+00	5.70E-01	1.61E-01	-3.20E+00	1.59E-04	-3.77E+00	5.64E-05
490053438	adenine phosphoribosyltransferase	1.22E+01	-2.53E+00	3.86E-06	-3.19E+00	3.04E-06	-6.53E-01	3.70E-03
490060889	luciferase	1.03E+01	-1.68E+00	1.21E-04	-3.18E+00	9.05E-06	-1.50E+00	2.72E-04
497682761	hypothetical protein	1.06E+01	-2.57E-01	4.53E-01	-3.18E+00	8.53E-05	-2.92E+00	1.09E-04
490060088	acyl-peptide hydrolase	1.26E+01	-1.01E+00	1.53E-03	-3.17E+00	8.60E-06	-2.16E+00	3.79E-05
490060203	ABC transporter	1.25E+01	-4.62E-01	1.37E-01	-3.17E+00	4.17E-05	-2.70E+00	7.40E-05
497684897	hypothetical protein	1.16E+01	-2.79E+00	4.03E-06	-3.17E+00	5.07E-06	-3.78E-01	5.94E-02
490051507	porphobilinogen deaminase	1.44E+01	1.32E+00	2.87E-04	-3.15E+00	7.36E-06	-4.48E+00	2.02E-06
497681714	ATPase	9.79E+00	-1.11E+00	1.33E-03	-3.15E+00	1.24E-05	-2.04E+00	7.03E-05
490061295	hypothetical protein	1.07E+01	-4.12E-01	1.66E-01	-3.14E+00	3.74E-05	-2.73E+00	6.01E-05
497683176	hypothetical protein	1.44E+01	-5.07E-01	1.15E-02	-3.14E+00	3.94E-06	-2.63E+00	5.14E-06
490057830	ATP-grasp superfamily enzyme	1.21E+01	-1.13E+00	1.19E-04	-3.14E+00	2.70E-06	-2.01E+00	8.58E-06
497683725	DNA polymerase subunit beta	1.31E+01	6.39E-01	1.22E-02	-3.14E+00	8.55E-06	-3.77E+00	3.34E-06
497684011	GDP-mannose 6-dehydrogenase	1.23E+01	-2.24E+00	7.36E-05	-3.13E+00	2.27E-05	-8.92E-01	9.80E-03
490059953	peptidase M24	9.84E+00	1.04E+00	2.62E-02	-3.13E+00	1.95E-04	-4.17E+00	3.79E-05
490054101	guanylate kinase	1.51E+01	-1.46E+00	6.46E-04	-3.12E+00	2.28E-05	-1.66E+00	4.40E-04
490055858	sulfate adenylyltransferase	1.40E+01	-4.12E-01	6.20E-02	-3.12E+00	8.24E-06	-2.71E+00	1.13E-05
497683456	thioester reductase	1.23E+01	-3.20E+00	7.43E-06	-3.11E+00	1.47E-05	8.22E-02	7.34E-01
490056624	peptide synthetase	1.37E+01	-3.54E+00	2.69E-05	-3.11E+00	7.75E-05	4.33E-01	2.31E-01
490056644	6-phospho-beta-glucosidase	9.75E+00	-4.03E-01	1.32E-02	-3.11E+00	2.23E-06	-2.71E+00	2.49E-06
490059462	ATP-binding protein	1.47E+01	-1.45E+00	3.94E-04	-3.11E+00	1.49E-05	-1.66E+00	2.49E-04
490055260	radical SAM protein	1.19E+01	-1.96E-01	3.10E-01	-3.10E+00	7.21E-06	-2.90E+00	6.80E-06
497684462	DSBA oxidoreductase	1.26E+01	-3.70E+00	1.15E-06	-3.09E+00	2.70E-06	6.15E-01	3.03E-03
490057400	hypothetical protein	1.35E+01	-6.03E-02	8.63E-01	-3.09E+00	6.90E-05	-3.03E+00	6.34E-05
497683989	SAM-dependent methyltransferase	1.31E+01	-2.32E+00	1.08E-05	-3.08E+00	5.79E-06	-7.53E-01	4.12E-03
497681088	UDP-N-acetylglucosamine 2-epimerase	1.30E+01	-1.97E+00	2.00E-05	-3.07E+00	5.34E-06	-1.10E+00	4.95E-04
497682351	protein-L-isoaspartate O-methyltransferase	1.28E+01	-1.90E+00	2.68E-04	-3.06E+00	3.74E-05	-1.16E+00	4.57E-03
490057415	dynein regulation protein LC7	1.34E+01	-1.88E+00	2.55E-04	-3.05E+00	3.37E-05	-1.18E+00	3.69E-03
497684912	aminotransferase	1.30E+01	-2.30E+00	6.14E-06	-3.04E+00	4.11E-06	-7.39E-01	2.35E-03
490056694	GntR family transcriptional regulator	1.35E+01	-2.01E+00	1.28E-03	-3.04E+00	2.22E-04	-1.03E+00	3.40E-02

497683145	serine/threonine protein kinase	1.19E+01	-3.20E+00	8.16E-03	-3.04E+00	1.47E-02	1.62E-01	8.67E-01
490052474	glyoxalase/bleomycin resistance protein/dioxygenase	1.35E+01	-2.99E+00	1.54E-04	-3.03E+00	2.13E-04	-3.80E-02	9.28E-01
490059479	ABC transporter ATP-binding protein	9.53E+00	9.09E-01	4.66E-03	-3.03E+00	1.84E-05	-3.93E+00	4.72E-06
497684175	hypothetical protein	1.40E+01	-1.52E+00	4.62E-04	-3.01E+00	2.37E-05	-1.49E+00	6.73E-04
490054165	50S ribosomal protein L10	1.51E+01	-8.03E-01	1.83E-02	-3.01E+00	4.24E-05	-2.20E+00	1.69E-04
497683539	ribosomal protein S12 methylthiotransferase	1.05E+01	8.74E-01	5.39E-03	-3.01E+00	1.84E-05	-3.88E+00	4.84E-06
490060364	hypothetical protein	1.16E+01	4.72E-01	2.90E-02	-3.01E+00	7.21E-06	-3.48E+00	3.24E-06
497684074	hypothetical protein, partial	4.02E+00	-7.64E+00	7.44E-05	-3.00E+00	1.14E-02	4.63E+00	1.26E-03
490051386	anti-sigma B factor antagonist	1.54E+01	-5.23E+00	2.60E-06	-3.00E+00	4.11E-05	2.23E+00	1.49E-04
490050636	conserved hypothetical protein	9.29E+00	-1.88E+00	1.28E-04	-3.00E+00	2.05E-05	-1.12E+00	2.32E-03
490055862	phosphoadenosine phosphosulfate reductase	1.17E+01	-8.92E-01	2.56E-02	-3.00E+00	1.09E-04	-2.10E+00	5.89E-04
497680886	ABC transporter	1.27E+01	-3.48E+00	1.04E-04	-2.98E+00	3.41E-04	5.03E-01	2.73E-01
490052952	peptide ABC transporter ATPase	1.26E+01	9.51E-01	7.82E-03	-2.98E+00	3.89E-05	-3.93E+00	8.62E-06
497682165	XRE family transcriptional regulator	1.04E+01	1.38E+00	5.22E-03	-2.96E+00	1.61E-04	-4.34E+00	2.01E-05
490055432	cytidine deaminase	1.27E+01	2.67E-01	2.97E-01	-2.96E+00	2.83E-05	-3.23E+00	1.48E-05
490058377	hypothetical protein	9.03E+00	-3.28E-01	1.47E-01	-2.96E+00	1.48E-05	-2.63E+00	1.87E-05
490051359	conserved hypothetical protein	1.25E+01	-2.79E+00	3.56E-05	-2.96E+00	4.05E-05	-1.71E-01	5.57E-01
490050986	monooxygenase	1.03E+01	-2.88E+00	1.78E-05	-2.95E+00	2.49E-05	-7.16E-02	7.84E-01
490060709	hypothetical protein	1.45E+01	8.30E-01	3.58E-03	-2.95E+00	1.10E-05	-3.78E+00	3.24E-06
490059693	cytochrome P450	1.26E+01	-2.57E+00	1.67E-06	-2.94E+00	1.81E-06	-3.69E-01	1.59E-02
490052652	valine dehydrogenase	1.42E+01	-6.55E-01	8.57E-03	-2.93E+00	8.89E-06	-2.28E+00	2.10E-05
490050882	endoribonuclease	1.36E+01	-2.66E+00	3.93E-06	-2.93E+00	5.07E-06	-2.72E-01	1.32E-01
497684562	hypothetical protein	1.33E+01	2.24E-01	3.00E-01	-2.93E+00	1.49E-05	-3.15E+00	7.86E-06
490050144	deacetoxycephalosporin C synthetase	1.07E+01	-1.71E+00	3.30E-05	-2.92E+00	5.50E-06	-1.21E+00	2.50E-04
490052184	acyl-CoA dehydrogenase	1.39E+01	-4.65E-01	3.32E-02	-2.92E+00	8.55E-06	-2.46E+00	1.38E-05
490058344	methionine ABC transporter ATP-binding protein	1.45E+01	-1.14E+00	3.06E-04	-2.92E+00	5.83E-06	-1.78E+00	3.87E-05
497682387	aminotransferase	9.53E+00	1.68E+00	6.45E-06	-2.91E+00	1.81E-06	-4.59E+00	2.18E-07
497684393	CRISPR-associated Cse1 family protein	1.34E+01	-3.81E+00	6.08E-06	-2.91E+00	3.30E-05	9.05E-01	9.88E-03
490051696	ABC transporter permease	1.14E+01	-2.33E+00	6.15E-06	-2.90E+00	5.07E-06	-5.72E-01	8.66E-03
490056746	hypothetical protein	1.22E+01	-3.00E+00	1.87E-06	-2.89E+00	3.94E-06	1.08E-01	4.93E-01

490057783	metal-sulfur cluster biosynthesis protein	1.39E+01	-3.98E-01	7.73E-02	-2.89E+00	1.39E-05	-2.49E+00	1.97E-05
490056081	methionine ABC transporter ATP-binding protein	1.08E+01	1.19E-01	8.90E-01	-2.87E+00	1.02E-02	-2.98E+00	7.79E-03
490057478	shikimate kinase	1.51E+01	1.25E+00	1.39E-04	-2.86E+00	5.40E-06	-4.11E+00	1.55E-06
490051617	hypothetical protein	1.38E+01	-7.64E-02	6.01E-01	-2.85E+00	3.93E-06	-2.78E+00	2.96E-06
497683343	L-lysine aminotransferase	1.39E+01	-3.27E+00	4.09E-06	-2.85E+00	1.25E-05	4.16E-01	7.40E-02
490060208	L-carnitine dehydratase	1.34E+01	-1.25E+00	1.42E-04	-2.85E+00	5.40E-06	-1.61E+00	4.68E-05
490059904	inositol-phosphate phosphatase	1.24E+01	-6.54E-01	5.25E-02	-2.84E+00	7.89E-05	-2.19E+00	2.57E-04
497683335	biotin carboxylase	1.18E+01	-2.89E+00	2.69E-06	-2.84E+00	5.07E-06	4.93E-02	7.67E-01
490060226	dehydrogenase	9.34E+00	8.06E-01	4.28E-03	-2.84E+00	1.39E-05	-3.65E+00	3.82E-06
490055717	proteasome subunit alpha	1.36E+01	-3.40E-01	5.53E-01	-2.84E+00	2.06E-03	-2.50E+00	3.45E-03
490051193	LacI family transcriptional regulator	1.35E+01	-9.46E-01	2.79E-03	-2.84E+00	1.84E-05	-1.89E+00	1.00E-04
490051417	MarR family transcriptional regulator	1.43E+01	-5.68E-01	1.79E-02	-2.83E+00	1.23E-05	-2.26E+00	2.46E-05
497683289	ATP-dependent DNA helicase	1.24E+01	5.09E-01	3.32E-03	-2.82E+00	2.50E-06	-3.33E+00	1.17E-06
490059124	pyridoxamine 5'-phosphate oxidase	1.13E+01	-1.41E+00	1.27E-04	-2.82E+00	7.74E-06	-1.40E+00	1.61E-04
490051627	ribonucleoside-diphosphate reductase	1.38E+01	6.92E-01	2.54E-02	-2.81E+00	4.22E-05	-3.51E+00	1.21E-05
490051912	GntR family transcriptional regulator	1.33E+01	2.78E-01	4.90E-02	-2.81E+00	2.74E-06	-3.09E+00	1.61E-06
490057051	Biotin carboxylase	1.32E+01	-2.70E+00	2.11E-05	-2.81E+00	2.77E-05	-1.06E-01	6.78E-01
490054713	hypothetical protein	1.06E+01	2.60E-01	2.75E-01	-2.81E+00	2.52E-05	-3.07E+00	1.31E-05
490051804	hypothetical protein	1.41E+01	-3.43E-01	2.45E-01	-2.80E+00	6.86E-05	-2.46E+00	1.11E-04
497681024	nitrilase	1.07E+01	1.34E+00	1.81E-03	-2.80E+00	6.12E-05	-4.14E+00	8.03E-06
490050147	conserved hypothetical protein	1.26E+01	-3.36E+00	4.11E-06	-2.80E+00	1.52E-05	5.59E-01	2.97E-02
490054145	50S ribosomal protein L29	1.45E+01	-1.16E+00	2.62E-02	-2.80E+00	6.12E-04	-1.64E+00	7.93E-03
497683835	peptide synthetase	1.21E+01	-3.27E+00	2.19E-06	-2.79E+00	6.51E-06	4.79E-01	2.39E-02
490051121	trehalose phosphatase	1.47E+01	-5.75E-01	3.29E-03	-2.79E+00	3.42E-06	-2.21E+00	5.57E-06
490059942	hypothetical protein	1.23E+01	-2.19E+00	2.43E-05	-2.78E+00	1.39E-05	-5.96E-01	1.99E-02
490059527	Lon protease	1.30E+01	-1.98E+00	5.73E-05	-2.78E+00	1.84E-05	-7.96E-01	7.67E-03
490056765	conserved hypothetical protein	1.37E+01	-1.61E+00	1.50E-05	-2.77E+00	3.04E-06	-1.16E+00	9.03E-05
497683661	hypothetical protein	1.36E+01	-2.34E+00	3.76E-06	-2.77E+00	3.75E-06	-4.31E-01	1.70E-02
490053479	enoyl-CoA hydratase	1.34E+01	-3.53E-03	9.81E-01	-2.77E+00	3.04E-06	-2.77E+00	2.38E-06
490056091	hypothetical protein	1.03E+01	-1.47E+00	6.54E-04	-2.77E+00	4.04E-05	-1.29E+00	1.68E-03

497683061	NmrA family protein	1.21E+01	-9.51E-01	1.66E-03	-2.76E+00	1.39E-05	-1.81E+00	7.54E-05
490052682	NUDIX hydrolase	1.36E+01	3.18E-01	1.87E-01	-2.76E+00	2.73E-05	-3.07E+00	1.28E-05
490057169	hypothetical protein	1.02E+01	-2.27E+00	9.65E-05	-2.75E+00	5.41E-05	-4.83E-01	1.16E-01
490058897	branched-chain alpha-keto acid dehydrogenase subunit E2	1.22E+01	1.28E+00	3.68E-04	-2.74E+00	1.42E-05	-4.02E+00	2.57E-06
490057310	6-phosphofructokinase	1.43E+01	4.65E-01	1.17E-01	-2.74E+00	6.25E-05	-3.21E+00	2.38E-05
497685350	oxidoreductase	1.36E+01	-1.61E+00	2.05E-04	-2.74E+00	2.30E-05	-1.13E+00	1.66E-03
490059562	Clavaminate synthase 2	1.25E+01	-3.70E+00	1.02E-05	-2.74E+00	6.44E-05	9.61E-01	1.10E-02
490060751	acetyltransferase	1.41E+01	9.93E-01	4.62E-04	-2.74E+00	6.05E-06	-3.73E+00	1.88E-06
490051946	hypothetical protein	1.07E+01	-2.40E+00	1.20E-04	-2.73E+00	9.04E-05	-3.31E-01	3.05E-01
490056071	argininosuccinate synthase	9.79E+00	-4.47E-01	2.70E-02	-2.73E+00	7.83E-06	-2.28E+00	1.28E-05
490050890	hypothetical protein	1.13E+01	-1.86E+00	4.25E-03	-2.72E+00	9.41E-04	-8.63E-01	1.06E-01
497682848	TetR family transcriptional regulator	1.27E+01	-2.37E+00	1.13E-03	-2.72E+00	8.42E-04	-3.44E-01	4.81E-01
490059108	cytochrome P450	1.34E+01	-3.79E+00	1.15E-06	-2.71E+00	2.89E-06	1.08E+00	1.02E-04
490055666	membrane protein	1.33E+01	-4.69E-01	6.17E-03	-2.71E+00	3.04E-06	-2.24E+00	4.05E-06
497683088	hypothetical protein	1.36E+01	-1.10E+00	2.11E-04	-2.70E+00	5.46E-06	-1.61E+00	3.80E-05
490055338	dynein regulation protein LC7	1.31E+01	-1.77E+00	1.49E-04	-2.69E+00	2.88E-05	-9.19E-01	5.58E-03
490050711	type 11 methyltransferase	1.40E+01	-3.16E+00	1.87E-06	-2.69E+00	5.79E-06	4.73E-01	1.80E-02
497681453	MaoC family dehydratase	1.37E+01	-7.78E-01	1.17E-02	-2.69E+00	3.76E-05	-1.91E+00	1.74E-04
497685265	LuxR family transcriptional regulator	1.04E+01	-1.61E+00	2.70E-05	-2.69E+00	5.34E-06	-1.08E+00	2.72E-04
490060516	hypothetical protein	1.20E+01	-1.17E+00	3.36E-04	-2.69E+00	9.26E-06	-1.52E+00	1.09E-04
490053036	NAD(P)H quinone oxidoreductase	1.43E+01	-1.42E+00	1.11E-03	-2.69E+00	6.14E-05	-1.27E+00	2.50E-03
490058668	precorrin-8X methylmutase	1.27E+01	1.99E-02	9.46E-01	-2.68E+00	3.76E-05	-2.70E+00	2.92E-05
497684806	GntR family transcriptional regulator	1.16E+01	3.93E-01	1.33E-01	-2.68E+00	4.05E-05	-3.07E+00	1.72E-05
490056676	hypothetical protein	1.47E+01	-2.24E-02	8.67E-01	-2.68E+00	2.82E-06	-2.66E+00	2.23E-06
497685246	hypothetical protein	1.39E+01	-1.80E+00	1.31E-04	-2.67E+00	2.83E-05	-8.71E-01	6.86E-03
490056872	AsnC family transcriptional regulator	1.32E+01	-7.50E-01	1.10E-02	-2.67E+00	3.10E-05	-1.92E+00	1.29E-04
490051614	3-phosphoshikimate 1-carboxyvinyltransferase	1.31E+01	3.06E-01	6.93E-02	-2.67E+00	5.79E-06	-2.97E+00	2.96E-06
490050161	conserved hypothetical protein	1.20E+01	-3.85E+00	2.59E-06	-2.66E+00	1.82E-05	1.18E+00	8.44E-04
490055448	HrcA family transcriptional regulator	1.07E+01	3.86E-01	3.54E-01	-2.66E+00	5.65E-04	-3.04E+00	2.40E-04
497682270	molybdenum cofactor biosynthesis protein MoaC	3.62E+00	4.35E+00	3.75E-04	-2.65E+00	6.72E-03	-7.00E+00	4.05E-05

490059888	hypothetical protein	1.29E+01	-2.10E+00	4.46E-05	-2.65E+00	2.31E-05	-5.43E-01	3.89E-02
490060901	hypothetical protein	1.20E+01	-2.56E+00	1.99E-06	-2.65E+00	3.17E-06	-8.39E-02	5.40E-01
490053854	cytochrome C biosynthesis protein	1.02E+01	2.67E-01	8.62E-02	-2.64E+00	5.07E-06	-2.91E+00	2.57E-06
490057306	TetR family transcriptional regulator	1.15E+01	-8.32E-01	1.18E-03	-2.64E+00	7.11E-06	-1.81E+00	2.78E-05
490056602	seryl-tRNA synthetase	1.22E+01	-1.12E+00	1.71E-02	-2.63E+00	4.07E-04	-1.51E+00	6.06E-03
497683342	isopenicillin N synthase	1.23E+01	-1.24E+00	7.17E-04	-2.63E+00	2.49E-05	-1.39E+00	5.05E-04
497682305	hypothetical protein	1.34E+01	-3.28E-01	1.80E-02	-2.63E+00	2.56E-06	-2.30E+00	2.57E-06
490054474	phosphomannomutase	1.39E+01	5.57E-01	1.02E-03	-2.62E+00	1.85E-06	-3.18E+00	8.19E-07
490058107	LuxR family transcriptional regulator	1.25E+01	-8.07E-01	6.02E-02	-2.61E+00	4.37E-04	-1.81E+00	2.57E-03
490055136	membrane protein	8.75E+00	-1.31E+00	2.83E-03	-2.61E+00	1.25E-04	-1.30E+00	3.98E-03
490055493	MarR family transcriptional regulator	1.44E+01	-3.44E-01	3.60E-02	-2.61E+00	5.07E-06	-2.27E+00	5.80E-06
490055022	hypothetical protein	1.49E+01	-4.21E+00	1.63E-04	-2.61E+00	2.84E-03	1.60E+00	2.35E-02
490054189	ribonuclease P	1.37E+01	5.25E-01	7.82E-03	-2.60E+00	5.79E-06	-3.13E+00	2.49E-06
490050167	oxidoreductase	1.35E+01	-2.70E+00	3.01E-05	-2.60E+00	5.53E-05	1.02E-01	7.10E-01
490061051	protein kinase	1.24E+01	-4.02E+00	3.11E-04	-2.59E+00	4.41E-03	1.43E+00	4.86E-02
490059045	glyoxalase	1.31E+01	1.98E+00	2.42E-04	-2.58E+00	9.21E-05	-4.56E+00	5.57E-06
497683082	delta-aminolevulinic acid dehydratase	1.13E+01	-4.14E-01	5.27E-01	-2.57E+00	6.53E-03	-2.16E+00	1.31E-02
497683347	putative regulatory protein (AfsR-like protein)	1.52E+01	-2.64E+00	8.11E-06	-2.57E+00	1.59E-05	7.25E-02	7.22E-01
490056700	cytochrome P450	8.68E+00	-2.87E-01	3.96E-01	-2.57E+00	2.33E-04	-2.28E+00	3.75E-04
490052108	hypothetical protein	1.16E+01	2.67E-01	1.91E-01	-2.57E+00	1.84E-05	-2.83E+00	8.76E-06
490054879	3-ketoacyl-ACP reductase	1.00E+01	-6.10E-01	1.83E-02	-2.57E+00	2.49E-05	-1.96E+00	7.43E-05
490055254	50S ribosomal protein L27	1.32E+01	6.24E-01	5.83E-03	-2.56E+00	8.89E-06	-3.19E+00	3.06E-06
497682579	transcriptional regulator	1.15E+01	3.14E-01	2.33E-01	-2.56E+00	6.05E-05	-2.87E+00	2.82E-05
497684047	hypothetical protein	1.26E+01	-9.34E-01	6.89E-03	-2.56E+00	6.40E-05	-1.62E+00	5.71E-04
490052921	hypothetical protein	1.13E+01	-3.64E-01	3.49E-01	-2.56E+00	4.75E-04	-2.19E+00	9.36E-04
490057877	tryptophan synthase subunit alpha	1.45E+01	-2.71E+00	6.82E-05	-2.56E+00	1.34E-04	1.48E-01	6.46E-01
497685168	hypothetical protein	1.35E+01	-3.28E+00	1.68E-06	-2.55E+00	6.07E-06	7.36E-01	2.00E-03
497683462	histidine kinase	1.34E+01	-2.20E+00	4.60E-06	-2.55E+00	5.07E-06	-3.46E-01	4.23E-02
490060205	oxidoreductase	1.35E+01	-2.53E+00	4.16E-06	-2.54E+00	7.16E-06	-1.48E-02	9.29E-01
497683948	hypothetical protein	1.42E+01	-4.49E-01	3.11E-01	-2.54E+00	9.50E-04	-2.09E+00	2.24E-03
490056313	serine hydroxymethyltransferase	1.43E+01	-2.39E-01	2.36E-01	-2.54E+00	1.91E-05	-2.30E+00	2.27E-05

497683211	cystathionine gamma-synthase	1.11E+01	-1.33E+00	9.50E-04	-2.54E+00	5.22E-05	-1.21E+00	2.05E-03
497684123	putative DNA-binding protein	9.49E+00	-7.50E-02	8.06E-01	-2.54E+00	1.14E-04	-2.46E+00	1.10E-04
490059601	glycosyltransferase family 1	1.48E+01	-2.32E+00	2.28E-05	-2.54E+00	2.39E-05	-2.15E-01	3.40E-01
490058146	glycyl-tRNA synthetase	1.36E+01	-1.44E-01	5.46E-01	-2.54E+00	4.30E-05	-2.39E+00	4.61E-05
490051829	LysR family transcriptional regulator	1.42E+01	-7.73E-01	1.06E-02	-2.54E+00	4.30E-05	-1.76E+00	2.31E-04
490051029	DtxR family transcriptional regulator	1.42E+01	-1.25E+00	4.95E-04	-2.53E+00	2.28E-05	-1.29E+00	5.52E-04
490057926	thiamine-phosphate pyrophosphorylase	9.96E+00	1.55E-01	1.88E-01	-2.53E+00	2.74E-06	-2.69E+00	1.73E-06
490058552	DNA repair protein RadA	1.08E+01	7.55E-01	3.54E-04	-2.53E+00	2.83E-06	-3.28E+00	1.01E-06
490054931	alpha/beta hydrolase	1.50E+01	-4.04E-01	1.39E-02	-2.52E+00	4.52E-06	-2.12E+00	5.57E-06
490052654	phosphoribosylaminoimidazole synthetase	1.40E+01	-1.37E-01	5.08E-01	-2.52E+00	2.38E-05	-2.39E+00	2.38E-05
490053470	globin	1.34E+01	7.56E-01	4.61E-03	-2.52E+00	1.84E-05	-3.28E+00	4.65E-06
490055879	AraC family transcriptional regulator	1.36E+01	-1.26E+00	8.85E-05	-2.52E+00	5.93E-06	-1.26E+00	1.09E-04
490058723	LuxR family transcriptional regulator	1.36E+01	-9.05E-01	1.27E-01	-2.52E+00	3.49E-03	-1.61E+00	2.34E-02
490059211	(4Fe-4S)-binding protein	1.35E+01	-2.43E+00	1.35E-05	-2.51E+00	1.85E-05	-8.81E-02	6.71E-01
497685110	5,10-methylenetetrahydromethanopterin reductase	1.32E+01	-2.43E+00	6.27E-06	-2.51E+00	9.05E-06	-8.16E-02	6.44E-01
497685044	hypothetical protein	1.30E+01	-3.05E+00	1.87E-06	-2.51E+00	6.07E-06	5.39E-01	8.46E-03
490057794	6-phosphogluconolactonase, partial	1.44E+01	8.38E-01	4.53E-04	-2.51E+00	5.07E-06	-3.34E+00	1.58E-06
490057615	NADP oxidoreductase	1.02E+01	5.23E-01	2.49E-02	-2.51E+00	2.04E-05	-3.03E+00	6.53E-06
490059933	3'-5' exonuclease	1.22E+01	-1.91E+00	4.80E-05	-2.50E+00	2.13E-05	-5.91E-01	2.08E-02
490054173	MaoC family dehydratase	1.35E+01	-1.02E+00	1.15E-04	-2.50E+00	3.93E-06	-1.47E+00	2.25E-05
490057293	ABC transporter permease	1.22E+01	1.25E+00	9.54E-04	-2.49E+00	4.28E-05	-3.75E+00	5.57E-06
490056027	hypothetical protein	1.27E+01	-1.93E+00	1.89E-04	-2.49E+00	7.70E-05	-5.59E-01	6.96E-02
490051790	hypothetical protein	1.26E+01	-8.45E-01	4.30E-04	-2.49E+00	5.07E-06	-1.64E+00	1.89E-05
490054139	30S ribosomal protein S8	1.13E+01	-2.43E-02	9.46E-01	-2.48E+00	1.52E-04	-2.46E+00	1.32E-04
490052908	hydrogen peroxide-inducible protein	1.35E+01	7.50E-01	1.10E-03	-2.48E+00	5.79E-06	-3.23E+00	2.03E-06
490057429	ankyrin	1.30E+01	-8.43E-01	1.60E-03	-2.48E+00	1.25E-05	-1.64E+00	6.45E-05
497680874	hypothetical protein	1.16E+01	1.39E+00	1.45E-03	-2.48E+00	1.09E-04	-3.87E+00	1.06E-05
490054120	30S ribosomal protein S13	1.40E+01	-6.65E-01	2.11E-01	-2.47E+00	2.65E-03	-1.80E+00	1.05E-02
490057733	enoyl-CoA hydratase	1.00E+01	1.91E-01	2.08E-01	-2.46E+00	6.58E-06	-2.66E+00	3.82E-06
490052942	magnesium or manganese-dependent protein phosphatase	1.21E+01	-2.34E+00	8.83E-06	-2.46E+00	1.23E-05	-1.17E-01	5.24E-01

490047179	MerR-family transcriptional regulator	1.03E+01	-3.17E-02	9.63E-01	-2.45E+00	3.27E-03	-2.42E+00	3.06E-03
490054198	thioredoxin	1.32E+01	-1.63E+00	1.87E-04	-2.45E+00	3.68E-05	-8.20E-01	7.91E-03
490059516	molecular chaperone GroES	1.23E+01	-2.36E-01	5.08E-01	-2.45E+00	3.88E-04	-2.22E+00	5.73E-04
490050159	PbsX family transcriptional regulator	1.38E+01	-2.52E+00	3.03E-06	-2.45E+00	5.79E-06	7.16E-02	6.35E-01
490052515	preprotein translocase SecA	1.23E+01	-5.48E-01	7.26E-03	-2.44E+00	7.83E-06	-1.89E+00	1.84E-05
490056066	N-acetylglutamate synthase	1.27E+01	-2.35E+00	1.14E-05	-2.44E+00	1.64E-05	-9.23E-02	6.34E-01
490056432	HAD family hydrolase	1.12E+01	2.04E+00	8.00E-05	-2.44E+00	4.81E-05	-4.48E+00	3.04E-06
490054143	50S ribosomal protein L14	1.39E+01	-1.36E+00	1.61E-02	-2.44E+00	1.52E-03	-1.08E+00	4.96E-02
490055080	endonuclease VII	1.27E+01	-3.38E+00	2.57E-04	-2.44E+00	2.07E-03	9.41E-01	9.43E-02
497683567	DNA topoisomerase IV subunit A	1.28E+01	6.20E-01	3.63E-03	-2.44E+00	7.29E-06	-3.06E+00	2.57E-06
490052433	cell division protein FtsE	1.29E+01	-1.16E+00	7.11E-03	-2.44E+00	2.51E-04	-1.28E+00	5.86E-03
490059199	fructose-2,6-bisphosphatase	1.29E+01	3.58E-01	2.09E-01	-2.43E+00	1.13E-04	-2.79E+00	4.61E-05
490057035	alpha/beta hydrolase	1.40E+01	-2.67E+00	4.16E-06	-2.43E+00	1.04E-05	2.35E-01	1.96E-01
490050038	MarR family transcriptional regulator	1.08E+01	4.89E-01	1.09E-02	-2.43E+00	7.49E-06	-2.92E+00	2.96E-06
497681084	uracil-DNA glycosylase	1.42E+01	4.33E-01	4.13E-02	-2.43E+00	1.84E-05	-2.86E+00	6.56E-06
490056077	acetyltransferase	1.21E+01	-3.33E+00	1.11E-05	-2.42E+00	7.59E-05	9.05E-01	9.64E-03
490060252	histidine kinase	9.56E+00	-2.82E+00	5.67E-04	-2.41E+00	1.90E-03	4.05E-01	4.29E-01
490056264	ATPase AAA	1.16E+01	-7.50E-01	3.72E-03	-2.41E+00	1.81E-05	-1.66E+00	8.16E-05
490053230	histidine kinase	1.22E+01	-7.87E-02	7.33E-01	-2.41E+00	4.12E-05	-2.33E+00	3.92E-05
497681216	adenylosuccinate lyase	1.36E+01	-2.09E-01	3.53E-01	-2.39E+00	4.28E-05	-2.19E+00	5.43E-05
490060228	techoic acid ABC transporter ATP-binding protein	1.18E+01	7.22E-01	9.89E-03	-2.39E+00	3.86E-05	-3.11E+00	9.00E-06
497685041	calcium-binding protein	1.18E+01	-3.32E+00	2.41E-06	-2.39E+00	1.46E-05	9.29E-01	1.26E-03
490054722	hypothetical protein	1.19E+01	-6.50E-01	1.97E-03	-2.39E+00	5.88E-06	-1.74E+00	1.70E-05
490055111	hypothetical protein	1.36E+01	-4.95E+00	1.16E-06	-2.39E+00	2.04E-05	2.57E+00	1.11E-05
490051148	cysteinyl-tRNA synthetase	1.33E+01	-3.87E-01	2.03E-02	-2.39E+00	5.79E-06	-2.00E+00	8.58E-06
490060210	3-hydroxyacyl-CoA dehydrogenase	1.27E+01	-7.47E-01	1.47E-03	-2.38E+00	8.12E-06	-1.63E+00	3.39E-05
497682943	hydrolase	1.43E+01	-2.54E+00	1.47E-03	-2.37E+00	3.10E-03	1.64E-01	7.67E-01
490050761	hypothetical protein	1.12E+01	-5.11E-01	5.83E-03	-2.37E+00	5.79E-06	-1.86E+00	1.13E-05
497681398	ATPase	1.29E+01	1.70E-02	9.73E-01	-2.37E+00	1.18E-03	-2.39E+00	1.01E-03
497682104	ATP-dependent helicase	1.30E+01	-2.20E+00	3.97E-05	-2.37E+00	4.17E-05	-1.72E-01	4.68E-01

490054708	oxppcycle protein	1.41E+01	-1.39E+00	3.29E-04	-2.37E+00	3.39E-05	-9.81E-01	2.57E-03
497683278	hydrolase	1.13E+01	-3.52E-01	9.25E-02	-2.37E+00	2.37E-05	-2.02E+00	3.97E-05
497684722	translation initiation factor 2	1.33E+01	-2.91E+00	3.40E-06	-2.37E+00	1.34E-05	5.42E-01	1.46E-02
490059323	transferase	1.48E+01	-2.30E+00	1.37E-04	-2.37E+00	1.74E-04	-6.96E-02	8.23E-01
490060315	sugar phosphotransferase	1.39E+01	-2.52E-01	1.34E-01	-2.36E+00	1.01E-05	-2.11E+00	1.26E-05
490054428	UDP-glucose 6-dehydrogenase	1.24E+01	2.97E-04	9.99E-01	-2.36E+00	7.24E-05	-2.36E+00	5.99E-05
497685194	5,10-methylenetetrahydrofolate reductase	1.33E+01	2.93E+00	1.57E-06	-2.36E+00	5.07E-06	-5.29E+00	2.01E-07
497681386	GntR family transcriptional regulator	1.18E+01	-2.82E-01	6.71E-01	-2.35E+00	9.48E-03	-2.07E+00	1.53E-02
490058484	SMI1_KNR4 domain-containing protein	1.16E+01	3.87E-01	1.69E-01	-2.35E+00	1.19E-04	-2.74E+00	4.50E-05
490059556	ABC-type dipeptide transport system, solute-binding protein	1.28E+01	-3.03E+00	4.04E-06	-2.35E+00	2.02E-05	6.82E-01	8.05E-03
490055329	isopropylmalate isomerase	1.28E+01	-1.28E-02	9.40E-01	-2.35E+00	6.80E-06	-2.34E+00	5.23E-06
497681801	reductase	1.34E+01	-9.25E-01	1.29E-03	-2.35E+00	1.93E-05	-1.42E+00	1.77E-04
490050197	DNA-binding protein	9.67E+00	-1.17E+00	9.20E-04	-2.34E+00	4.11E-05	-1.17E+00	1.24E-03
490056114	cytidylate kinase	1.36E+01	-1.82E+00	2.57E-04	-2.34E+00	1.06E-04	-5.20E-01	8.68E-02
490050760	hydroxyurea phosphotransferase	1.10E+01	1.78E+00	2.59E-04	-2.33E+00	9.77E-05	-4.12E+00	5.70E-06
490050170	beta-lactamase	1.26E+01	-3.59E+00	1.32E-06	-2.33E+00	7.16E-06	1.26E+00	9.42E-05
490058571	NADP oxidoreductase coenzyme F420-dependent	1.37E+01	9.79E-01	2.26E-03	-2.33E+00	4.13E-05	-3.31E+00	6.56E-06
490061049	alkanal monooxygenase	1.33E+01	-3.81E+00	2.09E-05	-2.33E+00	3.72E-04	1.48E+00	3.36E-03
497684117	hypothetical protein	1.31E+01	-2.36E+00	3.93E-06	-2.33E+00	7.10E-06	2.95E-02	8.44E-01
497683812	isopentenyl-diphosphate delta-isomerase	1.04E+01	-1.14E+00	7.41E-04	-2.33E+00	3.09E-05	-1.19E+00	8.00E-04
490054149	30S ribosomal protein S19	1.61E+01	3.99E-01	2.32E-02	-2.33E+00	7.91E-06	-2.72E+00	3.42E-06
490053887	NADH:ubiquinone oxidoreductase subunit H	1.43E+01	-2.94E+00	6.71E-04	-2.33E+00	3.32E-03	6.12E-01	2.73E-01
497681485	chromosome partitioning protein	1.28E+01	6.50E-01	2.26E-03	-2.32E+00	7.22E-06	-2.98E+00	2.49E-06
490052580	gamma-glutamyl cyclotransferase	1.02E+01	4.07E-01	1.60E-02	-2.32E+00	6.12E-06	-2.73E+00	2.62E-06
490054456	acyl-CoA synthetase	1.38E+01	5.69E-01	5.91E-03	-2.32E+00	9.11E-06	-2.89E+00	3.20E-06
490054938	peptidase C45	1.32E+01	-1.79E+00	6.95E-06	-2.32E+00	5.07E-06	-5.28E-01	4.29E-03
490057941	glucokinase	1.44E+01	5.67E-01	1.09E-02	-2.32E+00	1.76E-05	-2.89E+00	5.23E-06
490060004	regulatory protein	1.09E+01	3.90E-01	2.38E-02	-2.32E+00	7.67E-06	-2.71E+00	3.34E-06
490060430	Puromycin N-acetyltransferase	1.24E+01	1.70E+00	1.80E-05	-2.32E+00	7.52E-06	-4.01E+00	1.10E-06
490057927	transcriptional regulator	1.51E+01	-1.74E+00	1.66E-04	-2.32E+00	5.72E-05	-5.80E-01	3.91E-02

490061540	ABC-type Fe3+-hydroxamate transport system, solute-binding protein	1.06E+01	1.20E+00	2.68E-04	-2.31E+00	1.80E-05	-3.52E+00	2.61E-06
497681275	GntR family transcriptional regulator	9.47E+00	1.08E+00	2.23E-04	-2.31E+00	9.05E-06	-3.39E+00	2.03E-06
497685232	short-chain dehydrogenase	8.76E+00	-1.32E+00	2.82E-03	-2.31E+00	2.37E-04	-9.93E-01	1.39E-02
490055113	cytochrome P450	1.27E+01	-3.15E-02	8.03E-01	-2.31E+00	4.31E-06	-2.28E+00	3.05E-06
490055112	nucleoside triphosphate pyrophosphohydrolase	1.21E+01	7.84E-01	1.04E-03	-2.31E+00	8.33E-06	-3.09E+00	2.49E-06
490058806	membrane protein	1.26E+01	3.53E-01	1.67E-01	-2.30E+00	8.01E-05	-2.66E+00	3.28E-05
490052896	hypothetical protein	1.20E+01	-5.05E+00	1.15E-06	-2.30E+00	2.11E-05	2.75E+00	7.02E-06
490054237	cystathionine gamma-lyase	1.30E+01	1.45E-01	6.73E-01	-2.30E+00	4.01E-04	-2.45E+00	2.53E-04
497683809	glutamine amidotransferase	1.30E+01	-1.98E+00	7.15E-04	-2.30E+00	4.90E-04	-3.20E-01	3.97E-01
497683951	LysR family transcriptional regulator	1.13E+01	2.81E+00	1.45E-05	-2.30E+00	5.62E-05	-5.11E+00	2.03E-06
497682615	acetyltransferase	1.42E+01	1.25E-01	7.47E-01	-2.29E+00	6.98E-04	-2.42E+00	4.61E-04
490059259	peptidase M22	1.03E+01	-1.76E-01	4.72E-01	-2.29E+00	8.29E-05	-2.11E+00	1.04E-04
497681323	membrane protein	1.23E+01	4.43E-01	1.21E-01	-2.29E+00	1.32E-04	-2.73E+00	4.46E-05
490058380	hypothetical protein	1.30E+01	7.89E-01	2.09E-02	-2.29E+00	1.79E-04	-3.08E+00	3.31E-05
490054860	oxidoreductase	1.39E+01	-1.65E+00	1.09E-04	-2.29E+00	3.20E-05	-6.37E-01	1.57E-02
490057772	1-aminocyclopropane-1-carboxylate deaminase	1.51E+01	-9.60E-01	5.95E-03	-2.28E+00	1.11E-04	-1.32E+00	1.63E-03
497683638	glycosyl transferase	1.29E+01	4.20E-02	7.95E-01	-2.28E+00	9.86E-06	-2.32E+00	6.74E-06
490054041	glyceraldehyde-3-phosphate dehydrogenase	1.14E+01	-8.74E-01	2.04E-03	-2.28E+00	2.49E-05	-1.40E+00	2.30E-04
490057884	anthranilate synthase subunit I	1.29E+01	-3.35E-01	7.35E-02	-2.28E+00	1.72E-05	-1.94E+00	2.61E-05
490051425	glycerophosphoryl diester phosphodiesterase	1.28E+01	-6.66E-01	4.09E-02	-2.27E+00	1.90E-04	-1.61E+00	1.01E-03
497685129	ArsR family transcriptional regulator	1.09E+01	-2.57E-01	6.16E-02	-2.27E+00	5.07E-06	-2.02E+00	5.57E-06
490058154	2-isopropylmalate synthase	1.33E+01	5.34E-01	1.36E-02	-2.27E+00	1.84E-05	-2.80E+00	5.57E-06
490058041	XRE family transcriptional regulator	1.05E+01	-1.32E+00	1.75E-04	-2.26E+00	1.96E-05	-9.43E-01	1.30E-03
490053891	NADH:ubiquinone oxidoreductase subunit L	1.22E+01	-2.21E+00	2.92E-03	-2.26E+00	3.96E-03	-4.74E-02	9.31E-01
490058025	heme oxygenase	1.31E+01	2.40E-01	5.85E-01	-2.26E+00	1.70E-03	-2.50E+00	8.93E-04
497681192	DEAD/DEAH box helicase	1.28E+01	6.06E-01	7.14E-03	-2.25E+00	1.76E-05	-2.86E+00	4.84E-06
497685434	plasmid stabilization protein	1.04E+01	-4.26E+00	1.75E-05	-2.25E+00	6.37E-04	2.01E+00	1.02E-03
490051375	DNA polymerase III subunit delta	1.35E+01	8.36E-01	8.47E-03	-2.25E+00	8.73E-05	-3.09E+00	1.55E-05
490056068	acetylglutamate kinase	1.45E+01	-1.20E+00	5.82E-04	-2.25E+00	3.73E-05	-1.05E+00	1.58E-03
490053404	hypothetical protein	1.56E+01	6.24E-01	8.69E-02	-2.25E+00	4.60E-04	-2.87E+00	1.09E-04

497682512	ABC transporter substrate-binding protein	1.11E+01	-2.89E+00	2.17E-05	-2.24E+00	1.16E-04	6.50E-01	3.86E-02
490057514	Putative uroporphyrin-III methyltransferase	1.21E+01	1.68E+00	3.12E-05	-2.24E+00	1.41E-05	-3.93E+00	1.63E-06
490055878	oligoribonuclease	1.46E+01	2.37E-01	2.33E-01	-2.24E+00	3.04E-05	-2.48E+00	1.49E-05
490053878	glycoside hydrolase	1.29E+01	2.70E-01	5.77E-01	-2.24E+00	2.88E-03	-2.51E+00	1.42E-03
497685127	threonine dehydratase	1.35E+01	1.36E+00	3.71E-04	-2.24E+00	4.41E-05	-3.59E+00	4.56E-06
490051745	aldo/keto reductase	1.15E+01	-6.97E-01	6.11E-03	-2.23E+00	2.73E-05	-1.54E+00	1.39E-04
490050102	threonine synthase	1.38E+01	8.26E-01	2.28E-03	-2.23E+00	2.39E-05	-3.06E+00	4.92E-06
490054117	DNA-directed RNA polymerase subunit alpha	1.40E+01	-7.79E-01	1.46E-03	-2.23E+00	1.33E-05	-1.45E+00	7.43E-05
497683955	Galactose oxidase	1.37E+01	-1.83E+00	4.82E-05	-2.22E+00	2.91E-05	-3.92E-01	7.75E-02
490052906	alkyl hydroperoxide reductase	1.42E+01	-2.95E+00	2.79E-06	-2.22E+00	1.49E-05	7.31E-01	3.03E-03
490053914	LuxR family transcriptional regulator	1.37E+01	-1.33E+00	1.36E-04	-2.22E+00	1.81E-05	-8.91E-01	1.40E-03
490053936	DNA mismatch repair protein MutT	9.09E+00	5.59E-03	9.85E-01	-2.22E+00	1.14E-04	-2.22E+00	9.37E-05
490057379	oxidoreductase	1.24E+01	-2.62E-01	2.61E-01	-2.21E+00	6.89E-05	-1.95E+00	1.09E-04
490060439	hypothetical protein	1.37E+01	-2.75E+00	1.30E-04	-2.21E+00	5.83E-04	5.36E-01	1.66E-01
490054160	30S ribosomal protein S7	1.27E+01	-5.03E-02	7.78E-01	-2.20E+00	1.86E-05	-2.15E+00	1.56E-05
490059512	methyltransferase	1.06E+01	1.01E+00	7.55E-04	-2.20E+00	2.30E-05	-3.21E+00	3.82E-06
490052491	cysteine synthase	1.35E+01	-9.02E-01	3.58E-03	-2.20E+00	5.74E-05	-1.30E+00	7.49E-04
490053886	NADH dehydrogenase subunit G	1.30E+01	-2.71E+00	2.35E-06	-2.20E+00	8.24E-06	5.16E-01	8.32E-03
490057294	multidrug ABC transporter ATPase	1.25E+01	2.57E-01	3.64E-01	-2.20E+00	2.10E-04	-2.45E+00	9.91E-05
490050525	methylmalonate-semialdehyde dehydrogenase	9.97E+00	1.51E+00	6.45E-03	-2.19E+00	1.55E-03	-3.71E+00	8.71E-05
497682945	threonine synthase	1.20E+01	-1.08E+00	1.59E-04	-2.19E+00	8.55E-06	-1.11E+00	1.71E-04
490052483	nicotinate phosphoribosyltransferase	1.33E+01	1.72E+00	1.27E-04	-2.18E+00	5.55E-05	-3.90E+00	3.79E-06
490059485	hypothetical protein	1.10E+01	-5.81E-01	9.91E-03	-2.18E+00	2.27E-05	-1.60E+00	7.83E-05
490057320	tripeptidyl aminopeptidase	1.49E+01	8.10E-01	3.63E-03	-2.18E+00	3.72E-05	-2.99E+00	6.86E-06
490058675	4-phosphopantetheinyl transferase	1.23E+01	-7.30E-01	5.67E-04	-2.18E+00	5.46E-06	-1.45E+00	2.16E-05
490050350	hypothetical protein	1.14E+01	-3.82E+00	3.33E-06	-2.18E+00	6.09E-05	1.64E+00	2.18E-04
490059968	sulfate adenylyltransferase subunit 2	1.29E+01	-7.41E-01	5.05E-02	-2.17E+00	5.61E-04	-1.43E+00	4.16E-03
490059282	ATPase	9.15E+00	6.21E-01	4.72E-02	-2.17E+00	2.06E-04	-2.79E+00	4.63E-05
490053871	radical SAM protein	1.21E+01	8.82E-01	2.43E-03	-2.17E+00	3.77E-05	-3.05E+00	6.41E-06
497683559	TerD-family protein	1.39E+01	-2.67E+00	1.17E-05	-2.17E+00	4.81E-05	5.04E-01	4.50E-02
490053269	methyltransferase type 12	1.30E+01	9.63E-01	5.02E-03	-2.17E+00	1.23E-04	-3.13E+00	1.69E-05

490053431	oxidoreductase	1.41E+01	-1.83E+00	3.10E-05	-2.17E+00	2.28E-05	-3.31E-01	9.94E-02
497685037	hypothetical protein	1.37E+01	1.95E-01	1.56E-01	-2.16E+00	7.09E-06	-2.35E+00	3.82E-06
490059585	homoserine dehydrogenase	1.23E+01	-8.84E-03	9.68E-01	-2.16E+00	2.07E-05	-2.15E+00	1.59E-05
497683542	DEAD/DEAH box helicase	1.39E+01	7.06E-01	2.17E-02	-2.15E+00	1.43E-04	-2.86E+00	2.89E-05
497685356	PBS lyase	1.62E+01	-1.33E+00	2.54E-03	-2.15E+00	3.22E-04	-8.23E-01	2.87E-02
490054415	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	1.13E+01	3.97E-01	6.83E-02	-2.15E+00	3.98E-05	-2.55E+00	1.44E-05
490059052	haloacid dehalogenase	8.90E+00	8.61E-01	4.71E-03	-2.15E+00	6.73E-05	-3.01E+00	1.12E-05
490059586	homoserine kinase	1.26E+01	3.71E-01	2.17E-02	-2.14E+00	7.83E-06	-2.51E+00	3.34E-06
490058298	cell division protein FtsK	1.15E+01	9.60E-02	5.11E-01	-2.14E+00	1.09E-05	-2.24E+00	6.56E-06
497682172	S-adenosyl-L-homocysteine hydrolase	1.43E+01	-1.86E-01	3.28E-01	-2.14E+00	3.25E-05	-1.95E+00	4.02E-05
490051101	hypothetical protein	1.39E+01	-6.18E-01	1.63E-02	-2.13E+00	5.47E-05	-1.51E+00	2.65E-04
490053985	aminoglycoside phosphotransferase	1.26E+01	-1.40E+00	1.82E-04	-2.13E+00	3.32E-05	-7.36E-01	6.16E-03
490058944	phosphoribosylglycinamide synthetase	1.18E+01	1.33E+00	7.69E-04	-2.13E+00	1.00E-04	-3.46E+00	8.14E-06
497683467	hydrolase	1.29E+01	-5.66E-01	9.46E-03	-2.13E+00	2.13E-05	-1.56E+00	7.28E-05
497683461	dynein regulation protein LC7	1.68E+01	-9.29E-01	1.66E-03	-2.13E+00	3.74E-05	-1.20E+00	5.90E-04
497685206	hypothetical protein	1.49E+01	-3.85E+00	2.94E-06	-2.12E+00	6.14E-05	1.73E+00	1.48E-04
490050156	N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase	1.25E+01	-2.94E+00	1.32E-06	-2.12E+00	5.07E-06	8.18E-01	3.09E-04
497684037	hypothetical protein	1.27E+01	-8.54E-01	6.05E-02	-2.12E+00	1.74E-03	-1.27E+00	1.77E-02
490059303	tryptophanyl-tRNA synthetase	1.11E+01	1.19E+00	4.55E-04	-2.12E+00	3.76E-05	-3.32E+00	4.39E-06
497683714	GntR family transcriptional regulator	1.31E+01	2.23E-01	1.18E-01	-2.12E+00	7.83E-06	-2.34E+00	4.06E-06
490056617	transcriptional regulator	1.15E+01	-1.14E-01	7.77E-01	-2.12E+00	1.24E-03	-2.00E+00	1.46E-03
490057452	3,4-dihydroxy-2-butanone 4-phosphate synthase	1.21E+01	7.94E-02	6.27E-01	-2.11E+00	1.78E-05	-2.19E+00	1.10E-05
490050165	conserved hypothetical protein	1.30E+01	-3.14E+00	1.15E-06	-2.11E+00	4.11E-06	1.03E+00	6.22E-05
490057355	hypothetical protein	1.30E+01	-2.34E+00	4.60E-06	-2.11E+00	1.29E-05	2.31E-01	1.64E-01
490054094	uracil phosphoribosyltransferase	1.37E+01	3.99E-02	8.35E-01	-2.11E+00	2.73E-05	-2.15E+00	2.00E-05
490059261	O-sialoglycoprotein endopeptidase	1.15E+01	9.19E-01	6.25E-04	-2.11E+00	1.66E-05	-3.03E+00	3.01E-06
490052578	DeoR family transcripitonal regulator	8.23E+00	-9.72E-01	1.87E-03	-2.11E+00	5.35E-05	-1.14E+00	1.11E-03
490055076	hypothetical protein	1.41E+01	8.70E-02	6.74E-01	-2.11E+00	4.79E-05	-2.20E+00	3.24E-05
490054111	50S ribosomal protein L13	1.21E+01	-5.16E-01	3.03E-02	-2.11E+00	5.15E-05	-1.59E+00	1.79E-04

490058573	LuxR family transcriptional regulator	1.28E+01	-8.38E-01	4.13E-02	-2.10E+00	9.46E-04	-1.26E+00	1.02E-02
490059080	phosphoserine aminotransferase	1.05E+01	2.37E-01	6.94E-02	-2.10E+00	5.50E-06	-2.34E+00	2.78E-06
490056214	hypothetical protein	1.49E+01	-1.51E+00	7.23E-04	-2.10E+00	2.01E-04	-5.84E-01	6.35E-02
490054298	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.31E+01	-2.61E-01	4.28E-01	-2.09E+00	5.98E-04	-1.83E+00	1.06E-03
490054208	inositol-3-phosphate synthase	1.26E+01	-1.67E-02	9.04E-01	-2.09E+00	6.67E-06	-2.07E+00	5.23E-06
490050084	F0F1 ATP synthase subunit gamma	1.45E+01	1.75E-01	2.37E-01	-2.09E+00	1.19E-05	-2.26E+00	6.07E-06
490050315	methyltransferase	1.38E+01	-4.45E+00	2.52E-06	-2.09E+00	1.05E-04	2.36E+00	4.57E-05
490053240	histidine kinase	1.43E+01	-4.68E-01	5.21E-02	-2.09E+00	6.86E-05	-1.62E+00	2.14E-04
490057572	regulatory protein	1.34E+01	3.88E-01	4.78E-02	-2.09E+00	2.58E-05	-2.47E+00	9.23E-06
490051755	hypothetical protein	1.60E+01	-7.39E-02	6.76E-01	-2.08E+00	2.49E-05	-2.01E+00	2.31E-05
497683607	chromosome partitioning protein ParB	1.43E+01	-1.84E+00	1.71E-02	-2.08E+00	1.45E-02	-2.43E-01	7.19E-01
490057863	dihydropyrimidine dehydrogenase subunit A	1.23E+01	1.55E+00	1.35E-05	-2.08E+00	6.36E-06	-3.63E+00	8.24E-07
490050168	cytochrome P450	1.35E+01	-2.90E+00	2.71E-06	-2.08E+00	1.73E-05	8.24E-01	1.40E-03
490055747	membrane protein	1.24E+01	-3.58E+00	1.02E-05	-2.08E+00	2.19E-04	1.50E+00	1.04E-03
490055589	iron ABC transporter ATP-binding protein	1.28E+01	-7.98E-01	1.09E-01	-2.08E+00	3.66E-03	-1.28E+00	2.84E-02
490050212	alanine-phosphoribitol ligase	1.28E+01	-1.49E+00	5.16E-04	-2.07E+00	1.40E-04	-5.85E-01	4.84E-02
497683252	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	1.46E+01	-1.14E+00	5.91E-04	-2.07E+00	4.28E-05	-9.28E-01	2.20E-03
490059698	lipase	1.30E+01	-2.35E+00	3.46E-03	-2.06E+00	9.42E-03	2.91E-01	6.32E-01
490059042	hypothetical protein	1.01E+01	4.78E-01	9.47E-03	-2.06E+00	1.21E-05	-2.54E+00	3.92E-06
497681608	sporulation protein	1.16E+01	8.15E-01	1.46E-03	-2.06E+00	2.20E-05	-2.87E+00	4.16E-06
490054888	ribosome recycling factor	1.34E+01	-7.81E-01	1.73E-03	-2.06E+00	2.13E-05	-1.27E+00	1.76E-04
497681006	cyclase	1.09E+01	-4.42E-01	8.06E-02	-2.05E+00	1.10E-04	-1.61E+00	3.30E-04
497680988	hypothetical protein	1.44E+01	-1.13E+00	7.04E-03	-2.05E+00	5.48E-04	-9.17E-01	2.33E-02
497681311	guanylate kinase	1.15E+01	6.06E-01	1.01E-02	-2.05E+00	3.56E-05	-2.65E+00	8.58E-06
490052149	glucokinase	1.19E+01	-3.71E-01	4.29E-02	-2.05E+00	2.06E-05	-1.68E+00	4.02E-05
490054371	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	1.16E+01	5.37E-01	1.55E-02	-2.04E+00	3.25E-05	-2.58E+00	8.76E-06
490055754	ATP phosphoribosyltransferase	1.28E+01	-8.83E-02	8.69E-01	-2.04E+00	5.16E-03	-1.95E+00	5.69E-03
490053371	radical SAM protein	1.43E+01	1.82E-01	3.90E-01	-2.04E+00	6.96E-05	-2.22E+00	3.80E-05
497681131	hypothetical protein	1.39E+01	1.84E-01	2.10E-01	-2.04E+00	1.25E-05	-2.22E+00	6.22E-06
490054100	orotidine 5'-phosphate decarboxylase	1.45E+01	6.55E-01	3.04E-03	-2.04E+00	1.75E-05	-2.69E+00	4.06E-06

490051150	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1.00E+01	1.15E+00	7.53E-04	-2.03E+00	6.09E-05	-3.19E+00	6.22E-06
490052783	lipase	1.22E+01	1.47E+00	1.38E-05	-2.03E+00	5.79E-06	-3.50E+00	8.19E-07
497685032	glycosyl transferase	8.84E+00	5.65E-01	2.75E-01	-2.03E+00	6.18E-03	-2.60E+00	1.62E-03
490051727	NADP-dependent oxidoreductase	1.23E+01	-1.44E+00	1.30E-05	-2.03E+00	5.40E-06	-5.96E-01	1.44E-03
490055255	50S ribosomal protein L21	1.43E+01	-9.94E-01	2.17E-02	-2.03E+00	1.15E-03	-1.03E+00	2.43E-02
490054876	conserved hypothetical protein	1.10E+01	2.42E-01	1.64E-01	-2.03E+00	2.44E-05	-2.27E+00	1.12E-05
490060320	hypothetical protein	1.21E+01	-2.92E+00	4.44E-06	-2.03E+00	3.73E-05	8.94E-01	2.05E-03
490058227	RarC protein	9.15E+00	2.42E+00	1.78E-05	-2.02E+00	6.25E-05	-4.44E+00	2.23E-06
490059367	GlcNAc-PI de-N-acetylase	1.35E+01	-9.65E-01	1.43E-04	-2.02E+00	7.21E-06	-1.06E+00	1.11E-04
497685198	pyridoxamine 5'-phosphate oxidase	1.47E+01	4.15E-01	1.40E-02	-2.02E+00	1.01E-05	-2.44E+00	3.82E-06
490060383	pyruvate phosphate dikinase	9.08E+00	5.44E-01	1.92E-02	-2.02E+00	4.63E-05	-2.56E+00	1.22E-05
490052673	phosphoribosylamine--glycine ligase	1.40E+01	-4.47E-01	1.33E-01	-2.02E+00	3.19E-04	-1.57E+00	1.04E-03
497685398	hypothetical protein	1.59E+01	-2.24E+00	4.21E-05	-2.01E+00	1.07E-04	2.22E-01	3.64E-01
490057695	HAD family hydrolase	1.42E+01	6.12E-01	9.61E-02	-2.01E+00	8.91E-04	-2.62E+00	1.89E-04
490059788	translation initiation factor IF-2	1.30E+01	-3.57E-01	1.72E-02	-2.01E+00	7.11E-06	-1.65E+00	1.18E-05
490057426	Antagonist of KipI	1.31E+01	1.88E-01	1.56E-01	-2.01E+00	7.74E-06	-2.20E+00	4.18E-06
490052844	lectin PVL	1.47E+01	-4.36E+00	1.87E-06	-2.00E+00	7.92E-05	2.36E+00	2.91E-05
490057754	multidrug DMT transporter permease	9.95E+00	8.09E-01	4.87E-02	-2.00E+00	1.28E-03	-2.81E+00	1.87E-04
490053859	aromatic acid decarboxylase	1.35E+01	9.92E-01	2.58E-04	-2.00E+00	1.41E-05	-2.99E+00	2.49E-06
490053814	protease	1.32E+01	-8.50E-01	1.16E-03	-2.00E+00	2.40E-05	-1.15E+00	3.11E-04
497682009	gamma-glutamyl phosphate reductase	1.27E+01	-9.36E-01	3.94E-03	-2.00E+00	1.24E-04	-1.06E+00	2.79E-03
490050139	D-alanyl-D-alanine carboxypeptidase	1.22E+01	-1.46E+00	9.76E-05	-1.99E+00	3.20E-05	-5.28E-01	1.93E-02
497682613	phosphomethylpyrimidine synthase	1.22E+01	-7.48E-01	7.02E-02	-1.99E+00	1.55E-03	-1.24E+00	1.35E-02
490057467	rRNA cytosine-C5-methyltransferase	1.07E+01	1.68E+00	5.15E-04	-1.99E+00	3.27E-04	-3.67E+00	1.28E-05
490059700	amidase	1.27E+01	-2.42E+00	4.03E-03	-1.98E+00	1.45E-02	4.36E-01	4.98E-01
490060995	F420-dependent oxidoreductase	1.25E+01	-2.07E+00	1.77E-04	-1.98E+00	3.35E-04	9.34E-02	7.54E-01
490060317	glucose-methanol-choline oxidoreductase	1.41E+01	-2.39E+00	6.08E-06	-1.98E+00	2.34E-05	4.15E-01	3.61E-02
490058395	phosphatase	1.08E+01	7.92E-02	8.77E-01	-1.97E+00	5.00E-03	-2.05E+00	3.66E-03
490059040	RpiR family transcriptional regulator	1.34E+01	-4.70E-01	9.60E-02	-1.97E+00	2.50E-04	-1.50E+00	9.01E-04
490053097	conserved hypothetical protein	1.25E+01	-1.96E+00	1.08E-03	-1.97E+00	1.53E-03	-1.64E-02	9.67E-01

497681370	acetyltransferase	1.34E+01	4.30E-02	7.13E-01	-1.97E+00	5.79E-06	-2.01E+00	3.92E-06
490060448	MFS transporter	1.41E+01	-3.16E+00	1.67E-06	-1.97E+00	1.49E-05	1.19E+00	1.28E-04
497683553	hypothetical protein	1.33E+01	2.05E+00	8.83E-06	-1.96E+00	1.81E-05	-4.02E+00	1.22E-06
490057028	Germacradienol/germacrene D synthase	1.24E+01	-2.87E+00	2.11E-05	-1.96E+00	2.13E-04	9.11E-01	8.95E-03
497682688	peptidyl-prolyl cis-trans isomerase	1.22E+01	-1.10E-01	5.55E-01	-1.96E+00	4.43E-05	-1.85E+00	4.75E-05
497684029	2-amino-3-ketobutyrate CoA ligase	1.39E+01	-1.55E+00	6.22E-05	-1.96E+00	3.07E-05	-4.09E-01	4.62E-02
490059691	aminoglycoside 2'-N-acetyltransferase	1.32E+01	-8.98E-01	1.31E-02	-1.96E+00	4.28E-04	-1.06E+00	8.27E-03
497682822	RNA helicase	1.34E+01	1.54E-01	3.34E-01	-1.96E+00	2.28E-05	-2.11E+00	1.22E-05
490051647	DeoR family transcriptional regulator	1.14E+01	1.41E+00	4.00E-05	-1.96E+00	1.46E-05	-3.37E+00	1.73E-06
490059803	hypothetical protein	1.41E+01	-4.79E+00	1.15E-06	-1.96E+00	3.07E-05	2.83E+00	4.97E-06
490052798	hypothetical protein	1.43E+01	-1.77E+00	2.68E-05	-1.95E+00	2.66E-05	-1.81E-01	3.10E-01
490061204	lipase	1.38E+01	-7.42E-01	3.49E-03	-1.95E+00	3.98E-05	-1.21E+00	3.85E-04
490056660	succinate dehydrogenase	1.28E+01	-6.53E-01	2.48E-01	-1.95E+00	1.09E-02	-1.30E+00	5.07E-02
490050756	flavodoxin	1.26E+01	-2.63E+00	4.09E-06	-1.95E+00	2.49E-05	6.86E-01	4.04E-03
490046282	30S ribosomal protein S10	1.29E+01	-1.13E+00	9.35E-03	-1.94E+00	1.02E-03	-8.08E-01	4.74E-02
490055854	sulfate ABC transporter permease	1.10E+01	2.92E-01	2.88E-01	-1.94E+00	3.17E-04	-2.23E+00	1.28E-04
490058570	pantothenate synthetase	9.22E+00	1.97E+00	9.56E-04	-1.94E+00	1.53E-03	-3.91E+00	3.52E-05
497683373	ATP synthase subunit beta	1.27E+01	2.31E-01	1.94E-01	-1.94E+00	3.43E-05	-2.17E+00	1.62E-05
490057189	heat shock protein 90	1.31E+01	-8.22E-01	1.62E-02	-1.93E+00	3.78E-04	-1.11E+00	5.58E-03
490056760	oxidoreductase	1.44E+01	-5.75E-01	4.17E-02	-1.93E+00	2.10E-04	-1.36E+00	1.15E-03
490060232	phytoene synthase	1.19E+01	3.25E+00	2.39E-05	-1.93E+00	5.09E-04	-5.18E+00	4.05E-06
497682932	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	1.28E+01	4.06E-01	2.30E-01	-1.93E+00	9.26E-04	-2.34E+00	2.95E-04
490054317	branched-chain amino acid ABC transporter ATP-binding protein	1.23E+01	-1.93E+00	7.67E-04	-1.93E+00	1.15E-03	-2.31E-04	9.99E-01
490054877	hypothetical protein	1.25E+01	2.59E-01	4.03E-01	-1.92E+00	6.63E-04	-2.18E+00	2.98E-04
497681559	amidohydrolase	1.21E+01	1.10E-01	3.91E-01	-1.92E+00	9.79E-06	-2.03E+00	5.81E-06
497682262	esterase	1.37E+01	-9.98E-01	1.43E-04	-1.92E+00	9.86E-06	-9.21E-01	2.73E-04
490058283	copper-binding protein	1.54E+01	-1.68E-01	4.03E-01	-1.92E+00	7.30E-05	-1.75E+00	9.73E-05
497682013	putative bifunctional ribulose 5-phosphate reductase/CDP-ribitol pyrophosphorylase	1.26E+01	-1.06E-01	5.89E-01	-1.92E+00	6.14E-05	-1.81E+00	6.71E-05
490059842	ATP-dependent DNA helicase RecQ	1.20E+01	5.46E-01	8.62E-03	-1.92E+00	2.54E-05	-2.46E+00	6.45E-06
490056851	hypothetical protein	1.36E+01	-2.59E+00	1.67E-06	-1.92E+00	7.21E-06	6.77E-01	8.95E-04

490056886	chemotaxis protein CheY	1.29E+01	-4.04E-01	6.37E-03	-1.91E+00	5.79E-06	-1.51E+00	1.12E-05
490056356	acyl-ACP desaturase	1.07E+01	3.16E-01	1.60E-01	-1.91E+00	1.08E-04	-2.23E+00	4.09E-05
497683089	hypothetical protein	1.32E+01	-1.25E-01	4.33E-01	-1.91E+00	2.51E-05	-1.79E+00	2.73E-05
497681743	glycosyl transferase family 1	1.07E+01	-7.43E-02	8.00E-01	-1.91E+00	3.85E-04	-1.84E+00	4.13E-04
490050759	hypothetical protein	1.42E+01	2.08E-01	3.97E-01	-1.91E+00	2.12E-04	-2.12E+00	1.04E-04
497681868	hypothetical protein	1.43E+01	-4.42E-01	3.51E-02	-1.91E+00	4.70E-05	-1.47E+00	1.48E-04
497681732	phospho-2-dehydro-3-deoxyheptonate aldolase	1.33E+01	1.61E-01	3.30E-01	-1.90E+00	2.91E-05	-2.07E+00	1.57E-05
497683112	50S ribosomal protein L22	1.44E+01	3.81E-02	8.77E-01	-1.90E+00	1.41E-04	-1.94E+00	1.06E-04
490056110	glycosyl transferase	1.30E+01	-1.08E+00	4.18E-04	-1.90E+00	3.56E-05	-8.25E-01	2.13E-03
490053558	XRE family transcriptional regulator	9.14E+00	-7.75E-04	9.97E-01	-1.90E+00	1.11E-04	-1.90E+00	9.26E-05
497680879	hypothetical protein	1.36E+01	-1.33E+00	1.96E-04	-1.90E+00	4.90E-05	-5.67E-01	1.73E-02
490058700	orotate phosphoribosyltransferase	1.17E+01	2.75E+00	4.75E-05	-1.89E+00	4.72E-04	-4.64E+00	5.44E-06
490051432	16S rRNA methyltransferase	1.47E+01	-2.85E-01	1.93E-01	-1.89E+00	1.05E-04	-1.61E+00	2.06E-04
490054494	Crp/Fnr family transcriptional regulator	1.23E+01	9.83E-02	6.20E-01	-1.89E+00	6.78E-05	-1.99E+00	4.32E-05
497683509	PucR family transcriptional regulator	1.36E+01	8.44E-01	4.39E-04	-1.89E+00	1.39E-05	-2.74E+00	2.57E-06
490052563	zinc-binding dehydrogenase	1.05E+01	-6.00E-01	6.02E-03	-1.89E+00	2.91E-05	-1.29E+00	1.58E-04
490055528	ketol-acid reductoisomerase	1.27E+01	3.41E-01	1.66E-01	-1.89E+00	1.82E-04	-2.23E+00	6.45E-05
497683513	acetyltransferase	1.37E+01	-1.41E+00	7.86E-05	-1.89E+00	2.80E-05	-4.83E-01	1.97E-02
490051939	hypothetical protein	1.44E+01	-8.64E-01	5.55E-04	-1.89E+00	1.84E-05	-1.03E+00	2.96E-04
490055585	HNH nuclease	1.33E+01	-6.31E-02	8.66E-01	-1.89E+00	1.24E-03	-1.82E+00	1.31E-03
490051024	DNA primase	1.20E+01	-7.30E-01	1.01E-03	-1.89E+00	1.48E-05	-1.16E+00	1.16E-04
490053869	conserved hypothetical protein	1.25E+01	4.32E-01	2.27E-01	-1.88E+00	1.40E-03	-2.31E+00	4.20E-04
490050142	aldehyde dehydrogenase	8.97E+00	-1.65E+00	2.60E-05	-1.88E+00	2.27E-05	-2.34E-01	1.66E-01
490054628	competence damage-inducible protein A	1.39E+01	-4.00E+00	3.29E-06	-1.88E+00	1.57E-04	2.12E+00	7.12E-05
490059900	deoxyuridine 5'-triphosphate nucleotidohydrolase	9.97E+00	-1.37E-01	4.03E-01	-1.88E+00	3.13E-05	-1.74E+00	3.61E-05
490052553	ABC transporter	1.34E+01	-1.79E-01	3.37E-01	-1.88E+00	5.50E-05	-1.70E+00	7.44E-05
490054170	aspartate aminotransferase	1.27E+01	-2.59E-01	8.17E-02	-1.88E+00	1.48E-05	-1.62E+00	2.13E-05
497685427	acyl-CoA dehydrogenase	1.19E+01	5.36E-01	2.06E-02	-1.88E+00	6.68E-05	-2.41E+00	1.65E-05
497682940	N-acetyltransferase GCN5	1.43E+01	5.26E-01	2.04E-01	-1.87E+00	2.94E-03	-2.40E+00	7.27E-04
497681516	tyrosyl-tRNA synthetase	1.39E+01	-3.09E-01	9.11E-02	-1.87E+00	3.68E-05	-1.56E+00	7.22E-05

490057566	aldehyde dehydrogenase	1.16E+01	-1.19E+00	2.18E-02	-1.87E+00	4.34E-03	-6.81E-01	1.60E-01
490054166	50S ribosomal protein L1	1.17E+01	-2.89E-01	1.51E-01	-1.87E+00	6.72E-05	-1.58E+00	1.31E-04
490053291	ABC transporter substrate-binding protein	1.30E+01	-2.15E+00	3.10E-03	-1.87E+00	8.92E-03	2.82E-01	6.03E-01
490052791	transcriptional regulator	1.40E+01	-2.16E+00	1.90E-05	-1.87E+00	5.82E-05	2.97E-01	1.54E-01
490054136	30S ribosomal protein S5	1.32E+01	-5.64E-01	2.53E-02	-1.87E+00	1.16E-04	-1.30E+00	6.51E-04
497682129	IclR family transcriptional regulator	1.52E+01	-1.93E+00	3.86E-05	-1.86E+00	6.86E-05	6.58E-02	7.49E-01
497682071	acyl-CoA dehydrogenase	1.28E+01	-1.97E-01	3.33E-01	-1.86E+00	8.89E-05	-1.66E+00	1.31E-04
490056673	50S ribosomal protein L19	1.35E+01	-1.35E+00	1.40E-04	-1.86E+00	4.25E-05	-5.06E-01	2.24E-02
490051556	TetR family transcriptional regulator	1.23E+01	2.83E-02	9.42E-01	-1.86E+00	1.02E-03	-1.89E+00	8.35E-04
497681987	peptidase S41	1.32E+01	-1.70E+00	5.32E-04	-1.85E+00	5.09E-04	-1.54E-01	6.11E-01
490057930	glycine oxidase	1.14E+01	-4.07E-02	8.01E-01	-1.85E+00	2.45E-05	-1.81E+00	2.12E-05
497685451	hydrolase	1.47E+01	-2.90E+00	6.56E-06	-1.85E+00	8.76E-05	1.05E+00	1.38E-03
497683024	hypothetical protein	1.30E+01	1.47E-01	4.35E-01	-1.85E+00	6.57E-05	-1.99E+00	3.72E-05
490055486	hypothetical protein	1.02E+01	1.45E+00	1.42E-03	-1.84E+00	6.09E-04	-3.29E+00	2.68E-05
490057736	ABC transporter	1.37E+01	2.39E-01	3.46E-01	-1.84E+00	2.87E-04	-2.08E+00	1.28E-04
490055137	transcriptional regulator	1.37E+01	-2.42E-01	3.25E-01	-1.84E+00	2.43E-04	-1.60E+00	4.39E-04
490059244	50S ribosomal protein L4	1.29E+01	5.76E-01	1.02E-02	-1.84E+00	4.67E-05	-2.42E+00	1.07E-05
497685167	hypothetical protein	1.12E+01	-1.35E+00	6.05E-04	-1.84E+00	1.82E-04	-4.90E-01	6.91E-02
490054132	adenylate kinase	1.24E+01	-7.65E-02	4.97E-01	-1.83E+00	7.16E-06	-1.75E+00	6.14E-06
497682159	chemotaxis protein CheY	1.46E+01	-9.94E-01	8.43E-04	-1.83E+00	5.53E-05	-8.37E-01	2.66E-03
497682119	peptidase	1.29E+01	1.71E+00	4.60E-06	-1.83E+00	6.44E-06	-3.54E+00	6.01E-07
490056448	peptidase M48	1.41E+01	-1.44E+00	2.41E-03	-1.83E+00	1.06E-03	-3.91E-01	2.67E-01
490051255	cell division protein FtsH	1.26E+01	-1.11E-01	3.47E-01	-1.83E+00	8.33E-06	-1.72E+00	8.07E-06
490058790	IclR family transcriptional regulator	1.23E+01	-1.97E+00	1.35E-03	-1.82E+00	2.95E-03	1.43E-01	7.33E-01
490054831	ATP-dependent DNA helicase PcrA	1.14E+01	1.29E+00	1.87E-03	-1.82E+00	4.74E-04	-3.10E+00	2.61E-05
490052962	peptidase S9	1.13E+01	-4.04E-01	6.11E-03	-1.81E+00	6.80E-06	-1.41E+00	1.46E-05
490060766	ornithine cyclodeaminase	1.15E+01	2.37E+00	1.88E-05	-1.81E+00	1.06E-04	-4.18E+00	2.57E-06
490050677	short-chain dehydrogenase	1.16E+01	-2.77E+00	6.10E-06	-1.81E+00	6.86E-05	9.59E-01	1.58E-03
490058302	acetolactate synthase	1.01E+01	1.85E+00	3.19E-04	-1.80E+00	5.48E-04	-3.66E+00	1.32E-05
490060648	LuxR family transcriptional regulator	9.47E+00	1.80E+00	9.31E-03	-1.80E+00	1.33E-02	-3.61E+00	3.88E-04
490050353	DEAD/DEAH box helicase	1.33E+01	1.04E+00	1.81E-04	-1.80E+00	1.92E-05	-2.83E+00	2.57E-06

497683243	ATP-binding protein	1.13E+01	-7.65E-01	1.30E-03	-1.79E+00	2.69E-05	-1.03E+00	3.63E-04
497682609	aminotransferase	1.33E+01	3.14E-01	9.87E-02	-1.79E+00	5.53E-05	-2.11E+00	2.10E-05
497681611	glmZ(sRNA)-inactivating NTPase	1.36E+01	-1.91E-01	3.37E-01	-1.79E+00	9.41E-05	-1.60E+00	1.39E-04
490059917	ornithine carbamoyltransferase	1.56E+01	-5.61E-01	2.36E-02	-1.79E+00	1.27E-04	-1.23E+00	7.77E-04
490057664	acyl-CoA dehydrogenase	1.35E+01	-5.97E-01	1.03E-02	-1.79E+00	6.45E-05	-1.19E+00	4.50E-04
497684135	hypothetical protein	1.32E+01	-2.41E+00	8.11E-06	-1.79E+00	5.11E-05	6.22E-01	9.10E-03
490056193	hydrolase	1.35E+01	1.14E+00	9.70E-05	-1.79E+00	1.81E-05	-2.93E+00	2.24E-06
490052186	citrate lyase beta chain	9.84E+00	6.56E-01	2.75E-02	-1.78E+00	3.56E-04	-2.44E+00	5.88E-05
497683820	protein tyrosine/serine phosphatase	1.56E+01	-4.68E-01	7.90E-02	-1.78E+00	2.93E-04	-1.31E+00	1.26E-03
490054710	transaldolase	1.29E+01	-2.90E-01	2.01E-01	-1.78E+00	1.73E-04	-1.49E+00	3.72E-04
497685275	GCN5 family acetyltransferase	1.22E+01	-5.73E-01	3.96E-02	-1.78E+00	2.96E-04	-1.21E+00	1.94E-03
490053896	geranylgeranyl pyrophosphate synthase	1.23E+01	1.49E-01	3.50E-01	-1.78E+00	3.50E-05	-1.93E+00	1.92E-05
490051865	hypothetical protein	1.25E+01	-3.37E+00	1.70E-06	-1.78E+00	3.19E-05	1.60E+00	4.25E-05
490054105	S-adenosylmethionine synthase	1.26E+01	1.12E-01	5.47E-01	-1.77E+00	7.11E-05	-1.89E+00	4.32E-05
497681489	CTP synthetase	1.30E+01	3.43E-01	1.16E-01	-1.77E+00	1.21E-04	-2.12E+00	4.07E-05
490060509	hypothetical protein	1.15E+01	-2.03E+00	4.93E-05	-1.77E+00	1.44E-04	2.53E-01	2.75E-01
490057128	NUDIX hydrolase	1.10E+01	-3.18E-01	1.15E-01	-1.77E+00	8.01E-05	-1.45E+00	1.87E-04
490054072	adenine phosphoribosyltransferase	1.35E+01	-7.66E-01	7.95E-04	-1.77E+00	1.94E-05	-1.00E+00	2.54E-04
490059501	sugar transporter	1.37E+01	1.64E+00	2.09E-05	-1.77E+00	2.32E-05	-3.41E+00	1.73E-06
490057622	phenoxazinone synthase	1.16E+01	-2.82E+00	2.70E-05	-1.77E+00	4.41E-04	1.06E+00	5.39E-03
490054063	transcriptional regulator	1.41E+01	-2.86E-01	4.34E-02	-1.76E+00	1.34E-05	-1.48E+00	2.15E-05
490058239	hypothetical protein	1.22E+01	-1.93E+00	1.02E-05	-1.76E+00	2.44E-05	1.64E-01	2.98E-01
490053288	aconitate hydratase	1.29E+01	1.00E+00	2.11E-04	-1.76E+00	2.12E-05	-2.76E+00	2.68E-06
490054972	type 11 methyltransferase	1.43E+01	-1.14E-03	9.96E-01	-1.76E+00	6.44E-05	-1.76E+00	5.22E-05
497681070	putative electron transfer flavoprotein beta subunit, partial	8.92E+00	1.40E+00	6.92E-04	-1.76E+00	3.16E-04	-3.15E+00	1.43E-05
490054971	conserved hypothetical protein	8.15E+00	6.46E-03	9.79E-01	-1.75E+00	1.75E-04	-1.76E+00	1.43E-04
490058358	ABC transporter ATP-binding protein	1.17E+01	1.05E+00	5.27E-05	-1.75E+00	7.83E-06	-2.80E+00	1.57E-06
490060762	phosphoribosylglycinamide synthetase	1.46E+01	1.41E+00	1.94E-04	-1.75E+00	9.57E-05	-3.16E+00	5.34E-06
490052183	phosphatidylserine decarboxylase	1.05E+01	-5.29E-03	9.76E-01	-1.75E+00	2.73E-05	-1.75E+00	2.17E-05
497681423	peptide-binding protein	1.27E+01	-4.29E+00	3.74E-05	-1.75E+00	5.35E-03	2.54E+00	7.23E-04

490051619	RNA polymerase sigma factor RpoE	1.31E+01	9.53E-01	7.17E-03	-1.75E+00	5.17E-04	-2.70E+00	4.58E-05
497683348	isopenicillin N-epimerase	1.12E+01	-3.03E+00	4.47E-06	-1.75E+00	9.22E-05	1.29E+00	3.84E-04
490053899	membrane protein	1.39E+01	-1.09E+00	1.38E-02	-1.74E+00	2.33E-03	-6.50E-01	1.11E-01
497684177	hypothetical protein	1.38E+01	-1.75E+00	2.85E-05	-1.74E+00	4.43E-05	6.74E-03	9.69E-01
490057490	heme peroxidase	1.32E+01	-1.95E+00	2.68E-04	-1.74E+00	7.28E-04	2.11E-01	4.91E-01
490051741	PucR family transcriptional regulator	1.12E+01	-5.67E-01	2.83E-02	-1.74E+00	1.97E-04	-1.18E+00	1.32E-03
490054316	amino acid ABC transporter ATPase	1.35E+01	-3.07E+00	5.52E-05	-1.74E+00	1.53E-03	1.32E+00	5.32E-03
490053061	hypothetical protein	9.44E+00	7.82E-01	1.09E-02	-1.74E+00	3.16E-04	-2.52E+00	3.96E-05
497682584	XRE family transcriptional regulator	1.16E+01	2.11E+00	1.14E-05	-1.74E+00	4.30E-05	-3.86E+00	1.73E-06
490058297	hypothetical protein	1.32E+01	-3.40E-01	9.05E-02	-1.74E+00	8.14E-05	-1.40E+00	2.11E-04
490051256	hypoxanthine phosphoribosyltransferase	1.37E+01	8.06E-02	8.17E-01	-1.74E+00	1.55E-03	-1.82E+00	1.09E-03
490058912	amidohydrolase	1.38E+01	-2.12E+00	1.39E-05	-1.74E+00	5.43E-05	3.85E-01	5.75E-02
490053538	glutamyl-tRNA amidotransferase subunit A	1.30E+01	-4.19E-01	2.27E-01	-1.74E+00	1.79E-03	-1.32E+00	6.22E-03
490060991	acetyltransferase	1.27E+01	-9.25E-01	3.01E-03	-1.74E+00	1.81E-04	-8.12E-01	7.46E-03
497683966	O-acetylhomoserine aminocarboxypropyltransferase	1.16E+01	-3.20E+00	1.48E-06	-1.74E+00	1.84E-05	1.46E+00	3.12E-05
490050050	ABC transporter ATP-binding protein	1.20E+01	-5.20E-01	1.26E-02	-1.74E+00	4.79E-05	-1.22E+00	2.48E-04
497682030	membrane protein	9.29E+00	2.39E+00	3.09E-05	-1.73E+00	2.38E-04	-4.13E+00	3.79E-06
490051191	transcriptional regulator	1.30E+01	-3.64E-01	3.28E-01	-1.72E+00	2.89E-03	-1.36E+00	8.09E-03
490060580	dynein regulation protein LC7	1.32E+01	-1.16E+00	7.37E-03	-1.72E+00	1.61E-03	-5.60E-01	1.31E-01
490054402	hypothetical protein	9.95E+00	8.57E-01	4.20E-03	-1.72E+00	1.82E-04	-2.57E+00	2.02E-05
497682317	dihydropteroate synthase	1.24E+01	1.35E+00	2.09E-04	-1.72E+00	9.17E-05	-3.07E+00	5.37E-06
490053926	preprotein translocase SecA	1.48E+01	-1.10E+00	1.87E-04	-1.72E+00	3.07E-05	-6.19E-01	4.59E-03
490055025	hypothetical protein	1.27E+01	-2.92E+00	8.11E-06	-1.71E+00	1.66E-04	1.20E+00	9.07E-04
490059695	short-chain dehydrogenase	1.26E+01	-2.24E+00	4.21E-06	-1.71E+00	2.28E-05	5.27E-01	7.01E-03
497681065	hyaluronate lyase	1.51E+01	3.89E-01	1.32E-01	-1.71E+00	3.58E-04	-2.10E+00	1.04E-04
490057888	cytochrome P450	1.11E+01	-2.05E+00	3.68E-05	-1.71E+00	1.39E-04	3.47E-01	1.30E-01
490060520	cell surface protein	1.37E+01	-3.50E+00	9.66E-06	-1.71E+00	5.11E-04	1.79E+00	3.43E-04
490060159	potassium transporter TrkA	1.33E+01	6.65E-01	8.63E-03	-1.70E+00	1.16E-04	-2.37E+00	1.90E-05
490052935	hypothetical protein	1.23E+01	-1.77E-01	2.09E-01	-1.70E+00	2.27E-05	-1.53E+00	2.91E-05
490056330	malate dehydrogenase	1.32E+01	3.21E-01	3.86E-02	-1.70E+00	2.15E-05	-2.02E+00	7.45E-06
490053420	6-phosphogluconate dehydrogenase	1.37E+01	-1.33E+00	5.36E-05	-1.70E+00	2.49E-05	-3.76E-01	3.20E-02

490060217	amino acid oxidase	1.07E+01	1.37E-01	3.03E-01	-1.70E+00	1.88E-05	-1.84E+00	9.91E-06
497681422	LuxR family transcriptional regulator	1.18E+01	4.68E-01	3.73E-02	-1.70E+00	1.22E-04	-2.16E+00	3.01E-05
490058384	malate dehydrogenase	1.41E+01	1.07E+00	2.70E-03	-1.69E+00	3.86E-04	-2.77E+00	2.68E-05
490058389	peptide chain release factor 2	1.43E+01	1.58E-01	3.20E-01	-1.69E+00	4.16E-05	-1.85E+00	2.17E-05
490056167	conserved hypothetical protein	1.20E+01	1.06E+00	6.59E-04	-1.69E+00	9.02E-05	-2.76E+00	7.39E-06
490057142	regulatory protein	1.14E+01	-8.91E-03	9.61E-01	-1.69E+00	2.60E-05	-1.68E+00	2.10E-05
497681429	GntR family transcriptional regulator	1.44E+01	-4.61E-01	1.73E-01	-1.69E+00	1.70E-03	-1.23E+00	7.27E-03
490061010	monooxygenase	1.47E+01	-1.19E+00	7.78E-05	-1.69E+00	2.27E-05	-4.96E-01	8.46E-03
490055283	trigger factor	1.30E+01	-9.41E-02	4.60E-01	-1.69E+00	1.77E-05	-1.59E+00	1.69E-05
490056619	transferase	1.35E+01	-2.69E-01	3.61E-01	-1.68E+00	1.02E-03	-1.42E+00	2.17E-03
490050729	peptidoglycan bridge formation protein FemAB	1.03E+01	-1.88E+00	1.02E-05	-1.68E+00	2.66E-05	1.99E-01	2.03E-01
497682601	ABC transporter	1.18E+01	1.88E-01	5.75E-01	-1.68E+00	1.92E-03	-1.87E+00	9.88E-04
490057353	hypothetical protein	1.24E+01	-2.68E-01	4.71E-01	-1.68E+00	3.46E-03	-1.41E+00	7.10E-03
497683691	hypothetical protein	1.55E+01	-1.06E+00	7.07E-04	-1.68E+00	9.75E-05	-6.23E-01	1.23E-02
490057052	Arginase/agmatinase/formiminoglutamase	1.33E+01	-2.32E+00	3.33E-06	-1.67E+00	2.13E-05	6.45E-01	2.12E-03
490058409	bifunctional glucose-6-phosphate/mannose-6-phosphate isomerase	1.35E+01	-2.27E-02	9.35E-01	-1.67E+00	3.36E-04	-1.65E+00	3.10E-04
490059939	protoporphyrinogen oxidase	1.34E+01	-7.93E-01	2.09E-03	-1.67E+00	6.78E-05	-8.81E-01	1.61E-03
490051025	ABC transporter ATP-binding protein	1.23E+01	7.08E-01	2.68E-03	-1.67E+00	5.02E-05	-2.38E+00	7.86E-06
490054823	GMP synthase	1.30E+01	-2.73E-01	5.35E-01	-1.67E+00	7.65E-03	-1.40E+00	1.55E-02
497683533	regulatory protein	1.47E+01	-7.38E-01	3.23E-03	-1.67E+00	7.51E-05	-9.31E-01	1.34E-03
490054099	diguanylate cyclase	1.21E+01	3.98E-01	8.62E-02	-1.67E+00	2.07E-04	-2.07E+00	5.67E-05
490058906	RNA polymerase sigma factor	9.61E+00	-7.00E-01	8.32E-03	-1.67E+00	1.60E-04	-9.67E-01	2.30E-03
497685015	hypothetical protein	1.09E+01	-3.13E+00	4.43E-06	-1.66E+00	1.32E-04	1.46E+00	2.21E-04
490050391	3-beta hydroxysteroid dehydrogenase	1.36E+01	-4.09E+00	3.93E-06	-1.66E+00	4.28E-04	2.43E+00	5.08E-05
490054993	glutamate-1-semialdehyde 2,1-aminomutase	1.18E+01	-1.11E+00	1.55E-04	-1.66E+00	3.15E-05	-5.51E-01	7.11E-03
490056868	RpiR family transcriptional regulator	1.24E+01	2.35E-01	1.33E-01	-1.66E+00	3.44E-05	-1.89E+00	1.48E-05
490054819	succinate-semialdehyde dehydrogenase	1.31E+01	-7.96E-01	1.89E-04	-1.66E+00	8.91E-06	-8.63E-01	1.58E-04
490054150	50S ribosomal protein L2	1.36E+01	-5.18E-01	2.39E-02	-1.66E+00	1.28E-04	-1.14E+00	7.79E-04
497681050	hypothetical protein	9.85E+00	2.63E+00	1.11E-05	-1.66E+00	1.58E-04	-4.28E+00	2.32E-06
490059245	50S ribosomal protein L23	1.38E+01	-8.76E-01	1.18E-03	-1.66E+00	6.67E-05	-7.80E-01	2.75E-03
490055531	acetolactate synthase	1.34E+01	3.08E-02	8.07E-01	-1.65E+00	1.46E-05	-1.68E+00	9.59E-06

497685323	methyltransferase type 11	8.63E+00	-6.95E-02	5.85E-01	-1.65E+00	1.81E-05	-1.58E+00	1.64E-05
490057686	transcriptional regulator	1.31E+01	5.10E-01	9.20E-03	-1.65E+00	3.92E-05	-2.16E+00	8.94E-06
490060513	terpene synthase	1.25E+01	-2.57E+00	4.16E-06	-1.65E+00	4.76E-05	9.13E-01	8.62E-04
490055732	preprotein translocase subunit SecA	1.35E+01	2.29E-02	8.65E-01	-1.65E+00	1.63E-05	-1.68E+00	1.12E-05
490055502	branched-chain amino acid aminotransferase	1.31E+01	4.00E-01	2.49E-01	-1.65E+00	2.37E-03	-2.05E+00	6.87E-04
497681460	C4-dicarboxylate ABC transporter substrate-binding protein	1.38E+01	-6.26E-01	1.82E-03	-1.65E+00	2.20E-05	-1.03E+00	1.81E-04
490059171	N5,N10-methylenetetrahydromethanopterin reductase	9.09E+00	-2.36E+00	7.64E-05	-1.65E+00	7.10E-04	7.12E-01	3.25E-02
490053090	hypothetical protein	1.40E+01	3.92E-01	1.19E-01	-1.65E+00	3.65E-04	-2.04E+00	1.01E-04
490060233	phytoene dehydrogenase	8.94E+00	1.47E+00	1.78E-03	-1.64E+00	1.53E-03	-3.11E+00	4.63E-05
490051928	hypothetical protein	1.44E+01	-1.23E+00	9.76E-05	-1.64E+00	3.55E-05	-4.08E-01	2.72E-02
490056013	peroxiredoxin	1.21E+01	6.31E-01	1.90E-02	-1.64E+00	2.75E-04	-2.27E+00	4.32E-05
490050956	short-chain dehydrogenase	1.44E+01	-2.86E+00	1.14E-05	-1.64E+00	2.71E-04	1.23E+00	1.08E-03
490054135	50S ribosomal protein L30	1.54E+01	-1.25E+00	5.57E-03	-1.64E+00	2.21E-03	-3.88E-01	2.83E-01
490053496	phosphoglycolate phosphatase	1.37E+01	-7.60E-02	8.27E-01	-1.64E+00	2.06E-03	-1.56E+00	2.30E-03
490058310	Nocardamine synthetase	1.17E+01	1.68E+00	1.21E-03	-1.64E+00	2.06E-03	-3.32E+00	4.51E-05
490051754	hypothetical protein	1.31E+01	8.78E-02	7.65E-01	-1.64E+00	9.06E-04	-1.72E+00	5.97E-04
497682307	adenine glycosylase	1.24E+01	-5.05E-02	8.39E-01	-1.64E+00	3.43E-04	-1.58E+00	3.49E-04
497682225	transcription-repair coupling factor	1.30E+01	8.88E-01	2.92E-03	-1.63E+00	1.95E-04	-2.52E+00	1.89E-05
490060667	cytochrome P450	1.28E+01	-7.41E-01	5.13E-03	-1.63E+00	1.40E-04	-8.89E-01	2.79E-03
490055435	membrane protein	1.23E+01	3.74E-01	3.75E-02	-1.63E+00	4.95E-05	-2.00E+00	1.49E-05
490055572	hypothetical protein	1.29E+01	-1.27E+00	1.09E-02	-1.63E+00	5.31E-03	-3.53E-01	4.07E-01
490051506	uroporphyrin-III C-methyltransferase	1.28E+01	9.14E-01	7.07E-04	-1.63E+00	5.55E-05	-2.54E+00	5.86E-06
497683103	UDP-N-acetylenolpyruvoylglucosamine reductase	1.39E+01	1.30E-01	4.57E-01	-1.63E+00	8.43E-05	-1.76E+00	4.66E-05
490055334	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	1.40E+01	1.04E+00	4.46E-05	-1.62E+00	9.05E-06	-2.67E+00	1.57E-06
497682186	hypothetical protein	1.53E+01	7.96E-01	1.74E-03	-1.62E+00	6.74E-05	-2.42E+00	8.44E-06
497681812	alpha-glucosidase	1.37E+01	-5.18E-01	8.62E-03	-1.62E+00	4.28E-05	-1.10E+00	2.55E-04
497682087	LuxAB-like protein (oxygenase)	1.21E+01	-8.00E-01	4.89E-04	-1.62E+00	2.29E-05	-8.18E-01	5.73E-04
490052722	ornithine cyclodeaminase	1.33E+01	-2.52E+00	2.04E-05	-1.62E+00	2.85E-04	9.07E-01	4.84E-03
497682964	chorismate mutase	1.25E+01	-2.72E+00	1.14E-05	-1.62E+00	2.19E-04	1.10E+00	1.41E-03
490058946	amidophosphoribosyltransferase	1.28E+01	-3.52E-01	2.57E-02	-1.62E+00	2.49E-05	-1.26E+00	6.45E-05

490061374	beta-lactamase	1.28E+01	-1.04E+00	4.62E-04	-1.62E+00	7.30E-05	-5.72E-01	1.19E-02
490058788	ATPase	1.61E+01	1.08E+00	3.52E-02	-1.62E+00	9.42E-03	-2.69E+00	6.72E-04
490055122	exopolyphosphatase	1.34E+01	-5.32E-02	8.78E-01	-1.61E+00	1.96E-03	-1.56E+00	2.05E-03
497682046	signal peptide protein	9.91E+00	9.61E-01	9.46E-03	-1.61E+00	1.13E-03	-2.58E+00	8.51E-05
490059221	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	1.43E+01	-4.84E-01	2.09E-02	-1.61E+00	8.76E-05	-1.13E+00	4.76E-04
490055333	glutamyl-tRNA synthetase	1.35E+01	-3.51E-01	1.64E-01	-1.61E+00	4.69E-04	-1.26E+00	1.48E-03
490057423	GntR family transcriptional regulator	1.54E+01	-1.45E+00	2.39E-04	-1.61E+00	2.10E-04	-1.59E-01	4.75E-01
490058075	antibiotic biosynthesis monooxygenase	1.47E+01	-1.51E+00	7.05E-03	-1.61E+00	7.88E-03	-9.16E-02	8.39E-01
490060988	Isoform 2 of Ribosomal protein S6 modification B	8.67E+00	3.11E-02	8.79E-01	-1.60E+00	1.34E-04	-1.64E+00	1.02E-04
490050149	deacetoxycephalosporin C hydroxylase	1.36E+01	-1.89E+00	3.14E-04	-1.60E+00	1.10E-03	2.84E-01	3.55E-01
490061208	acetyltransferase	1.47E+01	-1.82E+00	2.57E-04	-1.60E+00	7.45E-04	2.18E-01	4.42E-01
490054464	2-phospho-L-lactate transferase	1.03E+01	1.10E+00	2.88E-02	-1.60E+00	8.53E-03	-2.70E+00	5.56E-04
490057208	peptidase M20	1.43E+01	3.25E-01	1.10E-01	-1.60E+00	1.41E-04	-1.92E+00	4.54E-05
490055173	LuxR family transcriptional regulator	1.36E+01	-1.77E+00	9.21E-05	-1.59E+00	2.32E-04	1.79E-01	4.27E-01
490058520	molybdopterin biosynthesis protein MoeA	1.25E+01	2.52E+00	1.77E-05	-1.59E+00	2.55E-04	-4.11E+00	2.96E-06
497683590	hypothetical protein	1.39E+01	-8.14E-01	6.20E-04	-1.59E+00	3.21E-05	-7.75E-01	1.06E-03
497683263	N-succinyldiaminopimelate aminotransferase	1.40E+01	1.30E+00	5.80E-05	-1.59E+00	3.33E-05	-2.89E+00	2.57E-06
490056069	acetylornithine aminotransferase	1.22E+01	-3.59E-01	5.85E-02	-1.59E+00	8.43E-05	-1.23E+00	2.69E-04
490051625	peptide deformylase	1.30E+01	5.08E-01	2.92E-03	-1.59E+00	1.64E-05	-2.09E+00	3.92E-06
497685291	methyltransferase	1.20E+01	-2.09E+00	1.55E-04	-1.58E+00	9.71E-04	5.07E-01	1.05E-01
490054881	lipoprotein oligopeptide binding protein	1.56E+01	-3.61E-01	1.99E-01	-1.58E+00	9.67E-04	-1.22E+00	3.17E-03
490050861	hypothetical protein	1.52E+01	1.32E-01	3.92E-01	-1.58E+00	5.25E-05	-1.71E+00	2.91E-05
490056578	nucleotide sugar-1-phosphate transferase	1.38E+01	-9.55E-02	6.92E-01	-1.58E+00	4.39E-04	-1.48E+00	5.34E-04
497683148	hypothetical protein	1.44E+01	-3.44E+00	1.87E-06	-1.57E+00	6.97E-05	1.86E+00	2.55E-05
490057082	radical SAM protein	1.24E+01	-5.12E-01	1.65E-02	-1.57E+00	1.00E-04	-1.05E+00	6.73E-04
490054199	thioredoxin reductase	1.05E+01	4.27E-01	1.76E-02	-1.57E+00	4.43E-05	-1.99E+00	1.17E-05
490061073	RNA polymerase subunit sigma-70	1.45E+01	-1.38E+00	3.19E-05	-1.57E+00	2.73E-05	-1.87E-01	2.03E-01
497685248	deaminase reductase	1.32E+01	-3.39E-01	4.17E-01	-1.56E+00	8.34E-03	-1.22E+00	2.20E-02
490059191	hypothetical protein	1.46E+01	-5.84E-01	1.36E-02	-1.56E+00	1.57E-04	-9.81E-01	1.53E-03
490052949	ABC transporter permease	1.53E+01	-8.65E-02	7.09E-01	-1.56E+00	3.77E-04	-1.48E+00	4.41E-04

490050131	hypothetical protein	1.12E+01	3.49E-01	2.37E-01	-1.56E+00	1.38E-03	-1.91E+00	4.24E-04
497682198	diaminopimelate decarboxylase	1.61E+01	-1.21E+00	3.58E-05	-1.56E+00	1.81E-05	-3.50E-01	2.15E-02
490051157	PhoU family transcriptional regulator	1.38E+01	-7.23E-01	1.23E-03	-1.56E+00	3.74E-05	-8.35E-01	7.69E-04
490060090	adenosine deaminase	1.21E+01	1.08E+00	3.50E-04	-1.56E+00	7.92E-05	-2.64E+00	5.70E-06
490058381	beta-N-acetylhexosaminidase	1.17E+01	2.45E+00	4.01E-05	-1.56E+00	6.10E-04	-4.01E+00	5.44E-06
490057421	membrane protein	1.05E+01	5.48E-01	1.10E-02	-1.56E+00	9.17E-05	-2.10E+00	1.75E-05
497681764	hypothetical protein	1.63E+01	-1.13E+00	2.35E-03	-1.55E+00	6.82E-04	-4.25E-01	1.34E-01
490051986	hypothetical protein	1.92E+01	-1.33E+00	3.46E-03	-1.55E+00	2.41E-03	-2.24E-01	5.14E-01
490055856	sulfate ABC transporter substrate-binding protein	1.45E+01	-7.59E-01	9.12E-04	-1.55E+00	3.68E-05	-7.91E-01	9.76E-04
490051570	molybdopterin biosynthesis MoeZ	1.28E+01	-2.57E-01	3.58E-01	-1.55E+00	1.20E-03	-1.29E+00	2.66E-03
490059489	catalase	1.40E+01	-3.22E+00	1.40E-06	-1.55E+00	2.72E-05	1.67E+00	1.47E-05
490054350	export associated protein	1.36E+01	-1.36E+00	1.43E-04	-1.54E+00	1.12E-04	-1.82E-01	3.40E-01
490057336	adenosylmethionine--8-amino-7-oxononanoate aminotransferase	9.92E+00	1.68E+00	1.14E-04	-1.54E+00	2.60E-04	-3.23E+00	6.17E-06
490056354	hydroxylase	1.25E+01	2.51E+00	2.05E-05	-1.54E+00	3.52E-04	-4.05E+00	3.42E-06
497683568	peptidase M16	1.17E+01	-1.82E-01	4.50E-01	-1.54E+00	5.67E-04	-1.36E+00	9.64E-04
490056480	methyltransferase type 12	1.25E+01	1.70E+00	8.68E-05	-1.54E+00	2.12E-04	-3.24E+00	5.39E-06
490051608	histidinol-phosphatase	1.21E+01	3.08E-01	3.18E-01	-1.54E+00	1.96E-03	-1.84E+00	6.74E-04
490060764	peptide synthetase	1.39E+01	1.93E+00	7.26E-05	-1.53E+00	3.43E-04	-3.46E+00	5.70E-06
490060358	3-oxoacyl-ACP reductase	1.33E+01	1.21E+00	3.36E-04	-1.53E+00	1.45E-04	-2.74E+00	7.44E-06
490055503	3-isopropylmalate dehydrogenase	1.29E+01	-2.38E-01	3.86E-01	-1.53E+00	1.16E-03	-1.29E+00	2.41E-03
497685124	hypothetical protein	9.64E+00	-1.14E-01	6.25E-01	-1.53E+00	4.75E-04	-1.41E+00	6.25E-04
497681281	dolichol-phosphate mannosyltransferase	1.16E+01	7.31E-01	1.03E-02	-1.53E+00	4.05E-04	-2.26E+00	4.51E-05
490051413	phosphoenolpyruvate carboxylase	1.27E+01	-7.39E-01	5.51E-04	-1.52E+00	2.30E-05	-7.85E-01	5.30E-04
490054134	50S ribosomal protein L15	7.86E+00	5.70E-01	8.88E-03	-1.52E+00	9.76E-05	-2.09E+00	1.71E-05
490059075	membrane protein	1.41E+01	-1.77E+00	4.29E-05	-1.52E+00	1.35E-04	2.47E-01	2.12E-01
490054228	DNA helicase	1.08E+01	1.73E+00	2.09E-05	-1.52E+00	5.92E-05	-3.25E+00	2.29E-06
490057075	antibiotic resistance macrolide glycosyltransferase	1.42E+01	-1.97E+00	8.11E-06	-1.52E+00	4.30E-05	4.53E-01	1.54E-02
497680944	phosphotransferase	1.10E+01	-3.18E+00	5.46E-06	-1.51E+00	3.13E-04	1.66E+00	1.61E-04
490054320	branched-chain amino acid ABC transporter substrate-binding protein	1.19E+01	-2.18E+00	2.56E-05	-1.51E+00	2.46E-04	6.71E-01	1.25E-02

490055279	ATP-dependent protease	1.30E+01	-8.66E-01	1.56E-03	-1.51E+00	1.32E-04	-6.44E-01	8.65E-03
490059894	potassium transporter TrkA	8.69E+00	5.12E-01	2.25E-02	-1.51E+00	1.81E-04	-2.02E+00	3.43E-05
490057674	1-acyl-sn-glycerol-3-phosphate acyltransferase	1.39E+01	-1.20E-01	4.63E-01	-1.51E+00	8.99E-05	-1.39E+00	1.13E-04
490050085	F0F1 ATP synthase subunit alpha	1.24E+01	5.21E-02	8.05E-01	-1.51E+00	2.46E-04	-1.56E+00	1.75E-04
490051366	DNA mismatch repair protein	1.34E+01	-1.47E+00	2.11E-05	-1.51E+00	2.91E-05	-3.86E-02	7.80E-01
490054331	30S ribosomal protein S1	1.31E+01	-2.69E-01	8.06E-02	-1.51E+00	4.34E-05	-1.24E+00	9.65E-05
490052559	methionine sulfoxide reductase A	1.41E+01	4.94E-03	9.84E-01	-1.50E+00	2.87E-04	-1.51E+00	2.42E-04
490058078	Putative integral membrane protein	1.77E+01	-1.89E+00	2.11E-05	-1.50E+00	9.91E-05	3.87E-01	5.20E-02
490059034	diguanylate cyclase	1.10E+01	-1.93E+00	8.86E-06	-1.50E+00	4.39E-05	4.28E-01	1.91E-02
490055277	valyl-tRNA synthetase	1.30E+01	-1.31E-01	3.69E-01	-1.50E+00	5.10E-05	-1.37E+00	6.55E-05
490050757	hypothetical protein	1.35E+01	-6.44E-01	5.83E-03	-1.50E+00	1.21E-04	-8.54E-01	1.92E-03
490053991	hypothetical protein	1.39E+01	-3.04E-01	4.45E-02	-1.50E+00	3.53E-05	-1.19E+00	8.83E-05
490053370	octanoyltransferase	1.27E+01	2.37E-02	9.00E-01	-1.50E+00	1.19E-04	-1.52E+00	9.12E-05
490056183	glycerol kinase	1.25E+01	2.63E-01	2.01E-01	-1.49E+00	2.57E-04	-1.76E+00	9.33E-05
490051122	alpha,alpha-trehalose-phosphate synthase	1.22E+01	-1.70E+00	9.66E-06	-1.49E+00	2.73E-05	2.05E-01	1.48E-01
490052934	GTP-binding protein YchF	1.35E+01	9.53E-01	1.01E-02	-1.49E+00	1.77E-03	-2.44E+00	1.14E-04
490050509	carotenoid oxygenase	1.10E+01	-1.42E+00	9.00E-04	-1.49E+00	1.04E-03	-7.29E-02	7.93E-01
497683441	dihydrofolate reductase	9.83E+00	8.74E-01	1.01E-02	-1.49E+00	1.15E-03	-2.36E+00	8.83E-05
490051594	hydrolase	1.13E+01	-3.39E-01	2.42E-01	-1.49E+00	1.61E-03	-1.15E+00	5.23E-03
497683825	metallo-beta-lactamase	1.40E+01	3.20E-01	4.48E-02	-1.48E+00	4.65E-05	-1.80E+00	1.49E-05
497681705	cell division protein DivIVA	1.41E+01	5.40E-01	1.30E-01	-1.48E+00	3.94E-03	-2.02E+00	7.10E-04
490057690	inorganic polyphosphate/ATP-NAD kinase	1.33E+01	3.11E-01	1.21E-01	-1.48E+00	2.01E-04	-1.79E+00	6.24E-05
497683124	Fis family transcriptional regulator	1.30E+01	-2.11E+00	1.70E-05	-1.48E+00	1.42E-04	6.27E-01	9.53E-03
490059741	cell division protein FtsY	8.98E+00	1.90E-02	9.12E-01	-1.48E+00	6.99E-05	-1.50E+00	5.41E-05
490055317	AsnC family transcriptional regulator	1.37E+01	-1.94E+00	1.49E-05	-1.48E+00	8.36E-05	4.68E-01	2.14E-02
497682607	hydrolase	1.33E+01	-4.69E-01	1.16E-02	-1.47E+00	5.88E-05	-1.00E+00	3.61E-04
490055584	hypothetical protein	1.31E+01	-6.45E-01	1.98E-02	-1.47E+00	5.69E-04	-8.26E-01	8.97E-03
497685442	acetyltransferase	1.19E+01	-3.04E+00	3.68E-05	-1.47E+00	2.30E-03	1.57E+00	1.42E-03
497682458	hypothetical protein	1.31E+01	-2.66E-02	8.75E-01	-1.47E+00	8.01E-05	-1.44E+00	7.29E-05
490055001	SAM-dependent methyltransferase	9.06E+00	1.69E-01	4.45E-01	-1.47E+00	4.76E-04	-1.64E+00	2.34E-04
497681971	metal ABC transporter substrate-binding protein	1.07E+01	-6.72E-01	4.86E-03	-1.47E+00	1.38E-04	-7.95E-01	2.84E-03

490051175	asparaginase	1.39E+01	7.42E-01	6.20E-03	-1.47E+00	3.00E-04	-2.21E+00	3.14E-05
497683460	ATP-binding protein	1.11E+01	-8.44E-02	6.57E-01	-1.47E+00	1.98E-04	-1.38E+00	2.29E-04
490055318	D-alanine--D-alanine ligase	1.35E+01	1.00E+00	1.37E-04	-1.47E+00	3.13E-05	-2.47E+00	2.96E-06
490054068	Holliday junction DNA helicase RuvB	1.16E+01	-1.97E-01	1.91E-01	-1.46E+00	5.82E-05	-1.27E+00	1.01E-04
497681576	NAD-dependent dehydratase	1.08E+01	-4.75E-01	2.77E-02	-1.46E+00	1.91E-04	-9.87E-01	1.28E-03
490055583	sporulation protein	1.42E+01	-7.20E-01	5.02E-03	-1.46E+00	2.07E-04	-7.43E-01	5.74E-03
490054885	30S ribosomal protein S2	1.22E+01	-1.90E-01	4.49E-01	-1.46E+00	9.34E-04	-1.27E+00	1.67E-03
490057328	prevent-host-death protein	1.16E+01	-8.67E-01	1.15E-02	-1.46E+00	1.43E-03	-5.91E-01	6.45E-02
490053383	porphobilinogen deaminase	1.18E+01	1.62E-01	3.83E-01	-1.46E+00	1.99E-04	-1.62E+00	9.61E-05
490055328	isopropylmalate isomerase	1.25E+01	3.32E-01	5.48E-02	-1.46E+00	8.01E-05	-1.79E+00	2.41E-05
490059828	tRNA delta(2)-isopentenylpyrophosphate transferase	1.47E+01	5.39E-01	5.13E-03	-1.45E+00	5.11E-05	-1.99E+00	9.38E-06
497684140	hypothetical protein	1.29E+01	-3.13E+00	3.42E-06	-1.45E+00	1.81E-04	1.68E+00	7.22E-05
490055919	cyclase	1.40E+01	3.37E-01	1.82E-01	-1.45E+00	8.40E-04	-1.79E+00	2.42E-04
490054357	maleylpyruvate isomerase	1.25E+01	-8.42E-03	9.71E-01	-1.45E+00	2.12E-04	-1.44E+00	1.84E-04
490057218	sporulation protein	8.61E+00	-1.68E-01	4.10E-01	-1.44E+00	3.36E-04	-1.28E+00	5.53E-04
497685533	acyl-CoA dehydrogenase	8.70E+00	-3.22E-01	1.10E-01	-1.44E+00	2.23E-04	-1.12E+00	7.24E-04
490051367	hypothetical protein	1.27E+01	-1.53E+00	1.48E-04	-1.44E+00	3.02E-04	9.25E-02	6.63E-01
490054424	membrane dipeptidase	1.41E+01	4.21E-01	4.99E-03	-1.44E+00	1.80E-05	-1.86E+00	4.61E-06
490058199	ATP-dependent Clp protease ClpP	1.27E+01	-8.96E-01	3.43E-03	-1.44E+00	4.61E-04	-5.42E-01	3.94E-02
490059740	acetyltransferase	1.29E+01	1.27E+00	1.63E-03	-1.44E+00	1.30E-03	-2.71E+00	4.14E-05
490059431	acetyltransferase	1.37E+01	-6.01E-01	8.57E-03	-1.44E+00	1.62E-04	-8.36E-01	2.30E-03
490051180	hypothetical protein	1.40E+01	1.30E+00	2.10E-04	-1.44E+00	1.88E-04	-2.74E+00	6.86E-06
490053010	hypothetical protein	1.26E+01	-5.31E-01	8.85E-03	-1.44E+00	9.02E-05	-9.05E-01	8.58E-04
490058363	hypothetical protein	1.41E+01	-1.80E-01	2.41E-01	-1.43E+00	7.25E-05	-1.26E+00	1.20E-04
497683136	RNA polymerase subunit sigma-24	1.51E+01	3.12E+00	1.16E-05	-1.43E+00	8.69E-04	-4.56E+00	3.24E-06
490059862	thiosulfate sulfurtransferase	1.27E+01	-1.61E-01	3.62E-01	-1.43E+00	1.69E-04	-1.27E+00	2.66E-04
490055042	potassium transporter TrkA	1.04E+01	1.37E+00	1.30E-03	-1.43E+00	1.58E-03	-2.80E+00	4.10E-05
490057118	N-acetyltransferase GCN5	1.45E+01	-2.45E+00	9.38E-06	-1.43E+00	2.00E-04	1.02E+00	9.85E-04
490054231	MarR family transcriptional regulator	1.37E+01	-1.06E+00	3.31E-03	-1.42E+00	1.12E-03	-3.65E-01	1.92E-01
490054144	30S ribosomal protein S17	1.40E+01	-1.29E+00	1.26E-04	-1.42E+00	1.10E-04	-1.37E-01	4.31E-01

490054330	SAM-dependent methyltransferase	1.32E+01	-4.41E-01	2.82E-01	-1.42E+00	1.08E-02	-9.80E-01	4.46E-02
490053065	aspartyl-tRNA synthetase	1.32E+01	-8.64E-01	8.71E-03	-1.42E+00	1.15E-03	-5.56E-01	6.33E-02
490054049	threonyl-tRNA synthetase	1.28E+01	2.78E-01	1.56E-01	-1.42E+00	2.45E-04	-1.70E+00	8.10E-05
497681368	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1.30E+01	2.06E-01	1.63E-01	-1.42E+00	5.74E-05	-1.62E+00	2.43E-05
490060765	peptide synthetase	1.32E+01	1.92E+00	7.47E-06	-1.42E+00	4.86E-05	-3.34E+00	1.61E-06
497681233	histidine kinase	1.31E+01	-2.76E+00	4.53E-06	-1.41E+00	1.74E-04	1.35E+00	1.84E-04
490053695	transcriptional regulator	1.32E+01	-3.07E-03	9.87E-01	-1.41E+00	1.09E-04	-1.41E+00	9.22E-05
490055141	DNA-binding protein	1.45E+01	-3.10E+00	1.30E-05	-1.41E+00	1.02E-03	1.69E+00	3.37E-04
497682657	DNA gyrase subunit B	1.47E+01	-6.05E-02	7.77E-01	-1.41E+00	3.77E-04	-1.35E+00	4.13E-04
490060107	XRE family transcriptional regulator	1.33E+01	3.99E-01	4.45E-02	-1.41E+00	1.82E-04	-1.81E+00	4.19E-05
497683518	riboflavin kinase	1.44E+01	1.37E+00	1.22E-04	-1.41E+00	1.53E-04	-2.77E+00	5.43E-06
490058694	acetyltransferase	1.28E+01	9.79E-01	3.76E-04	-1.40E+00	8.78E-05	-2.38E+00	6.07E-06
490057340	membrane protein	1.41E+01	2.43E-01	4.60E-01	-1.40E+00	4.56E-03	-1.65E+00	1.81E-03
490055121	conserved hypothetical protein	1.17E+01	1.35E-01	5.11E-01	-1.40E+00	4.07E-04	-1.54E+00	2.18E-04
490053055	hypothetical protein	1.25E+01	7.81E-01	2.01E-03	-1.40E+00	1.48E-04	-2.18E+00	1.39E-05
490051497	RNA polymerase sigma factor SigB	1.11E+01	9.76E-01	7.37E-03	-1.40E+00	1.92E-03	-2.38E+00	1.04E-04
497681720	methyltransferase type 12	9.44E+00	4.17E-02	8.61E-01	-1.40E+00	5.69E-04	-1.44E+00	4.27E-04
497682890	D-tyrosyl-tRNA(Tyr) deacylase	1.24E+01	3.50E-01	1.89E-02	-1.39E+00	3.30E-05	-1.74E+00	9.29E-06
490052927	exodeoxyribonuclease VII small subunit	1.42E+01	-3.04E-01	4.56E-01	-1.39E+00	1.23E-02	-1.09E+00	3.14E-02
490058431	hypothetical protein	1.36E+01	2.35E-01	1.07E-01	-1.39E+00	5.18E-05	-1.63E+00	2.01E-05
497681488	NUDIX hydrolase	1.43E+01	-3.39E-01	1.84E-01	-1.39E+00	1.09E-03	-1.05E+00	3.95E-03
497682015	ribonuclease E	1.35E+01	-4.61E-02	7.65E-01	-1.39E+00	7.47E-05	-1.35E+00	7.35E-05
497682158	hypothetical protein	1.27E+01	1.00E+00	3.86E-02	-1.39E+00	1.50E-02	-2.39E+00	9.88E-04
490054699	phosphoglycerate kinase	8.99E+00	8.25E-01	1.08E-03	-1.39E+00	1.10E-04	-2.21E+00	9.50E-06
490050285	short-chain dehydrogenase	1.38E+01	-5.86E-01	3.39E-03	-1.39E+00	6.34E-05	-8.00E-01	9.40E-04
490056459	hypothetical protein	1.25E+01	1.50E+00	2.40E-04	-1.39E+00	5.42E-04	-2.89E+00	1.17E-05
490054890	50S rRNA methyltransferase	1.25E+01	2.35E-01	1.98E-01	-1.38E+00	2.06E-04	-1.62E+00	7.60E-05
490059790	ribosome-binding factor A	1.39E+01	8.01E-02	6.80E-01	-1.38E+00	2.91E-04	-1.46E+00	1.84E-04
490060435	hypothetical protein	1.16E+01	-2.42E+00	2.44E-04	-1.38E+00	6.28E-03	1.04E+00	1.96E-02
490053517	hypothetical protein	1.25E+01	-3.36E-01	2.25E-02	-1.38E+00	3.51E-05	-1.04E+00	1.13E-04

490057910	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	1.40E+01	-4.43E-01	3.06E-02	-1.38E+00	2.04E-04	-9.36E-01	1.33E-03
490060463	sugar-binding protein	1.19E+01	-3.34E+00	1.48E-06	-1.38E+00	5.93E-05	1.96E+00	9.29E-06
490057864	glutamate synthase	1.26E+01	1.79E+00	5.46E-06	-1.38E+00	2.94E-05	-3.17E+00	1.22E-06
490060702	SAM-dependent methyltransferase	1.67E+01	-3.46E-01	5.57E-02	-1.38E+00	1.34E-04	-1.03E+00	5.24E-04
497683712	dehydrogenase	1.63E+01	1.52E-01	4.46E-01	-1.37E+00	3.99E-04	-1.52E+00	1.96E-04
497683853	amidohydrolase	1.41E+01	-1.61E+00	1.77E-05	-1.37E+00	5.74E-05	2.42E-01	1.17E-01
490055865	sulfite reductase	1.42E+01	-6.03E-02	7.13E-01	-1.37E+00	1.28E-04	-1.31E+00	1.35E-04
490058894	LuxR family transcriptional regulator	1.50E+01	9.10E-01	2.18E-04	-1.37E+00	4.24E-05	-2.28E+00	3.85E-06
490051126	cold-shock protein	1.48E+01	-3.41E+00	8.11E-06	-1.37E+00	1.19E-03	2.04E+00	1.25E-04
497681332	preprotein translocase subunit SecD	1.40E+01	-6.10E-01	1.30E-02	-1.36E+00	3.75E-04	-7.55E-01	6.63E-03
490052517	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	1.32E+01	-1.05E+00	1.24E-03	-1.36E+00	4.76E-04	-3.13E-01	1.71E-01
497681813	LacI family transcriptional regulator	1.68E+01	-2.29E-01	1.76E-01	-1.36E+00	1.46E-04	-1.13E+00	3.27E-04
490059515	malate dehydrogenase	1.43E+01	-4.88E-01	2.07E-02	-1.36E+00	2.13E-04	-8.74E-01	1.85E-03
490059534	ATP/GTP-binding protein	1.20E+01	-2.20E+00	1.48E-04	-1.36E+00	2.62E-03	8.40E-01	2.15E-02
490058249	ABC transporter ATP-binding protein	1.33E+01	-3.67E-01	2.49E-02	-1.36E+00	6.39E-05	-9.94E-01	2.71E-04
490051173	lyase	1.32E+01	3.12E+00	2.68E-05	-1.36E+00	2.83E-03	-4.48E+00	6.37E-06
490052765	protein disaggregation chaperone	1.27E+01	-8.25E-02	7.32E-01	-1.36E+00	9.34E-04	-1.28E+00	1.14E-03
490059915	phosphatase	1.34E+01	8.18E-01	3.74E-03	-1.36E+00	4.23E-04	-2.18E+00	3.24E-05
490053874	ubiquinone/menaquinone biosynthesis methyltransferase	1.33E+01	4.56E-01	1.07E-02	-1.36E+00	6.89E-05	-1.81E+00	1.42E-05
490052231	ornithine carbamoyltransferase	1.29E+01	1.86E+00	1.57E-04	-1.35E+00	1.19E-03	-3.21E+00	1.28E-05
490050174	hypothetical protein	1.40E+01	-2.74E+00	1.67E-06	-1.35E+00	3.92E-05	1.39E+00	2.78E-05
497682431	ATPase	9.10E+00	5.93E-01	3.76E-02	-1.35E+00	1.36E-03	-1.94E+00	1.75E-04
490056901	hypothetical protein	1.30E+01	-8.24E-01	2.97E-03	-1.35E+00	3.58E-04	-5.26E-01	2.89E-02
490057486	ATPase AAA	1.31E+01	9.82E-01	4.50E-04	-1.35E+00	1.30E-04	-2.33E+00	7.86E-06
490054893	iron ABC transporter ATP-binding protein	1.19E+01	6.84E-01	1.06E-02	-1.35E+00	5.69E-04	-2.03E+00	5.68E-05
490055932	polynucleotide phosphorylase	9.89E+00	1.16E+00	4.63E-05	-1.34E+00	3.44E-05	-2.50E+00	2.49E-06
490052457	oxidoreductase	1.21E+01	5.05E-01	1.79E-02	-1.34E+00	2.26E-04	-1.85E+00	3.76E-05
490055253	GTPase CgtA	1.45E+01	1.17E+00	1.41E-03	-1.34E+00	1.04E-03	-2.51E+00	3.48E-05
490060104	alcohol dehydrogenase	1.28E+01	-1.65E+00	2.82E-04	-1.34E+00	1.24E-03	3.11E-01	2.45E-01
490056752	RNA polymerase subunit sigma24	1.23E+01	1.23E+00	2.64E-04	-1.34E+00	2.51E-04	-2.57E+00	8.67E-06

490058102	pyruvate dehydrogenase E1	1.38E+01	4.80E-01	3.80E-03	-1.34E+00	3.25E-05	-1.82E+00	6.43E-06
490059395	sugar transporter	9.44E+00	8.22E-01	3.31E-03	-1.34E+00	4.10E-04	-2.16E+00	3.03E-05
490052651	hypothetical protein	1.12E+01	2.57E-03	9.87E-01	-1.34E+00	6.89E-05	-1.34E+00	5.61E-05
490055930	dihydrodipicolinate reductase	1.38E+01	-1.28E-01	3.28E-01	-1.34E+00	5.11E-05	-1.21E+00	6.94E-05
490056421	DNA-binding protein	1.10E+01	-2.97E-01	1.40E-01	-1.33E+00	3.69E-04	-1.04E+00	1.20E-03
490057591	ferredoxin	1.23E+01	1.29E+00	1.48E-03	-1.33E+00	1.88E-03	-2.62E+00	4.72E-05
490054981	aldehyde dehydrogenase	1.17E+01	-2.46E+00	7.43E-06	-1.33E+00	2.26E-04	1.13E+00	4.76E-04
497683256	DNA mismatch repair protein MutT	1.33E+01	-3.28E-01	5.57E-02	-1.33E+00	1.22E-04	-1.00E+00	4.57E-04
490052926	malonic semialdehyde reductase	1.09E+01	1.01E+00	2.30E-02	-1.33E+00	1.03E-02	-2.34E+00	5.59E-04
490057871	ribokinase	1.44E+01	7.26E-01	6.93E-04	-1.33E+00	4.72E-05	-2.06E+00	5.57E-06
497684188	hypothetical protein	1.17E+01	-1.41E+00	2.87E-03	-1.33E+00	5.73E-03	8.36E-02	8.10E-01
490055070	hypothetical protein	1.09E+01	3.04E-01	5.18E-02	-1.32E+00	7.59E-05	-1.63E+00	2.27E-05
490058708	molecular chaperone DnaJ	1.48E+01	2.19E-01	3.31E-01	-1.32E+00	8.65E-04	-1.54E+00	3.35E-04
490054891	ABC transporter substrate-binding protein	1.31E+01	1.43E+00	1.55E-04	-1.32E+00	3.49E-04	-2.76E+00	7.91E-06
490053511	serine hydroxymethyltransferase	1.30E+01	2.72E-01	1.20E-01	-1.32E+00	1.80E-04	-1.59E+00	5.65E-05
490054315	transcriptional regulator	1.28E+01	5.07E-01	5.32E-02	-1.32E+00	1.14E-03	-1.82E+00	1.79E-04
490054845	mannose-1-phosphate guanyltransferase	1.33E+01	-8.22E-01	2.07E-03	-1.32E+00	2.73E-04	-4.95E-01	2.71E-02
497685139	peptidoglycan-binding protein	1.34E+01	-2.36E+00	2.83E-06	-1.32E+00	5.57E-05	1.05E+00	1.48E-04
490057593	transposase IS150	1.29E+01	1.17E+00	2.08E-03	-1.31E+00	1.72E-03	-2.48E+00	5.33E-05
490050335	capsular polysaccharide biosynthesis protein CapB	1.33E+01	1.36E+00	1.19E-04	-1.31E+00	2.10E-04	-2.67E+00	5.80E-06
490057602	glycerol-3-phosphate dehydrogenase	1.11E+01	6.00E-01	2.22E-02	-1.31E+00	8.40E-04	-1.91E+00	9.96E-05
490054387	isoleucyl-tRNA synthase	1.30E+01	-1.77E-01	2.34E-01	-1.31E+00	9.91E-05	-1.13E+00	1.76E-04
490057549	phenylalanyl-tRNA synthetase subunit beta	1.26E+01	-1.80E-01	2.10E-01	-1.31E+00	8.21E-05	-1.13E+00	1.47E-04
490059940	hypothetical protein	1.46E+01	-4.35E-01	6.19E-02	-1.31E+00	6.78E-04	-8.72E-01	4.71E-03
490056978	acetyltransferase	1.49E+01	2.44E-01	1.30E-01	-1.31E+00	1.29E-04	-1.55E+00	4.46E-05
490055884	glutamine amidotransferase	1.28E+01	5.56E-01	4.34E-02	-1.30E+00	1.44E-03	-1.86E+00	1.94E-04
490059388	hypothetical protein	1.43E+01	-1.58E+00	2.13E-04	-1.30E+00	8.81E-04	2.81E-01	2.47E-01
490054886	elongation factor Ts	1.40E+01	-6.78E-02	7.19E-01	-1.30E+00	3.34E-04	-1.24E+00	3.81E-04
490058049	ketohydroxyglutarate aldolase	1.48E+01	7.25E-01	9.17E-03	-1.30E+00	7.71E-04	-2.03E+00	6.51E-05
490056565	ATP-dependent Clp protease ATP-binding protein	1.20E+01	-6.46E-01	9.95E-04	-1.30E+00	4.20E-05	-6.56E-01	1.21E-03

497684079	hypothetical protein	1.41E+01	-1.46E+00	2.69E-05	-1.30E+00	7.13E-05	1.58E-01	2.84E-01
497683104	DNA-directed RNA polymerase subunit beta	1.24E+01	3.45E-01	1.62E-02	-1.30E+00	3.58E-05	-1.65E+00	9.50E-06
490053537	glutamyl-tRNA amidotransferase subunit C	1.18E+01	3.62E-01	6.06E-02	-1.30E+00	2.66E-04	-1.66E+00	6.24E-05
490056603	hydrolase	1.67E+01	-2.03E-01	3.16E-01	-1.30E+00	5.39E-04	-1.09E+00	1.15E-03
490052229	aspartate decarboxylase	1.43E+01	1.25E+00	1.22E-03	-1.29E+00	1.53E-03	-2.54E+00	3.96E-05
490060346	Fe3+-hydroxamate ABC transporter	1.58E+01	1.17E+00	4.30E-04	-1.29E+00	3.87E-04	-2.47E+00	1.28E-05
490058534	glutamyl-tRNA reductase	1.34E+01	-2.09E-01	2.97E-01	-1.29E+00	5.03E-04	-1.08E+00	1.11E-03
490056793	MFS transporter	1.41E+01	-6.12E-02	6.89E-01	-1.29E+00	1.20E-04	-1.23E+00	1.28E-04
497685301	salicylate hydroxylase	1.41E+01	-1.57E+00	1.78E-05	-1.29E+00	6.94E-05	2.87E-01	6.72E-02
490054167	50S ribosomal protein L11	1.31E+01	-4.74E-03	9.72E-01	-1.29E+00	3.09E-05	-1.28E+00	2.48E-05
490053532	lysine decarboxylase	1.30E+01	3.90E-01	8.49E-03	-1.28E+00	3.32E-05	-1.67E+00	7.86E-06
490051655	deaminase	1.09E+01	-3.28E-01	2.41E-01	-1.28E+00	2.88E-03	-9.55E-01	1.04E-02
490050944	radical SAM protein	1.02E+01	4.40E-01	2.35E-02	-1.28E+00	2.04E-04	-1.72E+00	3.79E-05
497683372	F0F1 ATP synthase subunit A	1.36E+01	5.71E-01	5.06E-03	-1.28E+00	1.27E-04	-1.85E+00	1.72E-05
490051891	hypothetical protein	1.47E+01	-1.98E+00	6.92E-06	-1.28E+00	8.61E-05	7.06E-01	1.60E-03
490050132	DNA-binding protein	1.34E+01	-4.75E-01	1.96E-02	-1.27E+00	2.44E-04	-8.00E-01	2.35E-03
497683807	RNA-binding protein	1.34E+01	-1.02E+00	1.33E-03	-1.27E+00	6.20E-04	-2.55E-01	2.49E-01
490058441	dynein regulation protein LC7	1.48E+01	8.38E-01	1.04E-03	-1.27E+00	1.81E-04	-2.11E+00	1.24E-05
490051382	transferase	1.31E+01	8.54E-01	4.28E-03	-1.27E+00	8.84E-04	-2.12E+00	5.08E-05
497685154	regulatory protein	1.58E+01	3.41E-01	3.10E-01	-1.27E+00	7.49E-03	-1.61E+00	2.09E-03
490059704	pyridoxal-5'-phosphate-dependent protein subunit beta	1.27E+01	3.14E-01	5.36E-02	-1.27E+00	1.19E-04	-1.58E+00	3.24E-05
490056429	recombinase RecF	1.13E+01	4.98E-01	1.43E-02	-1.26E+00	2.24E-04	-1.76E+00	3.44E-05
490052118	GCN5 family N-acetyltransferase	1.45E+01	-1.05E+00	1.41E-03	-1.26E+00	8.33E-04	-2.09E-01	3.58E-01
490054423	phosphoribosylaminoimidazole carboxylase	1.29E+01	-1.35E-01	6.55E-01	-1.26E+00	4.66E-03	-1.12E+00	7.16E-03
490051407	ribose-phosphate pyrophosphokinase	1.10E+01	5.38E-01	1.32E-02	-1.25E+00	3.09E-04	-1.79E+00	4.10E-05
497682234	50S ribosomal protein L25	1.18E+01	1.97E+00	4.03E-06	-1.25E+00	4.81E-05	-3.23E+00	1.22E-06
490052111	hypothetical protein	1.30E+01	-1.33E+00	1.21E-03	-1.25E+00	2.48E-03	8.10E-02	7.70E-01
490053246	FAD-linked oxidoreductase	1.43E+01	-1.69E+00	2.86E-05	-1.25E+00	2.05E-04	4.46E-01	2.62E-02
497682842	hydroxyglutarate oxidase	1.15E+01	-4.45E-01	4.96E-02	-1.25E+00	6.92E-04	-8.02E-01	5.70E-03
490059782	Kinase	1.28E+01	8.95E-01	4.21E-04	-1.25E+00	1.14E-04	-2.14E+00	7.10E-06

490056610	ABC transporter	1.02E+01	3.67E-01	4.51E-02	-1.24E+00	2.24E-04	-1.61E+00	4.90E-05
490051410	peptidyl-tRNA hydrolase	1.26E+01	-3.69E-01	2.46E-02	-1.24E+00	1.02E-04	-8.75E-01	5.40E-04
490050087	F0F1 ATP synthase subunit B	1.34E+01	-8.24E-01	2.23E-03	-1.24E+00	3.99E-04	-4.20E-01	5.22E-02
490057882	hypothetical protein	1.57E+01	-7.52E-01	2.76E-02	-1.24E+00	4.57E-03	-4.90E-01	1.36E-01
490051798	hydrolase	1.18E+01	1.10E+00	5.26E-03	-1.24E+00	4.46E-03	-2.34E+00	1.44E-04
497683935	hypothetical protein	1.50E+01	5.45E-01	9.78E-02	-1.24E+00	5.80E-03	-1.78E+00	8.24E-04
497682153	signal peptide protein	1.18E+01	-4.96E-03	9.73E-01	-1.24E+00	5.27E-05	-1.23E+00	4.37E-05
497681946	multidrug ABC transporter ATP-binding protein	1.36E+01	-7.58E-01	4.72E-03	-1.24E+00	5.94E-04	-4.80E-01	4.24E-02
490059049	Hypothetical protein	1.12E+01	-1.79E-02	9.27E-01	-1.24E+00	2.75E-04	-1.22E+00	2.55E-04
490056854	hypothetical protein	1.46E+01	-7.76E-02	5.72E-01	-1.24E+00	9.51E-05	-1.16E+00	1.09E-04
497683083	lysyl-tRNA synthetase	1.35E+01	9.27E-01	1.25E-03	-1.24E+00	4.18E-04	-2.16E+00	2.10E-05
490058671	precorrin-4 C11-methyltransferase	1.38E+01	3.95E-01	1.84E-02	-1.24E+00	1.03E-04	-1.63E+00	2.16E-05
490058945	hypothetical protein	1.01E+01	7.58E-01	4.77E-03	-1.23E+00	6.10E-04	-1.99E+00	4.34E-05
497681649	aminopeptidase N	1.32E+01	-3.38E-01	9.81E-03	-1.23E+00	2.49E-05	-8.95E-01	9.58E-05
490054729	dihydrodipicolinate synthase	1.31E+01	3.48E+00	3.93E-06	-1.23E+00	9.06E-04	-4.71E+00	2.03E-06
490051846	hypothetical protein	1.32E+01	-4.05E-01	6.38E-02	-1.23E+00	6.70E-04	-8.25E-01	4.54E-03
490058360	hypothetical protein	1.30E+01	1.44E+00	9.65E-04	-1.23E+00	3.22E-03	-2.67E+00	4.91E-05
490059418	fumarate hydratase	1.27E+01	-1.25E-01	4.11E-01	-1.23E+00	1.74E-04	-1.10E+00	2.57E-04
490054097	carbamoyl phosphate synthase small subunit	1.46E+01	1.06E+00	4.18E-04	-1.22E+00	2.99E-04	-2.28E+00	1.13E-05
490057784	iron ABC transporter ATP-binding protein	1.29E+01	-9.61E-02	7.02E-01	-1.22E+00	2.04E-03	-1.13E+00	2.71E-03
490054142	50S ribosomal protein L24	1.35E+01	-1.06E-01	7.02E-01	-1.22E+00	3.37E-03	-1.12E+00	4.68E-03
497682612	serine/threonine protein kinase	1.44E+01	-1.13E+00	4.09E-05	-1.22E+00	4.25E-05	-9.05E-02	4.61E-01
490061030	terpene synthase	1.12E+01	-7.60E-01	1.89E-03	-1.22E+00	2.48E-04	-4.59E-01	2.49E-02
490059344	betaine-aldehyde dehydrogenase	1.12E+01	1.57E+00	1.83E-04	-1.22E+00	1.03E-03	-2.79E+00	1.31E-05
490051252	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	1.21E+01	-5.86E-01	2.89E-02	-1.22E+00	1.54E-03	-6.29E-01	2.87E-02
490055229	FAD-binding dehydrogenase	9.06E+00	5.24E-01	3.95E-02	-1.22E+00	1.33E-03	-1.74E+00	1.77E-04
490055127	peptide ABC transporter ATP-binding protein	1.41E+01	3.70E-01	1.18E-01	-1.21E+00	1.32E-03	-1.58E+00	2.85E-04
490059734	5-hydroxymethyluracil DNA glycosylase	1.23E+01	1.05E+00	1.09E-04	-1.21E+00	7.69E-05	-2.26E+00	3.95E-06
490059201	hypothetical protein	1.33E+01	1.64E+00	1.90E-05	-1.21E+00	1.28E-04	-2.84E+00	2.57E-06
490050516	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1.29E+01	1.93E+00	4.81E-05	-1.20E+00	8.20E-04	-3.14E+00	6.17E-06

490056249	N-acetyltransferase GCN5	1.18E+01	9.89E-02	6.38E-01	-1.20E+00	9.63E-04	-1.30E+00	5.54E-04
490051158	phosphoglyceromutase	1.22E+01	1.32E+00	6.35E-03	-1.20E+00	1.40E-02	-2.52E+00	3.16E-04
490057508	class IV aminotransferase	1.36E+01	5.29E-01	5.57E-02	-1.20E+00	2.51E-03	-1.72E+00	3.27E-04
490054153	50S ribosomal protein L3	1.35E+01	2.84E-03	9.88E-01	-1.19E+00	3.39E-04	-1.20E+00	2.88E-04
490058277	methylmalonate-semialdehyde dehydrogenase	1.34E+01	-2.42E-01	1.50E-01	-1.19E+00	2.64E-04	-9.51E-01	7.51E-04
497681797	peptidase	1.23E+01	2.48E-01	1.12E-01	-1.19E+00	1.66E-04	-1.44E+00	5.11E-05
490057889	imidazole glycerol phosphate synthase	1.43E+01	2.73E-01	6.71E-02	-1.19E+00	1.12E-04	-1.46E+00	3.29E-05
490055760	riboflavin synthase subunit alpha	1.37E+01	-1.72E-01	2.97E-01	-1.19E+00	2.85E-04	-1.02E+00	5.56E-04
497681756	ubiquinol-cytochrome C reductase	1.29E+01	-1.38E+00	5.04E-04	-1.19E+00	1.63E-03	1.89E-01	4.39E-01
497682786	DNA polymerase III subunit gamma/tau	1.34E+01	1.24E-01	6.16E-01	-1.19E+00	2.37E-03	-1.31E+00	1.26E-03
490052950	ABC transporter	1.43E+01	9.55E-01	9.95E-04	-1.18E+00	4.90E-04	-2.14E+00	2.09E-05
490058175	leucyl-tRNA synthetase	1.33E+01	1.18E+00	1.96E-04	-1.18E+00	2.89E-04	-2.36E+00	8.14E-06
490059371	DUF255 domain-containing protein	1.08E+01	8.78E-01	7.76E-04	-1.18E+00	2.51E-04	-2.06E+00	1.32E-05
490054698	glyceraldehyde-3-phosphate dehydrogenase	1.05E+01	1.21E+00	8.41E-05	-1.18E+00	1.39E-04	-2.39E+00	4.56E-06
490061079	acetyltransferase	1.58E+01	1.09E+00	1.77E-04	-1.18E+00	1.79E-04	-2.27E+00	6.37E-06
490056051	hypothetical protein	1.10E+01	9.63E-02	6.67E-01	-1.18E+00	1.43E-03	-1.27E+00	8.41E-04
497681631	acyltransferase	1.24E+01	-6.86E-01	5.60E-03	-1.18E+00	5.61E-04	-4.90E-01	3.13E-02
497681765	phage-shock protein	1.21E+01	-1.39E-01	3.23E-01	-1.17E+00	1.36E-04	-1.04E+00	2.23E-04
497681420	recombinase RecB	1.15E+01	1.45E+00	4.58E-05	-1.17E+00	2.02E-04	-2.63E+00	4.05E-06
497682134	phosphotransferase	1.52E+01	2.83E-01	2.28E-01	-1.17E+00	1.89E-03	-1.45E+00	5.36E-04
497683618	1-deoxy-D-xylulose-5-phosphate synthase	1.34E+01	-6.60E-02	7.00E-01	-1.16E+00	3.60E-04	-1.10E+00	4.24E-04
490054162	DNA-directed RNA polymerase subunit beta'	1.26E+01	-2.66E-02	8.74E-01	-1.16E+00	2.51E-04	-1.14E+00	2.43E-04
490052686	hypothetical protein	1.51E+01	-2.57E+00	1.33E-04	-1.16E+00	1.03E-02	1.41E+00	3.79E-03
497682032	ribose 5-phosphate isomerase	1.13E+01	7.16E-01	2.11E-03	-1.16E+00	2.64E-04	-1.88E+00	2.00E-05
490059102	glycosyl transferase	1.32E+01	-1.96E+00	1.23E-04	-1.16E+00	2.72E-03	8.02E-01	1.38E-02
490061238	3-ketoacyl-ACP reductase	1.34E+01	-1.79E+00	5.02E-05	-1.16E+00	7.08E-04	6.35E-01	1.21E-02
490058550	hypothetical protein	1.22E+01	1.32E+00	4.86E-04	-1.16E+00	1.43E-03	-2.47E+00	2.46E-05
490054484	acetyl-CoA synthetase	1.32E+01	-8.87E-01	3.12E-03	-1.15E+00	1.24E-03	-2.68E-01	2.44E-01
490053375	glutamine synthetase	1.30E+01	4.83E-01	5.90E-02	-1.15E+00	2.04E-03	-1.64E+00	2.89E-04
490055374	hypothetical protein	1.13E+01	3.87E-01	6.73E-02	-1.15E+00	8.16E-04	-1.54E+00	1.52E-04
490059733	ribonuclease III	1.41E+01	-8.98E-01	2.57E-04	-1.15E+00	1.09E-04	-2.51E-01	9.29E-02

490055920	metallophosphoesterase	1.44E+01	-1.17E+00	4.05E-03	-1.15E+00	6.49E-03	1.91E-02	9.51E-01
490059859	phosphodiesterase	1.49E+01	5.65E-01	9.47E-03	-1.14E+00	4.28E-04	-1.71E+00	4.52E-05
490054653	O-sialoglycoprotein endopeptidase	8.75E+00	6.30E-01	6.86E-03	-1.14E+00	5.19E-04	-1.77E+00	4.51E-05
490053279	peptidase	1.36E+01	5.83E-01	7.71E-03	-1.14E+00	4.03E-04	-1.72E+00	4.06E-05
497681586	antibiotic biosynthesis monooxygenase	1.01E+01	-7.64E-01	3.11E-03	-1.14E+00	6.10E-04	-3.76E-01	7.40E-02
490058834	penicillin-binding protein	1.30E+01	-2.01E+00	4.08E-04	-1.14E+00	1.01E-02	8.76E-01	2.81E-02
490051801	O-methyltransferase	1.37E+01	1.61E-03	9.93E-01	-1.14E+00	3.43E-04	-1.14E+00	2.93E-04
497682938	putative guanyltransferase	1.17E+01	1.26E+00	5.87E-04	-1.13E+00	1.53E-03	-2.39E+00	2.78E-05
490054600	hypothetical protein	1.43E+01	-3.07E+00	2.66E-05	-1.13E+00	6.27E-03	1.94E+00	3.54E-04
490054727	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase	1.46E+01	4.20E-01	3.32E-02	-1.13E+00	4.87E-04	-1.55E+00	7.95E-05
490051143	sugar ABC transporter ATP-binding protein	1.43E+01	-7.80E-01	1.22E-03	-1.13E+00	2.74E-04	-3.45E-01	5.67E-02
497685225	beta-lactamase	1.23E+01	-3.65E+00	1.15E-06	-1.12E+00	1.53E-04	2.53E+00	3.34E-06
490056431	DNA polymerase III subunit beta	1.17E+01	-2.39E-01	2.33E-01	-1.12E+00	1.02E-03	-8.85E-01	3.03E-03
490058538	glycerol acyltransferase	1.58E+01	1.22E+00	6.42E-05	-1.12E+00	1.53E-04	-2.34E+00	4.22E-06
490050024	pyruvate kinase	1.25E+01	5.08E-01	9.23E-03	-1.12E+00	2.73E-04	-1.62E+00	3.38E-05
490053893	NADH:ubiquinone oxidoreductase subunit N	1.42E+01	-4.63E+00	3.76E-06	-1.11E+00	5.65E-03	3.52E+00	1.46E-05
497685238	hypothetical protein	1.65E+01	3.26E-01	3.77E-02	-1.11E+00	1.69E-04	-1.44E+00	3.81E-05
497681692	DNA polymerase III subunit alpha	1.22E+01	-7.67E-01	2.69E-03	-1.11E+00	5.98E-04	-3.46E-01	8.78E-02
490056180	methionine synthase	1.31E+01	-1.09E+00	2.56E-03	-1.11E+00	3.48E-03	-2.13E-02	9.35E-01
497683556	diaminopimelate epimerase	1.44E+01	7.29E-01	1.34E-02	-1.11E+00	2.84E-03	-1.84E+00	1.78E-04
497681843	oxidoreductase	1.32E+01	-2.38E-03	9.87E-01	-1.11E+00	1.28E-04	-1.11E+00	1.08E-04
490057565	short-chain dehydrogenase	1.45E+01	-1.12E+00	6.94E-04	-1.11E+00	1.09E-03	1.01E-02	9.61E-01
490055931	zinc protease	8.32E+00	6.08E-01	3.71E-02	-1.11E+00	4.12E-03	-1.72E+00	3.81E-04
490056667	diadenosine tetraphosphatase	1.20E+01	1.13E+00	6.24E-03	-1.11E+00	9.75E-03	-2.23E+00	2.54E-04
490059720	IclR family transcriptional regulator	1.49E+01	8.09E-01	1.51E-02	-1.11E+00	5.43E-03	-1.91E+00	2.88E-04
490054702	electron transporter	1.19E+01	-1.23E-01	4.20E-01	-1.10E+00	3.03E-04	-9.82E-01	4.87E-04
490058396	hypothetical protein	1.50E+01	-1.89E+00	2.32E-05	-1.10E+00	5.38E-04	7.88E-01	2.67E-03
490053850	glutamate-1-semialdehyde aminotransferase	1.12E+01	8.14E-01	1.11E-03	-1.10E+00	3.43E-04	-1.92E+00	1.81E-05
497682435	esterase	1.10E+01	-5.12E-01	9.62E-03	-1.10E+00	3.18E-04	-5.91E-01	6.63E-03
490059304	phosphoesterase	1.65E+01	5.76E-01	9.59E-03	-1.10E+00	5.84E-04	-1.68E+00	5.56E-05

497681263	signal peptide protein	1.38E+01	-5.57E-01	2.79E-03	-1.10E+00	1.27E-04	-5.42E-01	4.20E-03
490060251	ATP-binding protein	1.21E+01	-1.70E+00	6.12E-05	-1.10E+00	8.55E-04	5.96E-01	1.48E-02
490055876	response regulator	1.44E+01	-1.24E+00	2.76E-05	-1.10E+00	7.59E-05	1.40E-01	2.68E-01
497682041	dynein regulation protein LC7	1.44E+01	8.92E-01	4.35E-03	-1.10E+00	2.35E-03	-1.99E+00	9.19E-05
490054319	ABC transporter permease	1.26E+01	-4.90E-01	8.46E-02	-1.10E+00	4.93E-03	-6.07E-01	5.22E-02
497681303	ribulose-phosphate 3-epimerase	1.19E+01	2.91E+00	1.80E-05	-1.09E+00	3.84E-03	-4.01E+00	5.57E-06
490053805	DNA topoisomerase IV subunit B	1.24E+01	6.83E-01	3.19E-03	-1.09E+00	4.34E-04	-1.78E+00	3.10E-05
497685379	DNA-binding protein	1.54E+01	1.18E-01	6.46E-01	-1.09E+00	4.16E-03	-1.21E+00	2.19E-03
490059291	purine biosynthesis protein purH	1.31E+01	4.35E-01	6.09E-02	-1.09E+00	1.67E-03	-1.53E+00	2.54E-04
490056454	ribosome-associated protein IOJAP	1.44E+01	1.17E+00	4.87E-04	-1.09E+00	1.03E-03	-2.26E+00	2.14E-05
497681016	glucosamine-6-phosphate deaminase	8.64E+00	1.28E+00	2.08E-03	-1.09E+00	6.76E-03	-2.37E+00	1.09E-04
497682020	rod shape-determining protein Mbl	1.19E+01	9.81E-01	2.69E-04	-1.09E+00	2.35E-04	-2.07E+00	8.57E-06
490054808	whiD	1.25E+01	2.33E+00	5.26E-05	-1.09E+00	3.88E-03	-3.42E+00	1.04E-05
490053816	phosphocarrier protein HPr	1.11E+01	1.01E-01	4.76E-01	-1.09E+00	2.32E-04	-1.19E+00	1.22E-04
490060241	alpha-galactosidase	1.26E+01	7.63E-03	9.70E-01	-1.09E+00	4.26E-04	-1.09E+00	3.59E-04
497681154	hypothetical protein	1.11E+01	-4.65E-01	3.29E-02	-1.08E+00	9.98E-04	-6.20E-01	1.35E-02
490051458	oxidoreductase	1.44E+01	-1.21E+00	1.88E-04	-1.08E+00	4.95E-04	1.27E-01	4.73E-01
490054040	hypothetical protein	1.08E+01	-6.26E-01	8.71E-03	-1.08E+00	8.91E-04	-4.56E-01	4.13E-02
490055924	ribonuclease	1.30E+01	7.77E-02	6.31E-01	-1.08E+00	4.22E-04	-1.16E+00	2.54E-04
490058394	NAD-glutamate dehydrogenase	1.27E+01	1.19E-01	5.20E-01	-1.08E+00	9.13E-04	-1.20E+00	4.61E-04
490052582	phosphomannomutase	1.29E+01	5.65E-02	6.57E-01	-1.08E+00	1.22E-04	-1.14E+00	7.78E-05
490051040	acetyl-CoA carboxylase	9.43E+00	-1.08E+00	4.55E-04	-1.08E+00	6.87E-04	2.48E-03	9.89E-01
497681983	phosphate starvation protein PhoH	1.23E+01	2.80E-01	1.26E-01	-1.07E+00	6.63E-04	-1.35E+00	1.70E-04
497681789	membrane protein	1.33E+01	-2.97E-01	1.36E-01	-1.07E+00	1.07E-03	-7.75E-01	4.90E-03
497682442	hypothetical protein	1.07E+01	-1.67E-01	5.16E-01	-1.07E+00	5.01E-03	-9.03E-01	9.87E-03
497685090	hypothetical protein	1.63E+01	1.37E+00	1.55E-04	-1.07E+00	8.38E-04	-2.44E+00	1.12E-05
497683997	MarR family transcriptional regulator	1.38E+01	-8.66E-02	4.23E-01	-1.07E+00	6.29E-05	-9.80E-01	7.95E-05
497683979	alpha/beta hydrolase	1.28E+01	-1.12E-02	9.69E-01	-1.07E+00	2.60E-03	-1.06E+00	2.39E-03
490057887	hypothetical protein	1.07E+01	2.46E+00	9.26E-06	-1.07E+00	9.06E-04	-3.52E+00	2.96E-06
490051185	thiosulfate sulfurtransferase	9.54E+00	1.85E-01	2.15E-01	-1.06E+00	2.89E-04	-1.25E+00	1.06E-04
490057810	FeS-binding protein	1.14E+01	-4.21E-02	7.98E-01	-1.06E+00	4.00E-04	-1.02E+00	4.32E-04

490061357	Moenomycin biosynthesis protein MoeN5	1.08E+01	-8.52E-01	4.07E-03	-1.06E+00	2.04E-03	-2.10E-01	3.59E-01
497682455	cytochrome P450	1.38E+01	-1.28E+00	4.45E-04	-1.06E+00	1.77E-03	2.22E-01	3.22E-01
490057468	methionyl-tRNA formyltransferase	1.23E+01	2.13E-01	3.57E-01	-1.06E+00	3.13E-03	-1.28E+00	1.09E-03
490050027	thioredoxin	1.41E+01	1.98E-01	4.01E-01	-1.06E+00	3.48E-03	-1.26E+00	1.29E-03
497681565	IclR family transcriptional regulator	1.34E+01	-1.07E+00	1.77E-04	-1.06E+00	2.75E-04	1.05E-02	9.45E-01
497682175	LytR family transcriptional regulator	1.01E+01	-2.28E-01	1.58E-01	-1.06E+00	4.04E-04	-8.30E-01	1.26E-03
497681406	glycine/betaine ABC transporter ATP-binding protein	1.34E+01	1.61E+00	1.88E-04	-1.06E+00	2.48E-03	-2.67E+00	1.89E-05
490059057	heat-shock protein Hsp90	1.24E+01	-1.05E+00	1.12E-03	-1.06E+00	1.61E-03	-6.01E-03	9.77E-01
490054647	copper-binding protein	1.40E+01	5.22E-01	2.30E-02	-1.06E+00	1.30E-03	-1.58E+00	1.36E-04
490052907	alkyl hydroperoxide reductase	1.36E+01	7.46E-02	7.65E-01	-1.05E+00	3.77E-03	-1.13E+00	2.34E-03
490059189	transcriptional antiterminator	9.78E+00	-1.36E+00	9.79E-05	-1.05E+00	5.41E-04	3.08E-01	9.84E-02
490054382	alanine racemase	1.30E+01	2.56E-01	1.40E-01	-1.05E+00	5.69E-04	-1.31E+00	1.57E-04
490060087	hypothetical protein	1.18E+01	6.80E-01	5.32E-03	-1.05E+00	9.02E-04	-1.73E+00	5.67E-05
490051916	hypothetical protein	1.23E+01	-1.84E+00	5.02E-05	-1.05E+00	1.33E-03	7.89E-01	5.03E-03
490050708	phosphopantetheine--protein transferase	1.36E+01	-3.89E-02	8.53E-01	-1.05E+00	1.35E-03	-1.01E+00	1.44E-03
490708573	glutamine amidotransferase	1.40E+01	3.72E-02	8.16E-01	-1.05E+00	3.69E-04	-1.09E+00	2.64E-04
497683293	NAD-dependent dehydratase	1.43E+01	5.78E-01	3.78E-03	-1.05E+00	2.72E-04	-1.63E+00	2.46E-05
490058130	DNA primase	1.16E+01	-7.33E-02	5.76E-01	-1.04E+00	1.81E-04	-9.68E-01	2.25E-04
490054828	LuxR family transcriptional regulator	1.57E+01	-5.52E-01	7.05E-03	-1.04E+00	4.41E-04	-4.87E-01	1.62E-02
490059730	methyltransferase	1.38E+01	1.10E+00	3.34E-05	-1.04E+00	6.68E-05	-2.13E+00	2.59E-06
490052594	transcriptional regulator	1.52E+01	-9.31E-01	1.57E-04	-1.04E+00	1.34E-04	-1.05E-01	4.26E-01
490061346	AMP-dependent synthetase	1.50E+01	-1.64E-01	3.80E-01	-1.04E+00	1.19E-03	-8.71E-01	2.53E-03
497683195	aldehyde dehydrogenase	1.33E+01	2.81E-01	7.80E-02	-1.03E+00	3.43E-04	-1.31E+00	8.29E-05
497681563	MarR family transcriptional regulator	1.47E+01	4.56E-01	1.46E-02	-1.03E+00	4.01E-04	-1.49E+00	5.06E-05
490057557	50S ribosomal protein L35	1.42E+01	-1.06E+00	2.14E-04	-1.03E+00	3.67E-04	2.66E-02	8.64E-01
490056669	aspartate aminotransferase	1.11E+01	2.62E-01	1.59E-01	-1.03E+00	9.67E-04	-1.29E+00	2.55E-04
497682456	peptide hydrolase	1.51E+01	2.78E-01	7.23E-02	-1.03E+00	2.93E-04	-1.31E+00	7.16E-05
497683188	dienelactone hydrolase	1.20E+01	-4.49E-01	1.04E-02	-1.03E+00	2.54E-04	-5.80E-01	4.24E-03
497684950	terpene synthase	1.39E+01	-1.27E+00	9.53E-05	-1.03E+00	4.14E-04	2.44E-01	1.49E-01
490052661	phosphoribosylformylglycinamidine synthase	1.48E+01	-1.09E+00	3.67E-04	-1.03E+00	7.41E-04	6.11E-02	7.35E-01

490058915	TetR family transcriptional regulator	1.27E+01	-1.99E-01	4.54E-01	-1.03E+00	7.20E-03	-8.27E-01	1.71E-02
490053265	F420-dependent oxidoreductase	1.38E+01	3.09E-01	1.14E-01	-1.02E+00	1.15E-03	-1.33E+00	2.53E-04
497681405	glutamate--ammonia ligase	1.65E+01	-5.85E-01	1.23E-03	-1.02E+00	1.03E-04	-4.37E-01	6.80E-03
497682747	hypothetical protein	1.34E+01	-2.42E+00	2.79E-06	-1.02E+00	2.17E-04	1.40E+00	3.66E-05
490059833	ATP-binding protein	1.20E+01	8.62E-01	2.84E-04	-1.02E+00	1.82E-04	-1.88E+00	7.86E-06
490054878	3-ketoacyl-ACP reductase	1.24E+01	-1.34E-01	3.20E-01	-1.02E+00	2.26E-04	-8.83E-01	4.10E-04
490050658	activator of HSP90 ATPase	1.21E+01	-5.35E-01	9.11E-02	-1.02E+00	1.16E-02	-4.81E-01	1.44E-01
497684104	parB-like partition protein	1.23E+01	5.12E-02	8.04E-01	-1.02E+00	1.68E-03	-1.07E+00	1.15E-03
490050597	thioredoxin	1.50E+01	-5.61E+00	1.16E-06	-1.01E+00	2.72E-03	4.60E+00	2.25E-06
497683030	regulator	1.37E+01	-6.56E-01	2.58E-03	-1.01E+00	4.12E-04	-3.58E-01	4.62E-02
490051097	N-acetylmuramic acid-6-phosphate etherase	1.30E+01	3.92E-01	1.66E-01	-1.01E+00	8.48E-03	-1.41E+00	1.53E-03
490055118	enolase	1.23E+01	9.12E-02	6.01E-01	-1.01E+00	8.94E-04	-1.10E+00	4.95E-04
490055580	hypothetical protein	1.31E+01	-1.34E-01	2.49E-01	-1.01E+00	1.08E-04	-8.77E-01	1.87E-04
497682960	endoribonuclease	9.90E+00	8.30E-01	3.43E-03	-1.01E+00	1.94E-03	-1.84E+00	7.33E-05
490054262	ABC transporter permease	1.36E+01	2.30E-01	2.75E-01	-1.01E+00	2.36E-03	-1.24E+00	7.23E-04
490057483	alanyl-tRNA synthetase	1.34E+01	-2.03E-02	8.89E-01	-1.01E+00	2.59E-04	-9.89E-01	2.47E-04
490053332	LuxR family transcriptional regulator	1.58E+01	-4.13E-01	1.74E-02	-1.01E+00	3.45E-04	-5.95E-01	4.54E-03
497681279	membrane protein	1.25E+01	-1.69E-01	3.37E-01	-1.01E+00	1.00E-03	-8.38E-01	2.24E-03
490050104	diaminopimelate decarboxylase	1.32E+01	-9.27E-02	5.22E-01	-1.01E+00	3.70E-04	-9.15E-01	5.32E-04
490054261	ABC transporter permease	1.13E+01	1.36E+00	1.90E-04	-1.01E+00	1.36E-03	-2.37E+00	1.49E-05
490053804	hypothetical protein	1.34E+01	-4.18E-01	2.72E-02	-1.01E+00	6.60E-04	-5.88E-01	8.56E-03
490054080	30S ribosomal protein S4	1.46E+01	2.80E-01	5.68E-02	-1.00E+00	2.37E-04	-1.28E+00	5.54E-05
497682597	XRE family transcriptional regulator	1.22E+01	-2.70E+00	2.76E-05	-1.00E+00	6.34E-03	1.70E+00	3.87E-04
497682425	alpha/beta hydrolase	1.31E+01	1.10E+00	1.18E-04	-1.00E+00	2.82E-04	-2.11E+00	6.42E-06
490054882	uracil-DNA glycosylase	1.55E+01	-9.52E-01	4.32E-04	-1.00E+00	4.98E-04	-4.84E-02	7.67E-01
490052695	XRE family transcriptional regulator	1.24E+01	-2.17E-01	3.07E-01	-9.99E-01	2.61E-03	-7.83E-01	7.55E-03
490058372	FAD-linked oxidase	1.19E+01	-6.93E-01	7.81E-04	-9.98E-01	1.79E-04	-3.05E-01	4.30E-02
490051760	ATP/GTP-binding protein	8.10E+00	9.85E-01	4.76E-04	-9.94E-01	6.80E-04	-1.98E+00	1.79E-05
490056082	ABC transporter permease	9.08E+00	2.68E-01	2.63E-01	-9.91E-01	4.83E-03	-1.26E+00	1.29E-03
490054205	RNA nucleotidyltransferase	1.43E+01	3.22E-01	2.65E-02	-9.90E-01	1.81E-04	-1.31E+00	3.61E-05
490056070	arginine repressor	1.39E+01	-2.94E-01	2.33E-01	-9.90E-01	5.39E-03	-6.96E-01	2.31E-02

490053226	membrane protein	1.12E+01	1.53E+00	4.63E-05	-9.88E-01	6.47E-04	-2.52E+00	5.70E-06
497683102	NAD-dependent dehydratase	1.30E+01	2.04E+00	1.71E-04	-9.87E-01	9.52E-03	-3.03E+00	2.88E-05
497682004	nicotinic acid mononucleotide adenylyltransferase	1.32E+01	5.44E-02	7.02E-01	-9.84E-01	3.33E-04	-1.04E+00	2.14E-04
490055603	GntR family transcriptional regulator	1.33E+01	9.18E-01	1.12E-03	-9.84E-01	1.17E-03	-1.90E+00	3.33E-05
490054214	alanine racemase	1.27E+01	3.01E-01	1.23E-01	-9.83E-01	1.44E-03	-1.28E+00	3.11E-04
490060440	hypothetical protein	1.46E+01	-3.91E+00	2.89E-06	-9.81E-01	3.40E-03	2.93E+00	1.16E-05
490051512	ferredoxin	1.41E+01	1.42E-01	4.09E-01	-9.77E-01	1.07E-03	-1.12E+00	4.61E-04
490059415	Magnesium or manganese-dependent protein phosphatase	1.46E+01	-1.28E+00	3.10E-05	-9.77E-01	1.81E-04	3.01E-01	4.22E-02
490051552	hypothetical protein	1.07E+01	2.63E+00	1.80E-05	-9.77E-01	4.10E-03	-3.61E+00	5.57E-06
490050917	arginyl-tRNA synthetase	1.27E+01	1.02E-01	5.11E-01	-9.72E-01	6.25E-04	-1.07E+00	3.24E-04
490056913	cytochrome P450	7.88E+00	5.28E-01	7.29E-02	-9.72E-01	9.65E-03	-1.50E+00	1.04E-03
490051489	5'-methylthioadenosine phosphorylase	1.23E+01	-6.06E-01	4.23E-03	-9.70E-01	5.85E-04	-3.64E-01	4.72E-02
497681728	5,10-methylenetetrahydrofolate reductase	1.54E+01	3.03E-01	2.81E-02	-9.69E-01	1.59E-04	-1.27E+00	3.33E-05
490060951	acetyltransferase	1.29E+01	8.80E-01	1.09E-03	-9.68E-01	9.90E-04	-1.85E+00	3.03E-05
490058681	adenylosuccinate synthetase	1.31E+01	9.75E-01	1.40E-03	-9.67E-01	2.17E-03	-1.94E+00	4.93E-05
490051538	magnesium transporter CorA	1.33E+01	3.34E+00	1.50E-05	-9.63E-01	1.07E-02	-4.30E+00	5.94E-06
490058026	Phenazine biosynthesis PhzC/PhzF protein	1.54E+01	1.09E-01	5.17E-01	-9.60E-01	1.05E-03	-1.07E+00	5.22E-04
490055040	RNA methyltransferase	1.27E+01	7.19E-01	2.27E-03	-9.59E-01	7.86E-04	-1.68E+00	3.72E-05
490057170	hypothetical protein	1.45E+01	7.76E-01	9.77E-03	-9.58E-01	5.49E-03	-1.73E+00	2.31E-04
490059326	amidohydrolase	1.23E+01	-7.28E-01	8.31E-03	-9.58E-01	3.37E-03	-2.30E-01	3.15E-01
490058112	peptidase M28	1.35E+01	4.14E-01	1.19E-01	-9.57E-01	7.38E-03	-1.37E+00	1.11E-03
497681388	hypothetical protein	1.29E+01	1.15E+00	2.26E-03	-9.56E-01	8.05E-03	-2.11E+00	1.26E-04
490052576	biotin carboxyl carrier protein	1.26E+01	1.08E+00	2.56E-04	-9.56E-01	7.08E-04	-2.03E+00	1.33E-05
490057298	acyl-CoA thioesterase	1.53E+01	6.85E-01	6.44E-03	-9.51E-01	1.93E-03	-1.64E+00	9.86E-05
490058168	hypothetical protein	1.02E+01	2.43E+00	7.44E-05	-9.51E-01	1.18E-02	-3.38E+00	1.81E-05
490053058	DNA-binding protein	1.48E+01	5.15E-01	1.69E-02	-9.51E-01	1.40E-03	-1.47E+00	1.25E-04
497682849	NADH dehydrogenase	1.31E+01	-5.66E-01	2.65E-02	-9.49E-01	4.04E-03	-3.83E-01	1.20E-01
497682215	NADH dehydrogenase	1.37E+01	1.53E+00	2.32E-05	-9.46E-01	4.03E-04	-2.48E+00	3.82E-06
490055439	adenosine deaminase	1.30E+01	-1.51E+00	2.42E-04	-9.45E-01	3.99E-03	5.65E-01	3.40E-02
497682788	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.32E+01	3.15E-01	1.85E-01	-9.44E-01	5.36E-03	-1.26E+00	1.13E-03

490052451	ABC transporter substrate-binding protein	1.17E+01	1.61E+00	5.54E-04	-9.41E-01	1.14E-02	-2.55E+00	6.45E-05
490050100	transcription termination factor Rho	1.44E+01	-1.02E+00	9.43E-05	-9.37E-01	2.12E-04	8.19E-02	5.27E-01
490059197	hypothetical protein	1.22E+01	1.29E+00	9.54E-04	-9.37E-01	6.95E-03	-2.23E+00	7.13E-05
490051530	translocase	1.33E+01	-4.16E-01	1.30E-01	-9.36E-01	9.73E-03	-5.20E-01	8.36E-02
497681284	AsnC family transcriptional regulator	1.29E+01	4.10E-01	1.30E-01	-9.35E-01	9.10E-03	-1.35E+00	1.38E-03
497684774	phosphohydrolase	1.21E+01	2.03E+00	1.01E-04	-9.35E-01	7.46E-03	-2.97E+00	1.90E-05
490059687	transcriptional regulator	1.33E+01	2.13E+00	1.16E-05	-9.34E-01	1.10E-03	-3.06E+00	3.40E-06
490055567	hypothetical protein	1.26E+01	5.11E-01	9.51E-02	-9.32E-01	1.48E-02	-1.44E+00	1.66E-03
490060420	penicillin-binding protein	1.24E+01	-3.45E-01	3.98E-02	-9.31E-01	6.10E-04	-5.86E-01	5.66E-03
497683895	hypothetical protein	1.35E+01	1.58E-01	3.72E-01	-9.31E-01	1.53E-03	-1.09E+00	5.94E-04
490059268	inosine 5'-monophosphate dehydrogenase	1.22E+01	1.35E+00	1.30E-04	-9.29E-01	1.30E-03	-2.28E+00	1.20E-05
490055240	alcohol dehydrogenase	1.10E+01	1.44E+00	3.36E-04	-9.28E-01	4.71E-03	-2.37E+00	3.31E-05
497683184	sugar ABC transporter ATPase	1.18E+01	9.28E-01	2.10E-04	-9.26E-01	3.17E-04	-1.85E+00	8.67E-06
497681272	hypothetical protein, partial	9.45E+00	6.44E-01	2.32E-02	-9.26E-01	7.07E-03	-1.57E+00	4.36E-04
490058986	alkaline D-peptidase	1.52E+01	1.00E+00	1.93E-04	-9.24E-01	4.39E-04	-1.93E+00	9.59E-06
490050482	acetyltransferase	1.10E+01	2.81E-01	2.39E-01	-9.21E-01	6.57E-03	-1.20E+00	1.56E-03
490057339	N-acetyltransferase GCN5	1.26E+01	2.97E+00	1.30E-05	-9.18E-01	6.85E-03	-3.88E+00	5.20E-06
490054086	3-dehydroquinate synthase	1.31E+01	-2.75E-01	1.45E-01	-9.18E-01	1.82E-03	-6.43E-01	9.12E-03
490052535	phosphoenolpyruvate carboxykinase	1.06E+01	1.96E+00	9.23E-05	-9.17E-01	6.36E-03	-2.88E+00	1.71E-05
490058320	membrane protein	1.45E+01	-9.81E-01	4.94E-04	-9.15E-01	1.07E-03	6.64E-02	7.00E-01
497683320	alpha-ketoglutarate decarboxylase	1.22E+01	9.86E-01	6.12E-05	-9.11E-01	1.36E-04	-1.90E+00	4.03E-06
490056523	30S ribosomal protein S6 modification enzyme RimK	1.27E+01	2.41E-01	1.27E-01	-9.10E-01	7.28E-04	-1.15E+00	1.83E-04
490053398	type II citrate synthase	1.37E+01	5.41E-01	1.41E-02	-9.08E-01	1.82E-03	-1.45E+00	1.36E-04
497683465	histidine kinase	1.39E+01	-1.34E+00	1.30E-05	-9.06E-01	1.29E-04	4.34E-01	4.97E-03
490055599	phosphohistidine phosphatase	9.98E+00	3.17E+00	2.02E-05	-9.05E-01	1.49E-02	-4.08E+00	7.86E-06
490056254	glycerol acyltransferase	1.47E+01	7.68E-01	7.78E-03	-9.03E-01	5.40E-03	-1.67E+00	2.00E-04
497681776	pyruvate dehydrogenase E1	1.43E+01	8.33E-01	7.13E-03	-9.02E-01	7.28E-03	-1.74E+00	2.31E-04
490057616	aldo/keto reductase	1.48E+01	-4.77E-01	1.79E-02	-8.99E-01	1.34E-03	-4.22E-01	3.74E-02
490055581	hypothetical protein	1.40E+01	9.72E-01	1.21E-03	-8.98E-01	2.70E-03	-1.87E+00	5.06E-05
490053047	pyruvate dehydrogenase E1 subunit alpha	1.32E+01	2.99E-01	2.33E-01	-8.98E-01	9.20E-03	-1.20E+00	2.05E-03

497682040	aminopeptidase N	1.25E+01	1.19E+00	5.29E-05	-8.96E-01	3.36E-04	-2.09E+00	5.20E-06
497682058	hisitidine kinase	1.51E+01	-2.16E-01	3.97E-01	-8.96E-01	1.10E-02	-6.79E-01	3.20E-02
490059196	FAD-dependent oxidoreductase	1.32E+01	-8.39E-01	8.29E-03	-8.95E-01	8.94E-03	-5.66E-02	8.26E-01
490058755	CRISPR-associated protein Cse4	1.46E+01	-1.78E+00	1.56E-04	-8.91E-01	7.49E-03	8.85E-01	6.99E-03
497683785	isochorismatase	1.28E+01	-8.36E-01	3.92E-03	-8.90E-01	4.35E-03	-5.40E-02	8.06E-01
497682218	type II restriction endonuclease subunit M	1.16E+01	1.92E-01	2.65E-01	-8.89E-01	1.59E-03	-1.08E+00	5.05E-04
497683911	transcriptional regulator	1.27E+01	-5.29E-01	5.87E-03	-8.89E-01	6.52E-04	-3.60E-01	3.87E-02
497683627	ATPase	1.09E+01	1.18E+00	4.63E-05	-8.89E-01	2.89E-04	-2.07E+00	4.61E-06
490053861	radical SAM protein	1.35E+01	-7.78E-04	9.97E-01	-8.87E-01	1.51E-03	-8.87E-01	1.33E-03
497681849	DNA primase	1.16E+01	-1.12E+00	5.81E-04	-8.87E-01	2.89E-03	2.34E-01	2.60E-01
497681424	transferase	1.29E+01	8.54E-01	8.06E-04	-8.86E-01	1.01E-03	-1.74E+00	2.68E-05
497683603	hypothetical protein	1.16E+01	-5.55E-01	6.83E-03	-8.85E-01	1.02E-03	-3.30E-01	6.84E-02
490061145	hypothetical protein	1.33E+01	-1.10E+00	1.77E-04	-8.84E-01	8.15E-04	2.15E-01	1.90E-01
490057818	excinuclease ABC subunit B	1.37E+01	3.41E-01	1.73E-01	-8.84E-01	9.04E-03	-1.23E+00	1.65E-03
490056993	cytochrome P450	1.46E+01	-1.40E+00	1.13E-04	-8.82E-01	1.80E-03	5.19E-01	1.94E-02
497683062	TetR family transcriptional regulator	1.45E+01	1.75E+00	6.19E-05	-8.82E-01	3.13E-03	-2.63E+00	1.08E-05
490054002	ABC transporter	1.47E+01	1.94E+00	2.37E-05	-8.80E-01	2.02E-03	-2.82E+00	5.57E-06
490052502	peroxiredoxin	1.39E+01	8.14E-01	1.93E-03	-8.80E-01	1.95E-03	-1.69E+00	5.51E-05
490059251	pantothenate kinase	1.40E+01	6.10E-01	2.05E-03	-8.79E-01	4.67E-04	-1.49E+00	2.69E-05
490053825	16S RNA G1207 methylase RsmC	1.43E+01	-3.06E-01	1.92E-01	-8.79E-01	7.14E-03	-5.73E-01	3.90E-02
490058535	REX family transcriptional regulator	1.26E+01	1.38E+00	4.17E-04	-8.76E-01	6.13E-03	-2.26E+00	4.11E-05
490051666	ABC transporter permease	1.14E+01	2.00E-02	9.30E-01	-8.75E-01	3.50E-03	-8.95E-01	2.74E-03
490058659	metallophosphoesterase	1.19E+01	6.42E-01	1.27E-02	-8.72E-01	4.64E-03	-1.51E+00	2.38E-04
490059756	hypothetical protein	1.28E+01	-4.31E-01	1.18E-01	-8.72E-01	1.31E-02	-4.41E-01	1.31E-01
490057939	membrane protein	1.21E+01	-4.09E-01	2.04E-02	-8.70E-01	8.57E-04	-4.61E-01	1.63E-02
497683258	ABC transporter permease	1.31E+01	-1.34E-01	3.27E-01	-8.69E-01	5.55E-04	-7.36E-01	1.16E-03
497682582	putative two-component system sensor kinase/response regulator, bifunctional protein	1.38E+01	3.45E-01	1.51E-01	-8.67E-01	7.95E-03	-1.21E+00	1.37E-03
490052493	beta-lactamase	1.22E+01	1.69E+00	3.67E-05	-8.66E-01	1.67E-03	-2.55E+00	6.53E-06
490051445	hypothetical protein	1.33E+01	-3.14E+00	1.90E-06	-8.65E-01	1.15E-03	2.27E+00	7.86E-06
490060366	TetR family transcriptional regulator	1.56E+01	3.13E-01	2.35E-02	-8.64E-01	2.68E-04	-1.18E+00	4.52E-05

497681120	cold-shock protein	1.35E+01	-1.02E+00	4.35E-03	-8.61E-01	1.40E-02	1.63E-01	5.55E-01
490059369	regulatory protein	1.25E+01	-1.28E-01	3.06E-01	-8.60E-01	3.76E-04	-7.32E-01	7.65E-04
490054802	molecular chaperone GroES	1.00E+01	1.52E+00	2.11E-05	-8.59E-01	5.67E-04	-2.38E+00	3.92E-06
490054109	phosphoglucosamine mutase	1.42E+01	-4.61E-01	1.08E-02	-8.57E-01	7.97E-04	-3.95E-01	2.72E-02
497683391	hypothetical protein	1.17E+01	-2.08E+00	4.44E-06	-8.56E-01	5.17E-04	1.23E+00	6.68E-05
490051579	peptidase M20	1.30E+01	7.75E-02	5.16E-01	-8.55E-01	3.18E-04	-9.33E-01	1.73E-04
490051515	succinyl-diaminopimelate desuccinylase	1.38E+01	3.39E-01	3.74E-02	-8.54E-01	7.97E-04	-1.19E+00	1.17E-04
497682167	membrane protein	1.35E+01	-3.62E-02	8.42E-01	-8.51E-01	2.02E-03	-8.15E-01	2.21E-03
490054721	Fe-S cluster assembly protein SufB	1.33E+01	7.30E-01	1.47E-02	-8.49E-01	1.10E-02	-1.58E+00	4.53E-04
497682012	gamma-glutamyl kinase	1.36E+01	-3.36E-01	7.00E-02	-8.49E-01	2.00E-03	-5.13E-01	1.90E-02
490057346	transcriptional regulator	1.01E+01	1.20E-01	6.24E-01	-8.47E-01	1.09E-02	-9.67E-01	5.43E-03
497682617	beta-lactamase	1.31E+01	3.41E-01	7.17E-02	-8.47E-01	2.27E-03	-1.19E+00	3.43E-04
497681957	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	1.83E+01	1.60E+00	1.23E-04	-8.46E-01	4.65E-03	-2.44E+00	1.84E-05
490055607	modulator of DNA gyrase	1.30E+01	-1.21E-01	4.10E-01	-8.46E-01	9.91E-04	-7.26E-01	1.91E-03
490056340	DSBA oxidoreductase	1.52E+01	-1.76E+00	5.08E-05	-8.45E-01	3.30E-03	9.18E-01	1.92E-03
490051447	hypothetical protein	1.39E+01	-1.46E+00	6.83E-04	-8.44E-01	1.43E-02	6.18E-01	4.51E-02
490057891	imidazole glycerol phosphate synthase	1.16E+01	8.36E-01	2.56E-03	-8.43E-01	3.68E-03	-1.68E+00	8.96E-05
490053302	AsnC family transcriptional regulator	1.56E+01	-4.72E-01	4.97E-03	-8.42E-01	3.99E-04	-3.70E-01	1.94E-02
490056489	aspartokinase	1.32E+01	8.57E-01	1.33E-03	-8.41E-01	2.18E-03	-1.70E+00	4.82E-05
497681617	excinuclease ABC subunit A	1.25E+01	-3.15E-02	8.71E-01	-8.39E-01	2.76E-03	-8.07E-01	2.92E-03
490054113	ABC transporter	1.15E+01	1.20E+00	9.57E-05	-8.38E-01	9.13E-04	-2.04E+00	8.94E-06
490052684	nucleoside-diphosphate kinase	1.36E+01	-4.26E+00	1.15E-06	-8.32E-01	1.62E-03	3.43E+00	2.23E-06
490055252	transferase	1.45E+01	8.19E-01	3.67E-04	-8.29E-01	5.15E-04	-1.65E+00	1.38E-05
490057574	5'-3' exonuclease	1.42E+01	1.31E+00	3.76E-05	-8.28E-01	5.86E-04	-2.14E+00	5.23E-06
490051743	beta-lactamase	1.09E+01	3.16E-01	2.53E-02	-8.27E-01	3.89E-04	-1.14E+00	6.13E-05
490054392	RNA pseudouridine synthase	1.32E+01	3.84E-01	1.12E-02	-8.26E-01	3.86E-04	-1.21E+00	4.51E-05
490055825	hypothetical protein	1.34E+01	-3.32E+00	4.79E-06	-8.26E-01	7.27E-03	2.49E+00	2.29E-05
490053875	acetyltransferase	1.39E+01	-9.34E-01	7.68E-04	-8.26E-01	2.16E-03	1.09E-01	5.42E-01
490054062	glutamine amidotransferase	1.43E+01	7.86E-01	2.04E-03	-8.23E-01	2.42E-03	-1.61E+00	6.38E-05
497683562	RNA polymerase sigma factor	1.33E+01	6.66E-02	6.48E-01	-8.16E-01	1.05E-03	-8.83E-01	6.08E-04

490050709	hypothetical protein	1.33E+01	-1.09E+00	4.24E-04	-8.16E-01	2.86E-03	2.78E-01	1.54E-01
490053069	methionyl-tRNA synthetase	1.21E+01	7.87E-01	2.92E-03	-8.12E-01	3.77E-03	-1.60E+00	9.71E-05
497684181	diaminopimelate epimerase, partial	1.56E+01	-1.00E+00	1.12E-03	-8.11E-01	4.76E-03	1.90E-01	3.60E-01
490054287	glutamine synthetase	1.12E+01	1.01E+00	1.24E-03	-8.10E-01	5.46E-03	-1.82E+00	7.35E-05
497682414	oxidoreductase	1.32E+01	3.20E-01	2.98E-02	-8.10E-01	5.70E-04	-1.13E+00	8.65E-05
490052209	ribonuclease H	1.28E+01	5.86E-01	1.12E-02	-8.10E-01	3.77E-03	-1.40E+00	1.94E-04
490051136	hypothetical protein	1.23E+01	2.23E-01	7.90E-02	-8.09E-01	3.78E-04	-1.03E+00	9.04E-05
490053868	cold-shock protein	1.12E+01	7.51E-03	9.63E-01	-8.08E-01	5.70E-04	-8.16E-01	4.76E-04
497683782	DNA-binding protein	1.25E+01	3.06E-01	7.30E-02	-8.08E-01	1.73E-03	-1.11E+00	2.82E-04
490059294	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	1.44E+01	-2.26E-01	1.77E-01	-8.08E-01	2.03E-03	-5.82E-01	8.86E-03
497683594	hypothetical protein	1.54E+01	3.78E-01	5.23E-02	-8.05E-01	3.07E-03	-1.18E+00	3.68E-04
497683091	acetyltransferase	1.46E+01	4.06E-01	3.73E-02	-8.01E-01	2.77E-03	-1.21E+00	2.89E-04
497682274	penicillin amidase	1.42E+01	-8.94E-01	2.35E-03	-8.00E-01	5.96E-03	9.37E-02	6.59E-01

[a] Identification is based on annotation by NCBI. **[b]** Description is based on NCBI annotation of protein similarity by BLAST. **[c]** Average normalized expression in the WT strain. **[d]** Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. **[e]**Adjusted P-value in *ΔbldG* as compared to the WT strain. **[f]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. **[g]** Adjusted P-value in *ΔbldA* as compared to the WT strain. **[h]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and **[i]** Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Table A.1.5: Proteins determined to be significantly (P = 0.01) over-expressed in the *ΔbldA* compared to the *ΔbldG* strains of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G -WT[e]	logFC A -WT[f]	adj.P.Val A-WT[g]	logFC A -G[h]	adj.P.Val A -G[i]
490058756	CRISPR-associated protein Cas2	5.73E+00	-9.07E+00	9.69E-08	2.69E-01	1.52E-01	9.34E+00	4.46E-08
490054719	spermidine/putrescine ABC transporter ATP-binding protein	9.14E+00	2.20E+00	1.92E-02	8.96E+00	3.07E-05	6.76E+00	9.98E-05
490057554	50S ribosomal protein L20	1.03E+01	1.73E+00	2.00E-03	7.84E+00	3.04E-06	6.12E+00	5.23E-06
490053262	cell division protein SepF	9.78E+00	1.07E+00	9.94E-04	7.08E+00	6.87E-07	6.00E+00	8.19E-07
490050666	endoribonuclease L-PSP	1.36E+01	-7.85E-01	5.23E-02	4.94E+00	1.49E-05	5.73E+00	5.81E-06
497682291	hypothetical protein	1.26E+01	-3.01E+00	1.09E-02	2.07E+00	6.40E-02	5.08E+00	1.16E-03
490051454	conserved hypothetical protein	1.23E+01	-5.21E+00	6.60E-05	-3.32E-01	5.94E-01	4.87E+00	1.13E-04
497683080	hypothetical protein	1.08E+01	-3.90E+00	2.83E-03	7.42E-01	4.46E-01	4.64E+00	1.55E-03
497684074	hypothetical protein, partial	4.02E+00	-7.64E+00	7.44E-05	-3.00E+00	1.14E-02	4.63E+00	1.26E-03
490050597	thioredoxin	1.50E+01	-5.61E+00	1.16E-06	-1.01E+00	2.72E-03	4.60E+00	2.25E-06
490057875	membrane protein	1.37E+01	-2.13E+00	4.38E-03	2.45E+00	3.37E-03	4.58E+00	1.11E-04
490058852	Hypothetical protein	1.35E+01	-2.54E+00	7.44E-05	1.99E+00	3.79E-04	4.53E+00	5.94E-06
490050798	tellurium resistance protein	1.31E+01	-3.62E+00	1.48E-06	8.52E-01	1.09E-03	4.47E+00	8.19E-07
490056196	transcriptional regulator	1.42E+01	-3.38E+00	8.89E-05	1.07E+00	3.26E-02	4.45E+00	2.73E-05
497682033	putative gamma-aminobutyrate permease	1.43E+01	-2.25E+00	4.76E-03	2.18E+00	8.07E-03	4.42E+00	1.94E-04
497684987	hypothetical protein	1.08E+01	-9.87E-01	8.85E-02	3.32E+00	6.75E-04	4.31E+00	1.48E-04
490051568	reductase	1.04E+01	-4.26E+00	1.87E-06	-6.06E-02	7.83E-01	4.20E+00	2.49E-06
490046206	whiK	1.45E+01	-1.86E+00	2.04E-05	2.27E+00	1.39E-05	4.13E+00	1.57E-06
490059845	GntR family transcriptional regulator	1.37E+01	-2.52E-01	7.66E-01	3.85E+00	2.66E-03	4.10E+00	1.68E-03
490059429	succinate dehydrogenase	1.39E+01	-5.60E-01	2.01E-01	3.44E+00	1.73E-04	4.00E+00	6.58E-05
490054479	ATP-binding protein	1.34E+01	-2.91E+00	8.85E-04	1.07E+00	8.70E-02	3.98E+00	2.23E-04
490055426	peptidase M4	1.28E+01	-9.57E-01	1.16E-01	2.92E+00	1.82E-03	3.88E+00	3.65E-04
497681787	regulator	1.49E+01	-3.15E+00	1.46E-04	7.25E-01	1.22E-01	3.88E+00	6.24E-05
497685016	hypothetical protein	1.44E+01	-3.95E+00	3.03E-06	-9.89E-02	6.81E-01	3.85E+00	4.31E-06
490060049	putative secreted FAD-linked oxidase	1.35E+01	-3.29E+00	2.79E-06	3.97E-01	6.54E-02	3.69E+00	2.57E-06
490053784	ATP-dependent helicase	1.16E+01	-8.05E-01	5.90E-02	2.84E+00	2.71E-04	3.65E+00	6.26E-05

490054247	membrane protein	1.36E+01	-2.22E+00	2.17E-05	1.39E+00	3.49E-04	3.60E+00	3.58E-06
490051661	superoxide dismutase	1.46E+01	-3.05E+00	4.07E-03	5.43E-01	5.08E-01	3.59E+00	2.39E-03
490060096	glyoxalase	1.25E+01	-3.43E+00	2.65E-04	1.32E-01	8.07E-01	3.56E+00	2.82E-04
497683991	polyketide synthase	1.25E+01	-7.41E-01	2.45E-02	2.79E+00	5.81E-05	3.54E+00	1.54E-05
490052127	carbonate dehydratase	1.32E+01	-1.71E+00	2.72E-05	1.83E+00	3.10E-05	3.53E+00	2.03E-06
497685018	hypothetical protein	1.42E+01	-3.27E+00	1.87E-06	2.49E-01	1.60E-01	3.52E+00	2.03E-06
490053893	NADH:ubiquinone oxidoreductase subunit N	1.42E+01	-4.63E+00	3.76E-06	-1.11E+00	5.65E-03	3.52E+00	1.46E-05
490059531	histidine kinase	1.38E+01	-2.79E+00	4.63E-05	6.83E-01	5.19E-02	3.48E+00	1.98E-05
490052943	fumarate reductase	1.24E+01	-1.32E+00	4.41E-03	2.14E+00	5.69E-04	3.46E+00	4.06E-05
490052684	nucleoside-diphosphate kinase	1.36E+01	-4.26E+00	1.15E-06	-8.32E-01	1.62E-03	3.43E+00	2.23E-06
490060539	calcium-binding protein	1.48E+01	-3.90E+00	7.40E-06	-4.96E-01	1.18E-01	3.41E+00	1.76E-05
490061303	histidine decarboxylase	1.34E+01	-3.22E+00	3.20E-04	1.54E-01	7.71E-01	3.38E+00	3.26E-04
497683312	dimethylallyltranstransferase	1.13E+01	-2.27E+00	2.91E-04	1.08E+00	1.59E-02	3.36E+00	4.82E-05
497682409	pilus biosynthesis protein TadE	1.41E+01	-3.81E+00	1.16E-03	-5.05E-01	5.25E-01	3.31E+00	3.10E-03
490061142	amidohydrolase	1.20E+01	-3.75E+00	1.50E-05	-5.07E-01	1.45E-01	3.24E+00	3.71E-05
490058785	membrane protein	1.29E+01	-3.02E+00	5.74E-05	1.52E-01	6.64E-01	3.18E+00	5.47E-05
497681558	hypothetical protein	1.19E+01	-1.28E+00	2.49E-03	1.88E+00	5.34E-04	3.16E+00	3.14E-05
490058329	amidase	1.27E+01	-2.43E+00	2.24E-04	7.21E-01	7.58E-02	3.15E+00	7.35E-05
490050319	glutamine synthetase	1.55E+01	-3.19E+00	1.87E-06	-6.18E-02	7.09E-01	3.13E+00	2.57E-06
497682770	hypothetical protein	1.13E+01	-1.93E+00	1.92E-05	1.19E+00	3.22E-04	3.12E+00	3.24E-06
490052035	short-chain dehydrogenase	1.36E+01	-3.82E+00	1.87E-06	-6.99E-01	7.34E-03	3.12E+00	4.39E-06
497684150	hypothetical protein	1.35E+01	-3.20E+00	4.69E-06	-1.34E-01	5.44E-01	3.06E+00	7.39E-06
497681093	hypothetical protein	1.23E+01	-8.52E-01	3.06E-02	2.17E+00	5.75E-04	3.02E+00	8.78E-05
497683069	permease	1.36E+01	-3.63E+00	1.15E-06	-6.14E-01	3.38E-03	3.01E+00	2.03E-06
490059837	LexA repressor	1.16E+01	-1.12E+00	6.18E-03	1.87E+00	7.01E-04	2.99E+00	5.16E-05
490052167	aminotransferase class III	9.70E+00	-6.58E-01	1.75E-01	2.33E+00	2.09E-03	2.99E+00	5.05E-04
497681010	dihydroxyacetone kinase subunit K	1.31E+01	-2.46E+00	1.87E-06	5.22E-01	4.17E-03	2.98E+00	1.58E-06
497682216	hypothetical protein	1.15E+01	-1.41E+00	7.41E-04	1.57E+00	6.52E-04	2.98E+00	2.10E-05
490059937	flavoprotein oxidoreductase	1.01E+01	-1.48E-02	9.68E-01	2.92E+00	5.22E-05	2.93E+00	4.11E-05
490060440	hypothetical protein	1.46E+01	-3.91E+00	2.89E-06	-9.81E-01	3.40E-03	2.93E+00	1.16E-05
497682154	sugar ABC transporter substrate-binding protein	1.14E+01	-3.16E+00	6.33E-06	-2.57E-01	2.78E-01	2.91E+00	1.18E-05

490059212	NADH:ubiquinone oxidoreductase subunit J	1.34E+01	-3.20E+00	4.16E-06	-3.61E-01	1.13E-01	2.84E+00	8.68E-06
490059927	ABC transporter substrate-binding protein	1.31E+01	-2.88E+00	4.69E-06	-4.33E-02	8.31E-01	2.84E+00	6.51E-06
497681271	hypothetical protein, partial	1.25E+01	3.41E-02	9.16E-01	2.87E+00	5.82E-05	2.84E+00	5.01E-05
490059803	hypothetical protein	1.41E+01	-4.79E+00	1.15E-06	-1.96E+00	3.07E-05	2.83E+00	4.97E-06
490054446	conserved hypothetical protein	1.22E+01	-3.59E+00	2.48E-05	-7.67E-01	5.42E-02	2.82E+00	1.04E-04
497681151	hypothetical protein	1.13E+01	-2.26E+00	4.34E-06	5.46E-01	7.13E-03	2.81E+00	2.62E-06
490051281	maltose O-acetyltransferase	1.39E+01	-1.92E+00	2.32E-05	8.89E-01	1.77E-03	2.81E+00	5.46E-06
490051269	hypothetical protein	1.03E+01	-2.22E+00	3.93E-06	5.59E-01	4.75E-03	2.78E+00	2.49E-06
490058537	RNA polymerase subunit sigma-24	1.13E+01	-3.42E+00	3.40E-06	-6.56E-01	1.41E-02	2.77E+00	9.80E-06
490052896	hypothetical protein	1.20E+01	-5.05E+00	1.15E-06	-2.30E+00	2.11E-05	2.75E+00	7.02E-06
490050055	hypothetical protein	1.37E+01	-2.97E+00	6.94E-06	-2.37E-01	2.95E-01	2.73E+00	1.28E-05
490051384	potassium transporter	1.37E+01	-1.07E+00	9.27E-04	1.63E+00	1.60E-04	2.70E+00	1.12E-05
497685046	hypothetical protein	1.26E+01	-1.59E+00	2.96E-02	1.11E+00	1.21E-01	2.70E+00	3.81E-03
490059675	membrane protein	1.28E+01	-2.35E+00	1.83E-04	3.50E-01	3.12E-01	2.70E+00	1.11E-04
490059168	ABC transporter ATP-binding protein	1.13E+01	-2.81E+00	4.44E-06	-1.24E-01	5.15E-01	2.69E+00	6.66E-06
490057070	histidine kinase	1.25E+01	-2.31E+00	2.95E-05	3.18E-01	1.92E-01	2.63E+00	2.00E-05
490055111	hypothetical protein	1.36E+01	-4.95E+00	1.16E-06	-2.39E+00	2.04E-05	2.57E+00	1.11E-05
490059209	NADH dehydrogenase subunit D	1.20E+01	-2.35E+00	3.62E-04	1.90E-01	6.26E-01	2.54E+00	3.11E-04
497681423	peptide-binding protein	1.27E+01	-4.29E+00	3.74E-05	-1.75E+00	5.35E-03	2.54E+00	7.23E-04
490059637	sporulation protein	1.34E+01	-1.09E+00	7.98E-05	1.45E+00	2.94E-05	2.54E+00	2.57E-06
497685225	beta-lactamase	1.23E+01	-3.65E+00	1.15E-06	-1.12E+00	1.53E-04	2.53E+00	3.34E-06
490050721	hypothetical protein	1.79E+01	-2.31E+00	2.43E-05	2.04E-01	3.71E-01	2.52E+00	2.04E-05
490055290	hypothetical protein	1.49E+01	-2.39E+00	5.12E-06	1.16E-01	4.91E-01	2.50E+00	5.57E-06
490055825	hypothetical protein	1.34E+01	-3.32E+00	4.79E-06	-8.26E-01	7.27E-03	2.49E+00	2.29E-05
490060508	nitroreductase	1.36E+01	-2.44E+00	7.55E-04	1.18E-02	9.80E-01	2.46E+00	9.77E-04
490057367	ATP-binding protein	1.51E+01	-2.77E+00	1.02E-05	-3.35E-01	1.57E-01	2.44E+00	2.27E-05
490059210	NADH dehydrogenase subunit F	1.43E+01	-2.99E+00	2.69E-06	-5.54E-01	1.18E-02	2.43E+00	6.85E-06
490061352	UDP-glucose 4-epimerase	1.22E+01	-1.69E+00	7.81E-06	7.37E-01	7.35E-04	2.43E+00	2.57E-06
490050391	3-beta hydroxysteroid dehydrogenase	1.36E+01	-4.09E+00	3.93E-06	-1.66E+00	4.28E-04	2.43E+00	5.08E-05
490059955	beta-glucosidase	1.47E+01	-2.03E+00	1.08E-05	3.95E-01	3.97E-02	2.42E+00	6.05E-06
490050062	3-hydroxybutyryl-CoA dehydrogenase	8.99E+00	4.18E-01	1.32E-02	2.83E+00	3.04E-06	2.41E+00	3.85E-06

490053447	CRISPR-associated protein	1.69E+01	8.38E-03	9.73E-01	2.41E+00	2.73E-05	2.40E+00	2.17E-05
490050315	methyltransferase	1.38E+01	-4.45E+00	2.52E-06	-2.09E+00	1.05E-04	2.36E+00	4.57E-05
490052844	lectin PVL	1.47E+01	-4.36E+00	1.87E-06	-2.00E+00	7.92E-05	2.36E+00	2.91E-05
490052605	RNA polymerase sigma70 factor	1.16E+01	-2.48E+00	2.19E-06	-1.70E-01	2.28E-01	2.31E+00	3.74E-06
497685273	hypothetical protein	1.35E+01	-1.94E+00	5.45E-05	3.32E-01	1.58E-01	2.28E+00	3.12E-05
490051445	hypothetical protein	1.33E+01	-3.14E+00	1.90E-06	-8.65E-01	1.15E-03	2.27E+00	7.86E-06
490061463	calcium-binding protein	1.37E+01	-1.07E+00	1.20E-04	1.20E+00	9.84E-05	2.27E+00	4.52E-06
490060425	hypothetical protein	1.43E+01	-1.17E+00	7.68E-03	1.09E+00	1.52E-02	2.26E+00	3.77E-04
490057416	histidine kinase	1.30E+01	-2.72E+00	1.87E-06	-4.57E-01	1.16E-02	2.26E+00	4.39E-06
490059920	endoribonuclease	1.19E+01	9.60E-02	6.81E-01	2.34E+00	5.15E-05	2.25E+00	5.08E-05
490050423	folylpolyglutamate synthase	1.12E+01	-9.85E-01	1.94E-04	1.26E+00	8.29E-05	2.24E+00	5.05E-06
490051786	HAD family hydrolase	1.15E+01	-1.07E+00	8.28E-03	1.17E+00	7.86E-03	2.24E+00	2.61E-04
490051386	anti-sigma B factor antagonist	1.54E+01	-5.23E+00	2.60E-06	-3.00E+00	4.11E-05	2.23E+00	1.49E-04
490056425	membrane protein	1.13E+01	-9.14E-01	4.99E-03	1.31E+00	1.23E-03	2.23E+00	6.70E-05
490055729	glutamine amidotransferase	1.35E+01	-1.96E+00	6.01E-05	2.60E-01	2.67E-01	2.22E+00	3.96E-05
497684179	diaminopimelate epimerase	1.06E+01	-4.33E-01	1.23E-01	1.79E+00	4.29E-04	2.22E+00	1.17E-04
490057023	regulatory protein	1.28E+01	-2.47E+00	1.39E-05	-2.75E-01	2.15E-01	2.20E+00	2.98E-05
490055033	aminotransferase	1.40E+01	-8.98E-01	1.68E-03	1.28E+00	4.00E-04	2.18E+00	2.27E-05
490058973	membrane protein	1.53E+01	-1.81E+00	6.18E-06	3.41E-01	2.92E-02	2.16E+00	4.06E-06
490052939	hypothetical protein	1.44E+01	-2.71E+00	1.86E-06	-5.77E-01	3.36E-03	2.13E+00	4.84E-06
497683200	pyridine nucleotide-disulfide oxidoreductase	1.05E+01	4.04E-01	4.04E-02	2.54E+00	1.09E-05	2.13E+00	1.79E-05
497684051	carbon starvation protein CstA	1.44E+01	-2.40E+00	3.93E-06	-2.69E-01	1.08E-01	2.13E+00	7.86E-06
490054628	competence damage-inducible protein A	1.39E+01	-4.00E+00	3.29E-06	-1.88E+00	1.57E-04	2.12E+00	7.12E-05
497681703	DNA-binding protein	1.09E+01	-9.07E-01	1.41E-02	1.19E+00	6.14E-03	2.10E+00	3.02E-04
490061097	DNA primase	1.14E+01	-6.96E-01	3.92E-03	1.40E+00	1.67E-04	2.10E+00	1.89E-05
490057267	transcriptional activator	1.45E+01	-1.07E+00	3.96E-03	9.80E-01	8.66E-03	2.05E+00	1.82E-04
490050764	conserved hypothetical protein	1.41E+01	-2.63E+00	4.60E-06	-5.89E-01	1.09E-02	2.04E+00	1.89E-05
490051126	cold-shock protein	1.48E+01	-3.41E+00	8.11E-06	-1.37E+00	1.19E-03	2.04E+00	1.25E-04
490056701	cytochrome P450	1.25E+01	-1.75E+00	1.33E-04	2.82E-01	2.49E-01	2.03E+00	7.53E-05
497681807	alpha-N-acetylglucosaminidase	1.45E+01	-1.84E+00	5.24E-05	1.82E-01	3.86E-01	2.02E+00	4.02E-05
490050995	hypothetical protein	1.31E+01	-1.92E+00	2.17E-05	9.49E-02	6.05E-01	2.02E+00	2.14E-05

497685434	plasmid stabilization protein	1.04E+01	-4.26E+00	1.75E-05	-2.25E+00	6.37E-04	2.01E+00	1.02E-03
490058342	membrane protein	1.33E+01	-1.08E+00	2.12E-04	9.30E-01	6.72E-04	2.01E+00	1.20E-05
497682610	transcriptional regulator	1.27E+01	-2.96E+00	1.09E-04	-9.56E-01	3.47E-02	2.01E+00	1.05E-03
497682392	hypothetical protein	1.37E+01	-2.40E+00	1.90E-06	-4.05E-01	1.23E-02	2.00E+00	4.72E-06
497683554	hypothetical protein	1.05E+01	-1.20E+00	1.43E-03	7.87E-01	1.50E-02	1.98E+00	1.31E-04
490058506	histidyl-tRNA synthetase	1.31E+01	-2.78E+00	2.69E-05	-8.07E-01	1.81E-02	1.98E+00	1.94E-04
497685457	hypothetical protein	1.54E+01	-2.05E+00	1.33E-04	-8.45E-02	7.67E-01	1.97E+00	2.07E-04
490060463	sugar-binding protein	1.19E+01	-3.34E+00	1.48E-06	-1.38E+00	5.93E-05	1.96E+00	9.29E-06
497683410	hypothetical protein	1.33E+01	-1.33E+00	7.73E-05	6.12E-01	5.99E-03	1.95E+00	1.48E-05
490054600	hypothetical protein	1.43E+01	-3.07E+00	2.66E-05	-1.13E+00	6.27E-03	1.94E+00	3.54E-04
490054000	AMP-dependent synthetase	1.36E+01	-1.78E+00	1.80E-05	1.56E-01	3.45E-01	1.94E+00	1.49E-05
490057727	oxidoreductase	1.40E+01	-1.51E-02	9.46E-01	1.92E+00	5.02E-05	1.94E+00	3.96E-05
497681029	alpha-mannosidase	1.44E+01	-1.10E+00	6.21E-05	8.30E-01	3.99E-04	1.93E+00	5.70E-06
490059598	nucleotide pyrophosphatase	1.34E+01	-1.77E+00	1.35E-05	1.57E-01	3.10E-01	1.93E+00	1.12E-05
497685343	hypothetical protein	1.54E+01	-2.63E+00	1.99E-06	-7.17E-01	1.28E-03	1.91E+00	8.05E-06
490058978	phosphate ABC transporter ATP-binding protein	1.25E+01	-2.38E+00	2.71E-06	-4.70E-01	9.27E-03	1.91E+00	7.63E-06
490060633	hypothetical protein	1.51E+01	-2.55E+00	4.16E-06	-6.50E-01	5.31E-03	1.90E+00	1.95E-05
490058590	XRE family transcriptional regulator	1.26E+01	-2.65E+00	1.06E-03	-7.51E-01	1.83E-01	1.90E+00	7.20E-03
490054541	DNA-binding protein	1.52E+01	-8.79E-01	3.19E-04	1.02E+00	2.20E-04	1.90E+00	8.76E-06
490057012	cation-binding protein	1.24E+01	-1.63E+00	2.96E-04	2.60E-01	3.23E-01	1.89E+00	1.75E-04
490051270	aldehyde dehydrogenase	1.32E+01	-2.92E+00	1.57E-04	-1.04E+00	3.19E-02	1.88E+00	1.98E-03
497681259	hypothetical protein	1.01E+01	2.34E+00	6.94E-06	4.22E+00	1.68E-06	1.88E+00	2.43E-05
490061466	hypothetical protein	1.48E+01	-2.15E+00	7.44E-05	-2.93E-01	2.74E-01	1.86E+00	1.96E-04
497683148	hypothetical protein	1.44E+01	-3.44E+00	1.87E-06	-1.57E+00	6.97E-05	1.86E+00	2.55E-05
490059976	glyoxalase	1.20E+01	-9.10E-01	2.00E-03	9.40E-01	2.55E-03	1.85E+00	6.45E-05
490055478	DNA-binding protein	1.26E+01	-1.23E+00	5.29E-05	6.14E-01	2.77E-03	1.84E+00	9.37E-06
490052842	hypothetical protein	1.24E+01	-2.25E+00	2.33E-04	-4.06E-01	2.47E-01	1.84E+00	8.63E-04
497681011	dihydroxyacetone kinase subunit DhaL	1.05E+01	-2.22E+00	1.70E-04	-3.90E-01	2.34E-01	1.83E+00	5.96E-04
490055964	septum formation initiator	1.08E+01	-2.30E+00	7.89E-04	-4.77E-01	2.92E-01	1.83E+00	3.38E-03
490059408	L-glyceraldehyde 3-phosphate reductase	1.50E+01	-2.20E+00	3.93E-06	-3.76E-01	2.70E-02	1.82E+00	1.08E-05
490060520	cell surface protein	1.37E+01	-3.50E+00	9.66E-06	-1.71E+00	5.11E-04	1.79E+00	3.43E-04

490055968	secretion protein	1.31E+01	-2.27E+00	6.36E-06	-5.08E-01	1.49E-02	1.76E+00	2.61E-05
490054419	chemotaxis protein CheY	1.34E+01	-2.03E+00	6.63E-05	-2.92E-01	2.40E-01	1.74E+00	1.84E-04
497685206	hypothetical protein	1.49E+01	-3.85E+00	2.94E-06	-2.12E+00	6.14E-05	1.73E+00	1.48E-04
490055036	histidinol-phosphatase	1.39E+01	-1.37E+00	2.87E-04	3.47E-01	1.32E-01	1.71E+00	1.11E-04
497682597	XRE family transcriptional regulator	1.22E+01	-2.70E+00	2.76E-05	-1.00E+00	6.34E-03	1.70E+00	3.87E-04
497681148	hypothetical protein	1.47E+01	-2.47E+00	2.28E-05	-7.68E-01	1.15E-02	1.70E+00	1.88E-04
490050164	glutamate N-acetyltransferase 2	1.34E+01	-2.08E+00	7.08E-06	-3.80E-01	3.67E-02	1.70E+00	2.27E-05
490055141	DNA-binding protein	1.45E+01	-3.10E+00	1.30E-05	-1.41E+00	1.02E-03	1.69E+00	3.37E-04
497683486	signal peptidase	1.36E+01	-9.30E-01	1.51E-02	7.56E-01	4.71E-02	1.69E+00	1.18E-03
497684140	hypothetical protein	1.29E+01	-3.13E+00	3.42E-06	-1.45E+00	1.81E-04	1.68E+00	7.22E-05
490059489	catalase	1.40E+01	-3.22E+00	1.40E-06	-1.55E+00	2.72E-05	1.67E+00	1.47E-05
497682739	hypothetical protein	1.41E+01	-1.02E+00	9.92E-05	6.50E-01	1.48E-03	1.67E+00	1.10E-05
490052166	apolipoprotein acyltransferase	1.23E+01	-1.51E+00	1.18E-04	1.52E-01	4.50E-01	1.67E+00	8.77E-05
497680944	phosphotransferase	1.10E+01	-3.18E+00	5.46E-06	-1.51E+00	3.13E-04	1.66E+00	1.61E-04
490055938	hypothetical protein	1.15E+01	-2.48E+00	4.40E-05	-8.16E-01	1.58E-02	1.66E+00	4.38E-04
490053882	NADH dehydrogenase subunit C	1.48E+01	-2.33E+00	8.00E-05	-6.73E-01	4.22E-02	1.66E+00	5.95E-04
490050350	hypothetical protein	1.14E+01	-3.82E+00	3.33E-06	-2.18E+00	6.09E-05	1.64E+00	2.18E-04
497682751	hypothetical protein	1.44E+01	-1.65E+00	1.30E-04	-1.84E-02	9.38E-01	1.63E+00	1.71E-04
497680901	cytochrome P450	1.27E+01	-1.53E+00	2.07E-03	1.00E-01	7.81E-01	1.63E+00	1.97E-03
497683042	transcriptional regulator	1.36E+01	-1.24E+00	2.64E-04	3.94E-01	6.69E-02	1.63E+00	7.95E-05
490051883	hypothetical protein	9.96E+00	-1.44E+00	1.19E-03	1.86E-01	5.35E-01	1.62E+00	8.37E-04
490050162	proclavaminate amidinohydrolase	9.99E+00	-2.20E+00	2.66E-04	-6.01E-01	1.06E-01	1.60E+00	1.82E-03
490051865	hypothetical protein	1.25E+01	-3.37E+00	1.70E-06	-1.78E+00	3.19E-05	1.60E+00	4.25E-05
497681584	DNA-binding protein	1.42E+01	-1.99E+00	1.14E-05	-4.00E-01	3.74E-02	1.59E+00	4.05E-05
490051924	hypothetical protein	1.26E+01	-1.81E+00	1.87E-05	-2.30E-01	1.85E-01	1.58E+00	4.38E-05
490057150	aldolase	1.06E+01	1.11E-02	9.69E-01	1.59E+00	3.49E-04	1.58E+00	3.12E-04
497685442	acetyltransferase	1.19E+01	-3.04E+00	3.68E-05	-1.47E+00	2.30E-03	1.57E+00	1.42E-03
490051231	membrane protein	1.36E+01	-2.19E+00	3.74E-05	-6.18E-01	2.63E-02	1.57E+00	2.61E-04
490061125	precorrin 6A synthase	1.45E+01	-1.90E+00	2.29E-05	-3.42E-01	8.72E-02	1.56E+00	7.62E-05
490054344	pseudouridine-5'-phosphate glycosidase	1.35E+01	-2.10E+00	2.79E-06	-5.82E-01	1.88E-03	1.52E+00	1.27E-05
497685105	amidohydrolase	1.39E+01	-2.22E+00	3.74E-05	-7.06E-01	1.62E-02	1.51E+00	3.42E-04

490057319	1-acyl-sn-glycerol-3-phosphate acyltransferase	1.51E+01	-2.00E+00	1.20E-04	-4.83E-01	9.42E-02	1.51E+00	6.43E-04
490055747	membrane protein	1.24E+01	-3.58E+00	1.02E-05	-2.08E+00	2.19E-04	1.50E+00	1.04E-03
490051541	hypothetical protein	1.31E+01	-1.04E+00	3.28E-04	4.60E-01	2.41E-02	1.50E+00	6.23E-05
497681054	sporulation protein	1.24E+01	-4.68E-01	6.20E-03	1.03E+00	1.74E-04	1.50E+00	2.18E-05
490054803	molecular chaperone GroEL	1.06E+01	-1.80E-02	9.52E-01	1.46E+00	8.66E-04	1.48E+00	7.10E-04
490061049	alkanal monooxygenase	1.33E+01	-3.81E+00	2.09E-05	-2.33E+00	3.72E-04	1.48E+00	3.36E-03
497683687	ATP-binding protein	9.36E+00	-2.11E+00	1.30E-05	-6.39E-01	7.62E-03	1.47E+00	9.39E-05
497685015	hypothetical protein	1.09E+01	-3.13E+00	4.43E-06	-1.66E+00	1.32E-04	1.46E+00	2.21E-04
497683966	O-acetylhomoserine aminocarboxypropyltransferase	1.16E+01	-3.20E+00	1.48E-06	-1.74E+00	1.84E-05	1.46E+00	3.12E-05
497683403	ATP-dependent DNA helicase	1.35E+01	-1.65E+00	1.77E-05	-2.08E-01	1.84E-01	1.45E+00	4.07E-05
490054308	hypothetical protein	1.24E+01	-5.29E-01	2.34E-01	9.08E-01	7.76E-02	1.44E+00	1.32E-02
490058757	CRISPR-associated protein Cas1	1.29E+01	-9.33E-01	1.12E-03	5.04E-01	2.77E-02	1.44E+00	1.50E-04
490056409	hypothetical protein	1.37E+01	-2.00E+00	1.91E-04	-5.64E-01	8.01E-02	1.44E+00	1.40E-03
497682075	biotin carboxyl carrier protein	1.12E+01	-7.06E-01	1.43E-02	7.23E-01	1.85E-02	1.43E+00	6.20E-04
490052686	hypothetical protein	1.51E+01	-2.57E+00	1.33E-04	-1.16E+00	1.03E-02	1.41E+00	3.79E-03
497682747	hypothetical protein	1.34E+01	-2.42E+00	2.79E-06	-1.02E+00	2.17E-04	1.40E+00	3.66E-05
490050174	hypothetical protein	1.40E+01	-2.74E+00	1.67E-06	-1.35E+00	3.92E-05	1.39E+00	2.78E-05
490060062	3-oxoadipate enol-lactonase	1.25E+01	-2.47E+00	1.91E-04	-1.10E+00	1.52E-02	1.37E+00	5.07E-03
490051893	hypothetical protein	1.33E+01	-1.26E+00	1.13E-04	1.07E-01	5.21E-01	1.36E+00	9.05E-05
490052137	IclR family transcriptional regulator	1.43E+01	-1.44E+00	2.44E-05	-8.78E-02	5.35E-01	1.36E+00	4.10E-05
490055057	acetyltransferase	1.03E+01	-1.34E+00	4.72E-04	1.74E-02	9.42E-01	1.35E+00	5.79E-04
490058055	molecular chaperone GroES	1.31E+01	-1.54E+00	1.88E-04	-1.88E-01	4.05E-01	1.35E+00	4.78E-04
497681233	histidine kinase	1.31E+01	-2.76E+00	4.53E-06	-1.41E+00	1.74E-04	1.35E+00	1.84E-04
490055544	metallophosphoesterase	1.57E+01	-1.04E+00	1.39E-04	2.89E-01	6.80E-02	1.33E+00	4.78E-05
490054316	amino acid ABC transporter ATPase	1.35E+01	-3.07E+00	5.52E-05	-1.74E+00	1.53E-03	1.32E+00	5.32E-03
490059532	hypothetical protein	1.26E+01	-1.41E+00	1.26E-04	-8.32E-02	6.62E-01	1.32E+00	2.15E-04
490059039	aldehyde dehydrogenase	1.27E+01	-1.82E+00	1.71E-05	-5.00E-01	1.49E-02	1.32E+00	1.02E-04
490060507	UDP-glucose 4-epimerase	1.53E+01	-1.40E+00	5.26E-05	-9.33E-02	5.59E-01	1.31E+00	9.26E-05
490052557	membrane protein	1.39E+01	3.30E-01	6.19E-02	1.62E+00	5.50E-05	1.29E+00	1.44E-04
497682011	hypothetical protein	1.31E+01	-1.41E+00	4.89E-04	-1.23E-01	6.20E-01	1.29E+00	1.05E-03
497683348	isopenicillin N-epimerase	1.12E+01	-3.03E+00	4.47E-06	-1.75E+00	9.22E-05	1.29E+00	3.84E-04

490060397	cytochrome P450	1.73E+01	4.76E-01	1.44E-01	1.76E+00	1.06E-03	1.28E+00	4.64E-03
497682279	mechanosensitive ion channel protein	1.35E+01	-8.55E-01	2.16E-02	4.18E-01	2.27E-01	1.27E+00	4.97E-03
490060993	esterase	1.49E+01	-2.00E+00	3.36E-05	-7.32E-01	8.00E-03	1.27E+00	4.54E-04
490054052	membrane protein	1.38E+01	-1.26E+00	1.80E-04	-7.08E-03	9.69E-01	1.26E+00	2.35E-04
490050170	beta-lactamase	1.26E+01	-3.59E+00	1.32E-06	-2.33E+00	7.16E-06	1.26E+00	9.42E-05
497681909	hypothetical protein	1.35E+01	-1.53E+00	1.11E-05	-2.73E-01	5.46E-02	1.25E+00	3.44E-05
490051901	hypothetical protein	1.49E+01	-2.03E+00	7.60E-05	-7.84E-01	1.27E-02	1.25E+00	1.23E-03
497683391	hypothetical protein	1.17E+01	-2.08E+00	4.44E-06	-8.56E-01	5.17E-04	1.23E+00	6.68E-05
490050956	short-chain dehydrogenase	1.44E+01	-2.86E+00	1.14E-05	-1.64E+00	2.71E-04	1.23E+00	1.08E-03
490058412	hypothetical protein	1.53E+01	-1.34E+00	5.15E-04	-1.15E-01	6.29E-01	1.23E+00	1.09E-03
490055475	methionyl-tRNA formyltransferase	1.18E+01	-1.88E+00	5.01E-05	-6.58E-01	1.38E-02	1.22E+00	5.97E-04
490055025	hypothetical protein	1.27E+01	-2.92E+00	8.11E-06	-1.71E+00	1.66E-04	1.20E+00	9.07E-04
497683380	UDP-glucose 4-epimerase	1.30E+01	-1.23E+00	1.69E-04	-3.07E-02	8.64E-01	1.20E+00	2.44E-04

[a] Identification is based on annotation by NCBI. **[b]** Description is based on NCBI annotation of protein similarity by BLAST. **[c]** Average normalized expression in the WT strain. **[d]** Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. **[e]** Adjusted P-value in *ΔbldG* as compared to the WT strain. **[f]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. **[g]** Adjusted P-value in *ΔbldA* as compared to the WT strain. **[h]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and **[i]** Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Table A.1.6: Proteins determined to be significantly (P = 0.01) under-expressed in the *ΔbldA* compared to the *ΔbldG* strains of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G -WT[e]	logFC A -WT[f]	adj.P.Val A-WT[g]	logFC A -G[h]	adj.P.Val A -G[i]
497683181	RNA polymerase	1.24E+01	6.61E-01	3.95E-01	-1.62E+01	3.04E-06	-1.68E+01	2.23E-06
490058437	metal ABC transporter substrate-binding protein	7.89E+00	1.84E+00	1.16E-03	-9.60E+00	1.55E-06	-1.14E+01	6.01E-07
490059712	hypothetical protein	8.12E+00	8.38E-01	3.35E-03	-1.04E+01	1.03E-07	-1.12E+01	4.46E-08
490056771	acetoacetyl-CoA synthetase	8.45E+00	-1.06E-01	6.65E-01	-1.13E+01	1.47E-07	-1.12E+01	1.05E-07
490059370	hypothetical protein	7.41E+00	2.60E+00	2.22E-01	-8.58E+00	5.30E-03	-1.12E+01	1.25E-03
490058488	trans-aconitate 2-methyltransferase	6.45E+00	5.05E+00	8.06E-04	-6.08E+00	4.59E-04	-1.11E+01	1.87E-05
497682574	alpha-galactosidase	1.32E+01	3.40E+00	2.96E-01	-7.73E+00	4.89E-02	-1.11E+01	1.06E-02
497681777	short-chain dehydrogenase	7.07E+00	2.88E+00	2.90E-05	-7.99E+00	1.12E-06	-1.09E+01	2.18E-07
490058414	F420-0--gamma-glutamyl ligase	7.74E+00	4.03E-01	4.93E-02	-1.01E+01	9.52E-08	-1.05E+01	4.46E-08
490053513	glycine cleavage system protein T	7.26E+00	8.88E-01	3.04E-03	-9.24E+00	1.87E-07	-1.01E+01	9.76E-08
490054322	hypothetical protein	6.74E+00	2.11E+00	2.57E-04	-7.93E+00	1.68E-06	-1.00E+01	5.97E-07
490050479	ABC transporter	6.25E+00	5.68E+00	1.36E-03	-3.59E+00	1.70E-02	-9.28E+00	1.35E-04
490055894	hydroxymethylglutaryl-CoA lyase	7.27E+00	-9.31E-01	2.62E-02	-1.02E+01	1.24E-06	-9.22E+00	1.48E-06
490056716	cold-shock protein	1.12E+01	-6.54E-01	7.78E-01	-9.61E+00	4.18E-03	-8.96E+00	5.25E-03
497683354	HAD-superfamily hydrolase	5.38E+00	3.57E+00	2.17E-03	-5.39E+00	3.89E-04	-8.95E+00	2.46E-05
490051788	hypothetical protein	6.33E+00	3.35E-01	2.49E-02	-8.27E+00	5.94E-08	-8.60E+00	4.46E-08
490051251	3-dehydroquinate dehydratase	9.96E+00	2.57E+00	2.88E-01	-5.90E+00	4.43E-02	-8.47E+00	9.45E-03
490058410	hypothetical protein	7.26E+00	5.63E-01	5.53E-01	-7.33E+00	2.10E-04	-7.89E+00	1.20E-04
490050011	histidine kinase	4.27E+00	3.04E+00	3.60E-02	-4.17E+00	1.43E-02	-7.21E+00	9.14E-04
497682270	molybdenum cofactor biosynthesis protein MoaC	3.62E+00	4.35E+00	3.75E-04	-2.65E+00	6.72E-03	-7.00E+00	4.05E-05
490056026	hypothetical protein	5.83E+00	-1.64E+00	1.14E-02	-8.59E+00	6.44E-06	-6.95E+00	1.14E-05
490057723	DNA polymerase III subunit epsilon	3.92E+00	3.41E+00	1.47E-03	-3.53E+00	1.85E-03	-6.93E+00	4.66E-05
497683463	hypothetical protein	8.65E+00	-8.05E-01	6.61E-01	-7.34E+00	5.57E-03	-6.53E+00	8.60E-03
490053924	magnesium or manganese-dependent protein phosphatase	7.37E+00	2.26E+00	2.11E-01	-4.24E+00	4.89E-02	-6.50E+00	7.99E-03
490050623	short-chain dehydrogenase	6.89E+00	-1.34E+00	1.49E-01	-7.67E+00	1.20E-04	-6.33E+00	2.75E-04
490057553	RNA methyltransferase	7.39E+00	1.35E+00	4.56E-01	-4.54E+00	4.34E-02	-5.89E+00	1.45E-02

490054091	transcription antitermination protein NusB	1.30E+01	1.93E+00	6.92E-04	-3.90E+00	3.07E-05	-5.84E+00	4.35E-06
490057931	thiamine biosynthesis protein ThiS	1.29E+01	9.19E-01	9.99E-02	-4.70E+00	9.73E-05	-5.62E+00	3.29E-05
490052915	catalase	1.15E+01	4.54E+00	5.45E-05	-8.57E-01	1.23E-01	-5.40E+00	2.88E-05
497685194	5,10-methylenetetrahydrofolate reductase	1.33E+01	2.93E+00	1.57E-06	-2.36E+00	5.07E-06	-5.29E+00	2.01E-07
490053713	carbonic anhydrase	9.46E+00	-1.70E+00	8.27E-02	-6.92E+00	2.25E-04	-5.22E+00	8.59E-04
490060232	phytoene synthase	1.19E+01	3.25E+00	2.39E-05	-1.93E+00	5.09E-04	-5.18E+00	4.05E-06
497683951	LysR family transcriptional regulator	1.13E+01	2.81E+00	1.45E-05	-2.30E+00	5.62E-05	-5.11E+00	2.03E-06
490051238	MarR family transcriptional regulator	1.17E+01	6.92E-01	1.12E-03	-4.10E+00	1.11E-06	-4.79E+00	4.00E-07
490054729	dihydrodipicolinate synthase	1.31E+01	3.48E+00	3.93E-06	-1.23E+00	9.06E-04	-4.71E+00	2.03E-06
490058700	orotate phosphoribosyltransferase	1.17E+01	2.75E+00	4.75E-05	-1.89E+00	4.72E-04	-4.64E+00	5.44E-06
497682387	aminotransferase	9.53E+00	1.68E+00	6.45E-06	-2.91E+00	1.81E-06	-4.59E+00	2.18E-07
490055769	carbon-nitrogen hydrolase	1.15E+01	3.89E+00	2.79E-06	-6.96E-01	1.47E-02	-4.58E+00	2.23E-06
490059045	glyoxalase	1.31E+01	1.98E+00	2.42E-04	-2.58E+00	9.21E-05	-4.56E+00	5.57E-06
497683136	RNA polymerase subunit sigma-24	1.51E+01	3.12E+00	1.16E-05	-1.43E+00	8.69E-04	-4.56E+00	3.24E-06
490051435	hypothetical protein	1.50E+01	7.95E-01	2.06E-02	-3.70E+00	1.86E-05	-4.50E+00	5.98E-06
490051173	Lyase	1.32E+01	3.12E+00	2.68E-05	-1.36E+00	2.83E-03	-4.48E+00	6.37E-06
490056432	HAD family hydrolase	1.12E+01	2.04E+00	8.00E-05	-2.44E+00	4.81E-05	-4.48E+00	3.04E-06
490051507	porphobilinogen deaminase	1.44E+01	1.32E+00	2.87E-04	-3.15E+00	7.36E-06	-4.48E+00	2.02E-06
490054418	amino acid transporter	1.53E+01	4.43E+00	2.11E-05	-3.60E-02	9.35E-01	-4.46E+00	2.51E-05
490058227	RarC protein	9.15E+00	2.42E+00	1.78E-05	-2.02E+00	6.25E-05	-4.44E+00	2.23E-06
490050625	alpha/beta hydrolase	1.40E+01	4.34E-01	2.12E-01	-3.95E+00	2.92E-05	-4.38E+00	1.42E-05
497682165	XRE family transcriptional regulator	1.04E+01	1.38E+00	5.22E-03	-2.96E+00	1.61E-04	-4.34E+00	2.01E-05
490059435	N-acetyl-1-D-myo-inosityl-2-amino-2	1.17E+01	9.01E-01	2.56E-04	-3.42E+00	1.68E-06	-4.32E+00	5.97E-07
490051538	magnesium transporter CorA	1.33E+01	3.34E+00	1.50E-05	-9.63E-01	1.07E-02	-4.30E+00	5.94E-06
490058786	N5,N10-methylene tetrahydromethanopterin reductase	1.08E+01	6.75E-01	2.49E-02	-3.61E+00	1.29E-05	-4.29E+00	4.77E-06
497681050	hypothetical protein	9.85E+00	2.63E+00	1.11E-05	-1.66E+00	1.58E-04	-4.28E+00	2.32E-06
490052171	inositol monophosphatase	1.03E+01	1.03E+00	5.87E-04	-3.22E+00	5.07E-06	-4.26E+00	1.64E-06
490060766	ornithine cyclodeaminase	1.15E+01	2.37E+00	1.88E-05	-1.81E+00	1.06E-04	-4.18E+00	2.57E-06
490059953	peptidase M24	9.84E+00	1.04E+00	2.62E-02	-3.13E+00	1.95E-04	-4.17E+00	3.79E-05
497681024	nitrilase	1.07E+01	1.34E+00	1.81E-03	-2.80E+00	6.12E-05	-4.14E+00	8.03E-06

497682030	membrane protein	9.29E+00	2.39E+00	3.09E-05	-1.73E+00	2.38E-04	-4.13E+00	3.79E-06
490050760	hydroxyurea phosphotransferase	1.10E+01	1.78E+00	2.59E-04	-2.33E+00	9.77E-05	-4.12E+00	5.70E-06
490057478	shikimate kinase	1.51E+01	1.25E+00	1.39E-04	-2.86E+00	5.40E-06	-4.11E+00	1.55E-06
490058520	molybdopterin biosynthesis protein MoeA	1.25E+01	2.52E+00	1.77E-05	-1.59E+00	2.55E-04	-4.11E+00	2.96E-06
497682231	cellulose-binding protein	1.37E+01	-1.40E-01	3.20E-01	-4.23E+00	1.11E-06	-4.09E+00	8.19E-07
490055599	phosphohistidine phosphatase	9.98E+00	3.17E+00	2.02E-05	-9.05E-01	1.49E-02	-4.08E+00	7.86E-06
497681691	hypothetical protein	1.43E+01	3.71E+00	7.44E-05	-3.44E-01	4.49E-01	-4.06E+00	5.72E-05
490056354	hydroxylase	1.25E+01	2.51E+00	2.05E-05	-1.54E+00	3.52E-04	-4.05E+00	3.42E-06
490058897	branched-chain alpha-keto acid dehydrogenase subunit E2	1.22E+01	1.28E+00	3.68E-04	-2.74E+00	1.42E-05	-4.02E+00	2.57E-06
497683553	hypothetical protein	1.33E+01	2.05E+00	8.83E-06	-1.96E+00	1.81E-05	-4.02E+00	1.22E-06
490060430	Puromycin N-acetyltransferase	1.24E+01	1.70E+00	1.80E-05	-2.32E+00	7.52E-06	-4.01E+00	1.10E-06
497681303	ribulose-phosphate 3-epimerase	1.19E+01	2.91E+00	1.80E-05	-1.09E+00	3.84E-03	-4.01E+00	5.57E-06
490058381	beta-N-acetylhexosaminidase	1.17E+01	2.45E+00	4.01E-05	-1.56E+00	6.10E-04	-4.01E+00	5.44E-06
497681908	hypothetical protein	1.32E+01	6.21E-01	8.13E-04	-3.37E+00	1.11E-06	-3.99E+00	4.00E-07
490057878	tryptophan synthase subunit beta	1.09E+01	-4.71E-01	1.69E-01	-4.45E+00	1.57E-05	-3.98E+00	1.92E-05
497681074	hypothetical protein	1.10E+01	3.68E+00	1.87E-06	-2.98E-01	1.39E-01	-3.97E+00	2.03E-06
497683724	lipoate-protein ligase A	1.17E+01	6.95E-01	1.91E-02	-3.26E+00	1.73E-05	-3.95E+00	5.57E-06
490059479	ABC transporter ATP-binding protein	9.53E+00	9.09E-01	4.66E-03	-3.03E+00	1.84E-05	-3.93E+00	4.72E-06
490052952	peptide ABC transporter ATPase	1.26E+01	9.51E-01	7.82E-03	-2.98E+00	3.89E-05	-3.93E+00	8.62E-06
490057514	Putative uroporphyrin-III methyltransferase	1.21E+01	1.68E+00	3.12E-05	-2.24E+00	1.41E-05	-3.93E+00	1.63E-06
497685319	DNA-binding protein	1.60E+01	3.16E+00	1.11E-04	-7.51E-01	9.48E-02	-3.91E+00	4.51E-05
490058570	pantothenate synthetase	9.22E+00	1.97E+00	9.56E-04	-1.94E+00	1.53E-03	-3.91E+00	3.52E-05
490052483	nicotinate phosphoribosyltransferase	1.33E+01	1.72E+00	1.27E-04	-2.18E+00	5.55E-05	-3.90E+00	3.79E-06
490057339	N-acetyltransferase GCN5	1.26E+01	2.97E+00	1.30E-05	-9.18E-01	6.85E-03	-3.88E+00	5.20E-06
497683539	ribosomal protein S12 methylthiotransferase	1.05E+01	8.74E-01	5.39E-03	-3.01E+00	1.84E-05	-3.88E+00	4.84E-06
497680874	hypothetical protein	1.16E+01	1.39E+00	1.45E-03	-2.48E+00	1.09E-04	-3.87E+00	1.06E-05
497682584	XRE family transcriptional regulator	1.16E+01	2.11E+00	1.14E-05	-1.74E+00	4.30E-05	-3.86E+00	1.73E-06
490058356	PTS sugar transporter subunit IIA	1.30E+01	3.43E+00	2.19E-06	-3.62E-01	8.10E-02	-3.79E+00	2.23E-06
497681632	dephospho-CoA kinase	1.27E+01	-8.85E-02	7.88E-01	-3.88E+00	2.22E-05	-3.79E+00	1.89E-05
490060709	hypothetical protein	1.45E+01	8.30E-01	3.58E-03	-2.95E+00	1.10E-05	-3.78E+00	3.24E-06
497683725	DNA polymerase subunit beta	1.31E+01	6.39E-01	1.22E-02	-3.14E+00	8.55E-06	-3.77E+00	3.34E-06

497683433	short-chain dehydrogenase	9.44E+00	5.70E-01	1.61E-01	-3.20E+00	1.59E-04	-3.77E+00	5.64E-05
490057293	ABC transporter permease	1.22E+01	1.25E+00	9.54E-04	-2.49E+00	4.28E-05	-3.75E+00	5.57E-06
490060751	acetyltransferase	1.41E+01	9.93E-01	4.62E-04	-2.74E+00	6.05E-06	-3.73E+00	1.88E-06
490050525	methylmalonate-semialdehyde dehydrogenase	9.97E+00	1.51E+00	6.45E-03	-2.19E+00	1.55E-03	-3.71E+00	8.71E-05
490050094	hypothetical protein	1.42E+01	4.75E-01	1.09E-02	-3.22E+00	2.82E-06	-3.69E+00	1.57E-06
490060082	polyketide cyclase	1.07E+01	2.81E+00	1.29E-03	-8.61E-01	1.67E-01	-3.67E+00	4.20E-04
490057467	rRNA cytosine-C5-methyltransferase	1.07E+01	1.68E+00	5.15E-04	-1.99E+00	3.27E-04	-3.67E+00	1.28E-05
490058302	acetolactate synthase	1.01E+01	1.85E+00	3.19E-04	-1.80E+00	5.48E-04	-3.66E+00	1.32E-05
490060226	dehydrogenase	9.34E+00	8.06E-01	4.28E-03	-2.84E+00	1.39E-05	-3.65E+00	3.82E-06
490057863	dihydropyrimidine dehydrogenase subunit A	1.23E+01	1.55E+00	1.35E-05	-2.08E+00	6.36E-06	-3.63E+00	8.24E-07
490051552	hypothetical protein	1.07E+01	2.63E+00	1.80E-05	-9.77E-01	4.10E-03	-3.61E+00	5.57E-06
490060648	LuxR family transcriptional regulator	9.47E+00	1.80E+00	9.31E-03	-1.80E+00	1.33E-02	-3.61E+00	3.88E-04
497680947	hypothetical protein	1.36E+01	-8.12E-01	2.94E-03	-4.41E+00	2.50E-06	-3.59E+00	3.08E-06
497685127	threonine dehydratase	1.35E+01	1.36E+00	3.71E-04	-2.24E+00	4.41E-05	-3.59E+00	4.56E-06
490057009	hypothetical protein	1.40E+01	-1.06E-01	4.92E-01	-3.70E+00	2.23E-06	-3.59E+00	1.88E-06
490055325	DNA-binding protein	1.43E+01	4.66E+00	5.43E-06	1.08E+00	1.10E-02	-3.58E+00	2.27E-05
497681361	DSBA oxidoreductase	1.28E+01	1.35E-01	3.64E-01	-3.43E+00	2.50E-06	-3.56E+00	1.65E-06
497682119	peptidase	1.29E+01	1.71E+00	4.60E-06	-1.83E+00	6.44E-06	-3.54E+00	6.01E-07
490061074	Telomere-associated protein	1.07E+01	2.79E+00	3.03E-06	-7.39E-01	2.84E-03	-3.53E+00	2.03E-06
497683598	transcriptional regulator	1.26E+01	3.14E+00	1.67E-06	-3.96E-01	2.79E-02	-3.53E+00	1.57E-06
490057887	hypothetical protein	1.07E+01	2.46E+00	9.26E-06	-1.07E+00	9.06E-04	-3.52E+00	2.96E-06
490061540	ABC-type Fe3+-hydroxamate transport system, solute-binding protein	1.06E+01	1.20E+00	2.68E-04	-2.31E+00	1.80E-05	-3.52E+00	2.61E-06
490051627	ribonucleoside-diphosphate reductase	1.38E+01	6.92E-01	2.54E-02	-2.81E+00	4.22E-05	-3.51E+00	1.21E-05
490052783	Lipase	1.22E+01	1.47E+00	1.38E-05	-2.03E+00	5.79E-06	-3.50E+00	8.19E-07
490053387	arsenate reductase	1.07E+01	7.35E-02	8.04E-01	-3.41E+00	2.44E-05	-3.49E+00	1.72E-05
490051245	amino acid ABC transporter substrate-binding protein	1.35E+01	9.67E-02	6.29E-01	-3.38E+00	5.79E-06	-3.48E+00	3.92E-06
490060364	hypothetical protein	1.16E+01	4.72E-01	2.90E-02	-3.01E+00	7.21E-06	-3.48E+00	3.24E-06
490060764	peptide synthetase	1.39E+01	1.93E+00	7.26E-05	-1.53E+00	3.43E-04	-3.46E+00	5.70E-06
490058944	phosphoribosylglycinamide synthetase	1.18E+01	1.33E+00	7.69E-04	-2.13E+00	1.00E-04	-3.46E+00	8.14E-06
497683819	hypothetical protein	1.21E+01	-1.33E+00	5.13E-03	-4.78E+00	1.49E-05	-3.45E+00	5.06E-05

490053866	sodium:proton antiporter	1.28E+01	3.55E+00	8.97E-05	1.11E-01	8.06E-01	-3.44E+00	1.29E-04
490054808	whiD	1.25E+01	2.33E+00	5.26E-05	-1.09E+00	3.88E-03	-3.42E+00	1.04E-05
490059501	sugar transporter	1.37E+01	1.64E+00	2.09E-05	-1.77E+00	2.32E-05	-3.41E+00	1.73E-06
497681275	GntR family transcriptional regulator	9.47E+00	1.08E+00	2.23E-04	-2.31E+00	9.05E-06	-3.39E+00	2.03E-06
490058168	hypothetical protein	1.02E+01	2.43E+00	7.44E-05	-9.51E-01	1.18E-02	-3.38E+00	1.81E-05
490051647	DeoR family transcriptional regulator	1.14E+01	1.41E+00	4.00E-05	-1.96E+00	1.46E-05	-3.37E+00	1.73E-06
490057794	6-phosphogluconolactonase, partial	1.44E+01	8.38E-01	4.53E-04	-2.51E+00	5.07E-06	-3.34E+00	1.58E-06
490060765	peptide synthetase	1.32E+01	1.92E+00	7.47E-06	-1.42E+00	4.86E-05	-3.34E+00	1.61E-06
497683289	ATP-dependent DNA helicase	1.24E+01	5.09E-01	3.32E-03	-2.82E+00	2.50E-06	-3.33E+00	1.17E-06
490058310	Nocardamine synthetase	1.17E+01	1.68E+00	1.21E-03	-1.64E+00	2.06E-03	-3.32E+00	4.51E-05
490059303	tryptophanyl-tRNA synthetase	1.11E+01	1.19E+00	4.55E-04	-2.12E+00	3.76E-05	-3.32E+00	4.39E-06
490058571	NADP oxidoreductase coenzyme F420-dependent	1.37E+01	9.79E-01	2.26E-03	-2.33E+00	4.13E-05	-3.31E+00	6.56E-06
490051139	hydroxyurea phosphotransferase	1.17E+01	-2.02E-01	7.34E-01	-3.50E+00	7.48E-04	-3.30E+00	9.00E-04
490055486	hypothetical protein	1.02E+01	1.45E+00	1.42E-03	-1.84E+00	6.09E-04	-3.29E+00	2.68E-05
497683802	acetyl-CoA acetyltransferase	1.20E+01	-8.62E-01	6.23E-04	-4.15E+00	1.31E-06	-3.29E+00	2.03E-06
490058552	DNA repair protein RadA	1.08E+01	7.55E-01	3.54E-04	-2.53E+00	2.83E-06	-3.28E+00	1.01E-06
490053470	globin	1.34E+01	7.56E-01	4.61E-03	-2.52E+00	1.84E-05	-3.28E+00	4.65E-06
497682498	hypothetical protein	1.07E+01	3.47E-02	8.21E-01	-3.22E+00	2.75E-06	-3.25E+00	2.03E-06
490054228	DNA helicase	1.08E+01	1.73E+00	2.09E-05	-1.52E+00	5.92E-05	-3.25E+00	2.29E-06
490056480	methyltransferase type 12	1.25E+01	1.70E+00	8.68E-05	-1.54E+00	2.12E-04	-3.24E+00	5.39E-06
490052908	hydrogen peroxide-inducible protein	1.35E+01	7.50E-01	1.10E-03	-2.48E+00	5.79E-06	-3.23E+00	2.03E-06
490057710	peptidase	1.32E+01	-4.84E-01	4.42E-01	-3.72E+00	8.77E-04	-3.23E+00	1.57E-03
490056986	Putative dehydrogenase	1.23E+01	2.49E+00	6.27E-06	-7.40E-01	4.07E-03	-3.23E+00	3.06E-06
490055432	cytidine deaminase	1.27E+01	2.67E-01	2.97E-01	-2.96E+00	2.83E-05	-3.23E+00	1.48E-05
490057336	adenosylmethionine--8-amino-7-oxononanoate aminotransferase	9.92E+00	1.68E+00	1.14E-04	-1.54E+00	2.60E-04	-3.23E+00	6.17E-06
497682234	50S ribosomal protein L25	1.18E+01	1.97E+00	4.03E-06	-1.25E+00	4.81E-05	-3.23E+00	1.22E-06
490054220	30S ribosomal protein S6	1.15E+01	-9.17E-01	2.99E-03	-4.13E+00	4.33E-06	-3.21E+00	7.28E-06
490052231	ornithine carbamoyltransferase	1.29E+01	1.86E+00	1.57E-04	-1.35E+00	1.19E-03	-3.21E+00	1.28E-05
490057310	6-phosphofructokinase	1.43E+01	4.65E-01	1.17E-01	-2.74E+00	6.25E-05	-3.21E+00	2.38E-05
490059512	methyltransferase	1.06E+01	1.01E+00	7.55E-04	-2.20E+00	2.30E-05	-3.21E+00	3.82E-06

490059990	O-methyltransferase	1.01E+01	2.60E+00	7.18E-04	-5.87E-01	2.46E-01	-3.19E+00	3.24E-04
490055254	50S ribosomal protein L27	1.32E+01	6.24E-01	5.83E-03	-2.56E+00	8.89E-06	-3.19E+00	3.06E-06
490051150	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1.00E+01	1.15E+00	7.53E-04	-2.03E+00	6.09E-05	-3.19E+00	6.22E-06
490054474	phosphomannomutase	1.39E+01	5.57E-01	1.02E-03	-2.62E+00	1.85E-06	-3.18E+00	8.19E-07
490057864	glutamate synthase	1.26E+01	1.79E+00	5.46E-06	-1.38E+00	2.94E-05	-3.17E+00	1.22E-06
490052575	septum formation protein Maf	1.03E+01	-1.75E+00	2.21E-03	-4.92E+00	1.96E-05	-3.17E+00	1.29E-04
490060762	phosphoribosylglycinamide synthetase	1.46E+01	1.41E+00	1.94E-04	-1.75E+00	9.57E-05	-3.16E+00	5.34E-06
490050037	hypothetical protein	9.80E+00	3.73E+00	1.29E-06	5.67E-01	6.96E-03	-3.16E+00	2.23E-06
490060039	hypothetical protein	1.39E+01	-7.06E-01	1.84E-02	-3.86E+00	8.15E-06	-3.16E+00	1.48E-05
497681070	putative electron transfer flavoprotein beta subunit, partial	8.92E+00	1.40E+00	6.92E-04	-1.76E+00	3.16E-04	-3.15E+00	1.43E-05
497684562	hypothetical protein	1.33E+01	2.24E-01	3.00E-01	-2.93E+00	1.49E-05	-3.15E+00	7.86E-06
490053329	quinolinate synthetase	1.19E+01	2.94E+00	5.49E-06	-2.08E-01	3.26E-01	-3.15E+00	5.57E-06
490050516	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1.29E+01	1.93E+00	4.81E-05	-1.20E+00	8.20E-04	-3.14E+00	6.17E-06
490053269	methyltransferase type 12	1.30E+01	9.63E-01	5.02E-03	-2.17E+00	1.23E-04	-3.13E+00	1.69E-05
490054189	ribonuclease P	1.37E+01	5.25E-01	7.82E-03	-2.60E+00	5.79E-06	-3.13E+00	2.49E-06
490051870	acetyltransferase	1.26E+01	-4.74E-01	3.72E-02	-3.59E+00	5.08E-06	-3.12E+00	5.98E-06
490060233	phytoene dehydrogenase	8.94E+00	1.47E+00	1.78E-03	-1.64E+00	1.53E-03	-3.11E+00	4.63E-05
490060228	techoic acid ABC transporter ATP-binding protein	1.18E+01	7.22E-01	9.89E-03	-2.39E+00	3.86E-05	-3.11E+00	9.00E-06
490054831	ATP-dependent DNA helicase PcrA	1.14E+01	1.29E+00	1.87E-03	-1.82E+00	4.74E-04	-3.10E+00	2.61E-05
490055112	nucleoside triphosphate pyrophosphohydrolase	1.21E+01	7.84E-01	1.04E-03	-2.31E+00	8.33E-06	-3.09E+00	2.49E-06
490051375	DNA polymerase III subunit delta	1.35E+01	8.36E-01	8.47E-03	-2.25E+00	8.73E-05	-3.09E+00	1.55E-05
490051912	GntR family transcriptional regulator	1.33E+01	2.78E-01	4.90E-02	-2.81E+00	2.74E-06	-3.09E+00	1.61E-06
490054146	50S ribosomal protein L16	1.28E+01	2.17E+00	7.81E-04	-9.06E-01	5.50E-02	-3.08E+00	1.63E-04
490058380	hypothetical protein	1.30E+01	7.89E-01	2.09E-02	-2.29E+00	1.79E-04	-3.08E+00	3.31E-05
497684806	GntR family transcriptional regulator	1.16E+01	3.93E-01	1.33E-01	-2.68E+00	4.05E-05	-3.07E+00	1.72E-05
490052682	NUDIX hydrolase	1.36E+01	3.18E-01	1.87E-01	-2.76E+00	2.73E-05	-3.07E+00	1.28E-05
497682317	dihydropteroate synthase	1.24E+01	1.35E+00	2.09E-04	-1.72E+00	9.17E-05	-3.07E+00	5.37E-06
490054713	hypothetical protein	1.06E+01	2.60E-01	2.75E-01	-2.81E+00	2.52E-05	-3.07E+00	1.31E-05
490059687	transcriptional regulator	1.33E+01	2.13E+00	1.16E-05	-9.34E-01	1.10E-03	-3.06E+00	3.40E-06

497683567	DNA topoisomerase IV subunit A	1.28E+01	6.20E-01	3.63E-03	-2.44E+00	7.29E-06	-3.06E+00	2.57E-06
497681781	hypothetical protein	1.23E+01	2.26E+00	3.02E-04	-7.92E-01	5.39E-02	-3.06E+00	8.05E-05
490050102	threonine synthase	1.38E+01	8.26E-01	2.28E-03	-2.23E+00	2.39E-05	-3.06E+00	4.92E-06
490053871	radical SAM protein	1.21E+01	8.82E-01	2.43E-03	-2.17E+00	3.77E-05	-3.05E+00	6.41E-06
490055162	signal peptide protein	1.12E+01	-1.79E-01	4.87E-01	-3.23E+00	2.18E-05	-3.05E+00	2.14E-05
490055448	HrcA family transcriptional regulator	1.07E+01	3.86E-01	3.54E-01	-2.66E+00	5.65E-04	-3.04E+00	2.40E-04
490059261	O-sialoglycoprotein endopeptidase	1.15E+01	9.19E-01	6.25E-04	-2.11E+00	1.66E-05	-3.03E+00	3.01E-06
490057615	NADP oxidoreductase	1.02E+01	5.23E-01	2.49E-02	-2.51E+00	2.04E-05	-3.03E+00	6.53E-06
497683102	NAD-dependent dehydratase	1.30E+01	2.04E+00	1.71E-04	-9.87E-01	9.52E-03	-3.03E+00	2.88E-05
490057400	hypothetical protein	1.35E+01	-6.03E-02	8.63E-01	-3.09E+00	6.90E-05	-3.03E+00	6.34E-05
497681726	phytoene dehydrogenase	1.12E+01	1.17E+00	9.15E-02	-1.85E+00	2.56E-02	-3.02E+00	2.47E-03
490059052	haloacid dehalogenase	8.90E+00	8.61E-01	4.71E-03	-2.15E+00	6.73E-05	-3.01E+00	1.12E-05
490053859	aromatic acid decarboxylase	1.35E+01	9.92E-01	2.58E-04	-2.00E+00	1.41E-05	-2.99E+00	2.49E-06
490057320	tripeptidyl aminopeptidase	1.49E+01	8.10E-01	3.63E-03	-2.18E+00	3.72E-05	-2.99E+00	6.86E-06
490056081	methionine ABC transporter ATP-binding protein	1.08E+01	1.19E-01	8.90E-01	-2.87E+00	1.02E-02	-2.98E+00	7.79E-03
497681485	chromosome partitioning protein	1.28E+01	6.50E-01	2.26E-03	-2.32E+00	7.22E-06	-2.98E+00	2.49E-06
490051614	3-phosphoshikimate 1-carboxyvinyltransferase	1.31E+01	3.06E-01	6.93E-02	-2.67E+00	5.79E-06	-2.97E+00	2.96E-06
497681264	phosphoenolpyruvate-protein phosphotransferase	1.15E+01	2.54E+00	1.87E-06	-4.26E-01	1.19E-02	-2.97E+00	1.68E-06
497684774	phosphohydrolase	1.21E+01	2.03E+00	1.01E-04	-9.35E-01	7.46E-03	-2.97E+00	1.90E-05
490052787	cytochrome P450	1.36E+01	2.21E+00	8.10E-05	-7.51E-01	2.29E-02	-2.96E+00	2.29E-05
490053054	hypothetical protein	1.14E+01	-6.56E-01	1.85E-01	-3.59E+00	2.51E-04	-2.94E+00	6.22E-04
490056193	hydrolase	1.35E+01	1.14E+00	9.70E-05	-1.79E+00	1.81E-05	-2.93E+00	2.24E-06
490050038	MarR family transcriptional regulator	1.08E+01	4.89E-01	1.09E-02	-2.43E+00	7.49E-06	-2.92E+00	2.96E-06
497682761	hypothetical protein	1.06E+01	-2.57E-01	4.53E-01	-3.18E+00	8.53E-05	-2.92E+00	1.09E-04
490057951	histidine kinase	9.33E+00	2.07E+00	4.21E-04	-8.46E-01	3.90E-02	-2.92E+00	9.01E-05
490059255	alanine racemase	1.25E+01	2.27E+00	3.36E-05	-6.48E-01	2.31E-02	-2.91E+00	1.27E-05
490053854	cytochrome C biosynthesis protein	1.02E+01	2.67E-01	8.62E-02	-2.64E+00	5.07E-06	-2.91E+00	2.57E-06
490054379	cell division protein FtsZ	1.15E+01	1.48E+00	4.13E-02	-1.43E+00	6.19E-02	-2.91E+00	2.86E-03
490053822	epimerase	1.08E+01	3.36E+00	1.57E-06	4.61E-01	1.63E-02	-2.90E+00	2.57E-06
490055260	radical SAM protein	1.19E+01	-1.96E-01	3.10E-01	-3.10E+00	7.21E-06	-2.90E+00	6.80E-06
490054456	acyl-CoA synthetase	1.38E+01	5.69E-01	5.91E-03	-2.32E+00	9.11E-06	-2.89E+00	3.20E-06

497683263	N-succinyldiaminopimelate aminotransferase	1.40E+01	1.30E+00	5.80E-05	-1.59E+00	3.33E-05	-2.89E+00	2.57E-06
490057941	glucokinase	1.44E+01	5.67E-01	1.09E-02	-2.32E+00	1.76E-05	-2.89E+00	5.23E-06
490056459	hypothetical protein	1.25E+01	1.50E+00	2.40E-04	-1.39E+00	5.42E-04	-2.89E+00	1.17E-05
490052535	phosphoenolpyruvate carboxykinase	1.06E+01	1.96E+00	9.23E-05	-9.17E-01	6.36E-03	-2.88E+00	1.71E-05
497681608	sporulation protein	1.16E+01	8.15E-01	1.46E-03	-2.06E+00	2.20E-05	-2.87E+00	4.16E-06
497682579	transcriptional regulator	1.15E+01	3.14E-01	2.33E-01	-2.56E+00	6.05E-05	-2.87E+00	2.82E-05
490053404	hypothetical protein	1.56E+01	6.24E-01	8.69E-02	-2.25E+00	4.60E-04	-2.87E+00	1.09E-04
497683596	hypothetical protein	9.33E+00	2.20E+00	6.08E-06	-6.67E-01	3.50E-03	-2.87E+00	2.96E-06
497681972	Fur family transcriptional regulator	1.37E+01	-1.38E+00	2.36E-03	-4.25E+00	1.46E-05	-2.87E+00	6.96E-05
497681084	uracil-DNA glycosylase	1.42E+01	4.33E-01	4.13E-02	-2.43E+00	1.84E-05	-2.86E+00	6.56E-06
497683542	DEAD/DEAH box helicase	1.39E+01	7.06E-01	2.17E-02	-2.15E+00	1.43E-04	-2.86E+00	2.89E-05
497681192	DEAD/DEAH box helicase	1.28E+01	6.06E-01	7.14E-03	-2.25E+00	1.76E-05	-2.86E+00	4.84E-06
490059201	hypothetical protein	1.33E+01	1.64E+00	1.90E-05	-1.21E+00	1.28E-04	-2.84E+00	2.57E-06
490050353	DEAD/DEAH box helicase	1.33E+01	1.04E+00	1.81E-04	-1.80E+00	1.92E-05	-2.83E+00	2.57E-06
490052108	hypothetical protein	1.16E+01	2.67E-01	1.91E-01	-2.57E+00	1.84E-05	-2.83E+00	8.76E-06
490057021	siderophore biosynthesis protein	1.24E+01	3.02E+00	2.69E-05	2.02E-01	5.05E-01	-2.82E+00	4.63E-05
490054002	ABC transporter	1.47E+01	1.94E+00	2.37E-05	-8.80E-01	2.02E-03	-2.82E+00	5.57E-06
497683664	iron ABC transporter substrate-binding protein	1.27E+01	2.20E+00	2.72E-05	-6.17E-01	2.10E-02	-2.81E+00	1.08E-05
490057754	multidrug DMT transporter permease	9.95E+00	8.09E-01	4.87E-02	-2.00E+00	1.28E-03	-2.81E+00	1.87E-04
490055042	potassium transporter TrkA	1.04E+01	1.37E+00	1.30E-03	-1.43E+00	1.58E-03	-2.80E+00	4.10E-05
490058358	ABC transporter ATP-binding protein	1.17E+01	1.05E+00	5.27E-05	-1.75E+00	7.83E-06	-2.80E+00	1.57E-06
490058154	2-isopropylmalate synthase	1.33E+01	5.34E-01	1.36E-02	-2.27E+00	1.84E-05	-2.80E+00	5.57E-06
490059282	ATPase	9.15E+00	6.21E-01	4.72E-02	-2.17E+00	2.06E-04	-2.79E+00	4.63E-05
490057955	ribokinase	1.24E+01	2.80E+00	4.85E-05	7.90E-03	9.80E-01	-2.79E+00	6.07E-05
490059199	fructose-2,6-bisphosphatase	1.29E+01	3.58E-01	2.09E-01	-2.43E+00	1.13E-04	-2.79E+00	4.61E-05
490059344	betaine-aldehyde dehydrogenase	1.12E+01	1.57E+00	1.83E-04	-1.22E+00	1.03E-03	-2.79E+00	1.31E-05
490051617	hypothetical protein	1.38E+01	-7.64E-02	6.01E-01	-2.85E+00	3.93E-06	-2.78E+00	2.96E-06
490051736	3-oxoacyl-ACP synthase	1.20E+01	1.71E+00	9.70E-03	-1.06E+00	8.12E-02	-2.77E+00	1.25E-03
490054178	hypothetical protein	1.27E+01	-5.44E-01	1.03E-01	-3.32E+00	4.30E-05	-2.77E+00	8.74E-05
497683518	riboflavin kinase	1.44E+01	1.37E+00	1.22E-04	-1.41E+00	1.53E-04	-2.77E+00	5.43E-06
490053479	enoyl-CoA hydratase	1.34E+01	-3.53E-03	9.81E-01	-2.77E+00	3.04E-06	-2.77E+00	2.38E-06

490058384	malate dehydrogenase	1.41E+01	1.07E+00	2.70E-03	-1.69E+00	3.86E-04	-2.77E+00	2.68E-05
490053288	aconitate hydratase	1.29E+01	1.00E+00	2.11E-04	-1.76E+00	2.12E-05	-2.76E+00	2.68E-06
490056167	conserved hypothetical protein	1.20E+01	1.06E+00	6.59E-04	-1.69E+00	9.02E-05	-2.76E+00	7.39E-06
490054891	ABC transporter substrate-binding protein	1.31E+01	1.43E+00	1.55E-04	-1.32E+00	3.49E-04	-2.76E+00	7.91E-06
490056814	acetyltransferase	1.22E+01	-5.06E-01	9.66E-03	-3.25E+00	3.04E-06	-2.75E+00	3.79E-06
497681053	glutamate racemase	1.07E+01	2.35E+00	1.19E-03	-3.97E-01	4.20E-01	-2.75E+00	6.96E-04
497682256	hypothetical protein	1.26E+01	2.83E+00	2.14E-04	8.45E-02	8.45E-01	-2.74E+00	3.24E-04
490058484	SMI1_KNR4 domain-containing protein	1.16E+01	3.87E-01	1.69E-01	-2.35E+00	1.19E-04	-2.74E+00	4.50E-05
490060358	3-oxoacyl-ACP reductase	1.33E+01	1.21E+00	3.36E-04	-1.53E+00	1.45E-04	-2.74E+00	7.44E-06
490051180	hypothetical protein	1.40E+01	1.30E+00	2.10E-04	-1.44E+00	1.88E-04	-2.74E+00	6.86E-06
497683509	PucR family transcriptional regulator	1.36E+01	8.44E-01	4.39E-04	-1.89E+00	1.39E-05	-2.74E+00	2.57E-06
497681323	membrane protein	1.23E+01	4.43E-01	1.21E-01	-2.29E+00	1.32E-04	-2.73E+00	4.46E-05
490061295	hypothetical protein	1.07E+01	-4.12E-01	1.66E-01	-3.14E+00	3.74E-05	-2.73E+00	6.01E-05
490052580	gamma-glutamyl cyclotransferase	1.02E+01	4.07E-01	1.60E-02	-2.32E+00	6.12E-06	-2.73E+00	2.62E-06
497682686	nosiheptide resistance regulatory protein	1.43E+01	2.49E+00	2.68E-05	-2.35E-01	3.48E-01	-2.73E+00	2.14E-05
490054149	30S ribosomal protein S19	1.61E+01	3.99E-01	2.32E-02	-2.33E+00	7.91E-06	-2.72E+00	3.42E-06
490054966	membrane protein	1.56E+01	-1.46E+00	8.63E-05	-4.18E+00	2.02E-06	-2.72E+00	5.70E-06
490059776	4-aminobutyrate aminotransferase	1.39E+01	2.06E+00	9.38E-05	-6.57E-01	3.26E-02	-2.72E+00	2.84E-05
490060004	regulatory protein	1.09E+01	3.90E-01	2.38E-02	-2.32E+00	7.67E-06	-2.71E+00	3.34E-06
490059740	acetyltransferase	1.29E+01	1.27E+00	1.63E-03	-1.44E+00	1.30E-03	-2.71E+00	4.14E-05
490055858	sulfate adenylyltransferase	1.40E+01	-4.12E-01	6.20E-02	-3.12E+00	8.24E-06	-2.71E+00	1.13E-05
490056644	6-phospho-beta-glucosidase	9.75E+00	-4.03E-01	1.32E-02	-3.11E+00	2.23E-06	-2.71E+00	2.49E-06
490058668	precorrin-8X methylmutase	1.27E+01	1.99E-02	9.46E-01	-2.68E+00	3.76E-05	-2.70E+00	2.92E-05
490060203	ABC transporter	1.25E+01	-4.62E-01	1.37E-01	-3.17E+00	4.17E-05	-2.70E+00	7.40E-05
490051619	RNA polymerase sigma factor RpoE	1.31E+01	9.53E-01	7.17E-03	-1.75E+00	5.17E-04	-2.70E+00	4.58E-05
490054464	2-phospho-L-lactate transferase	1.03E+01	1.10E+00	2.88E-02	-1.60E+00	8.53E-03	-2.70E+00	5.56E-04
490058111	hypothetical protein	1.48E+01	2.12E+00	7.16E-06	-5.71E-01	7.47E-03	-2.69E+00	3.79E-06
490058788	ATPase	1.61E+01	1.08E+00	3.52E-02	-1.62E+00	9.42E-03	-2.69E+00	6.72E-04
490051466	TetR family transcriptional regulator	1.14E+01	2.53E+00	1.23E-04	-1.65E-01	6.28E-01	-2.69E+00	1.09E-04
490054100	orotidine 5'-phosphate decarboxylase	1.45E+01	6.55E-01	3.04E-03	-2.04E+00	1.75E-05	-2.69E+00	4.06E-06
490052584	membrane protein	1.32E+01	2.07E+00	1.78E-05	-6.15E-01	1.11E-02	-2.69E+00	6.58E-06

490057926	thiamine-phosphate pyrophosphorylase	9.96E+00	1.55E-01	1.88E-01	-2.53E+00	2.74E-06	-2.69E+00	1.73E-06
497681406	glycine/betaine ABC transporter ATP-binding protein	1.34E+01	1.61E+00	1.88E-04	-1.06E+00	2.48E-03	-2.67E+00	1.89E-05
490050335	capsular polysaccharide biosynthesis protein CapB	1.33E+01	1.36E+00	1.19E-04	-1.31E+00	2.10E-04	-2.67E+00	5.80E-06
490058360	hypothetical protein	1.30E+01	1.44E+00	9.65E-04	-1.23E+00	3.22E-03	-2.67E+00	4.91E-05
490055334	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	1.40E+01	1.04E+00	4.46E-05	-1.62E+00	9.05E-06	-2.67E+00	1.57E-06
490058806	membrane protein	1.26E+01	3.53E-01	1.67E-01	-2.30E+00	8.01E-05	-2.66E+00	3.28E-05
490056676	hypothetical protein	1.47E+01	-2.24E-02	8.67E-01	-2.68E+00	2.82E-06	-2.66E+00	2.23E-06
490057733	enoyl-CoA hydratase	1.00E+01	1.91E-01	2.08E-01	-2.46E+00	6.58E-06	-2.66E+00	3.82E-06
497681311	guanylate kinase	1.15E+01	6.06E-01	1.01E-02	-2.05E+00	3.56E-05	-2.65E+00	8.58E-06
490054057	lauroyl acyltransferase	1.33E+01	2.11E+00	4.79E-06	-5.42E-01	6.27E-03	-2.65E+00	2.94E-06
490055874	conserved hypothetical protein	1.42E+01	2.08E+00	4.44E-06	-5.58E-01	4.53E-03	-2.64E+00	2.57E-06
490060090	adenosine deaminase	1.21E+01	1.08E+00	3.50E-04	-1.56E+00	7.92E-05	-2.64E+00	5.70E-06
497683176	hypothetical protein	1.44E+01	-5.07E-01	1.15E-02	-3.14E+00	3.94E-06	-2.63E+00	5.14E-06
490058377	hypothetical protein	9.03E+00	-3.28E-01	1.47E-01	-2.96E+00	1.48E-05	-2.63E+00	1.87E-05
497683062	TetR family transcriptional regulator	1.45E+01	1.75E+00	6.19E-05	-8.82E-01	3.13E-03	-2.63E+00	1.08E-05
497681420	recombinase RecB	1.15E+01	1.45E+00	4.58E-05	-1.17E+00	2.02E-04	-2.63E+00	4.05E-06
490057695	HAD family hydrolase	1.42E+01	6.12E-01	9.61E-02	-2.01E+00	8.91E-04	-2.62E+00	1.89E-04
490057591	ferredoxin	1.23E+01	1.29E+00	1.48E-03	-1.33E+00	1.88E-03	-2.62E+00	4.72E-05
490059708	methylmalonyl-CoA carboxyltransferase	1.31E+01	2.07E+00	3.11E-05	-5.51E-01	2.91E-02	-2.62E+00	1.27E-05
497685032	glycosyl transferase	8.84E+00	5.65E-01	2.75E-01	-2.03E+00	6.18E-03	-2.60E+00	1.62E-03
490055271	nucleoside diphosphate kinase	1.46E+01	1.99E+00	4.32E-03	-5.99E-01	2.76E-01	-2.59E+00	1.54E-03
490054371	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	1.16E+01	5.37E-01	1.55E-02	-2.04E+00	3.25E-05	-2.58E+00	8.76E-06
497682046	signal peptide protein	9.91E+00	9.61E-01	9.46E-03	-1.61E+00	1.13E-03	-2.58E+00	8.51E-05
490054402	hypothetical protein	9.95E+00	8.57E-01	4.20E-03	-1.72E+00	1.82E-04	-2.57E+00	2.02E-05
490056752	RNA polymerase subunit sigma24	1.23E+01	1.23E+00	2.64E-04	-1.34E+00	2.51E-04	-2.57E+00	8.67E-06
490060383	pyruvate phosphate dikinase	9.08E+00	5.44E-01	1.92E-02	-2.02E+00	4.63E-05	-2.56E+00	1.22E-05
490052948	GTP-binding protein TypA	1.23E+01	1.72E+00	3.59E-04	-8.38E-01	1.75E-02	-2.56E+00	5.75E-05
490055841	hypothetical protein	1.30E+01	-7.87E-01	1.51E-03	-3.35E+00	3.04E-06	-2.56E+00	5.70E-06
490053321	cysteine desulfurase	1.14E+01	1.91E+00	7.82E-05	-6.49E-01	2.20E-02	-2.56E+00	2.21E-05
490052493	beta-lactamase	1.22E+01	1.69E+00	3.67E-05	-8.66E-01	1.67E-03	-2.55E+00	6.53E-06

490052451	ABC transporter substrate-binding protein	1.17E+01	1.61E+00	5.54E-04	-9.41E-01	1.14E-02	-2.55E+00	6.45E-05
490054415	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	1.13E+01	3.97E-01	6.83E-02	-2.15E+00	3.98E-05	-2.55E+00	1.44E-05
490058695	hydrolase	8.43E+00	2.59E+00	6.47E-06	4.75E-02	8.06E-01	-2.55E+00	8.90E-06
490052229	aspartate decarboxylase	1.43E+01	1.25E+00	1.22E-03	-1.29E+00	1.53E-03	-2.54E+00	3.96E-05
490052663	hypothetical protein	1.46E+01	1.90E+00	4.29E-03	-6.41E-01	2.28E-01	-2.54E+00	1.34E-03
490051506	uroporphyrin-III C-methyltransferase	1.28E+01	9.14E-01	7.07E-04	-1.63E+00	5.55E-05	-2.54E+00	5.86E-06
490059042	hypothetical protein	1.01E+01	4.78E-01	9.47E-03	-2.06E+00	1.21E-05	-2.54E+00	3.92E-06
497681796	glutamine synthetase	1.21E+01	2.38E+00	1.62E-03	-1.57E-01	7.69E-01	-2.53E+00	1.53E-03
490052497	PTS sugar transporter	1.11E+01	2.69E+00	1.60E-05	1.61E-01	5.03E-01	-2.53E+00	2.62E-05
490051692	sugar kinase	1.15E+01	2.02E+00	2.32E-05	-5.08E-01	2.84E-02	-2.52E+00	1.02E-05
490057777	hypothetical protein	1.37E+01	1.66E+00	4.55E-04	-8.61E-01	1.62E-02	-2.52E+00	6.59E-05
490053061	hypothetical protein	9.44E+00	7.82E-01	1.09E-02	-1.74E+00	3.16E-04	-2.52E+00	3.96E-05
497682225	transcription-repair coupling factor	1.30E+01	8.88E-01	2.92E-03	-1.63E+00	1.95E-04	-2.52E+00	1.89E-05
490053226	membrane protein	1.12E+01	1.53E+00	4.63E-05	-9.88E-01	6.47E-04	-2.52E+00	5.70E-06
490051158	phosphoglyceromutase	1.22E+01	1.32E+00	6.35E-03	-1.20E+00	1.40E-02	-2.52E+00	3.16E-04
490057587	proteasome subunit beta	1.40E+01	-1.19E+00	3.43E-04	-3.71E+00	3.42E-06	-2.52E+00	1.06E-05
490055253	GTPase CgtA	1.45E+01	1.17E+00	1.41E-03	-1.34E+00	1.04E-03	-2.51E+00	3.48E-05
490059586	homoserine kinase	1.26E+01	3.71E-01	2.17E-02	-2.14E+00	7.83E-06	-2.51E+00	3.34E-06
490053878	glycoside hydrolase	1.29E+01	2.70E-01	5.77E-01	-2.24E+00	2.88E-03	-2.51E+00	1.42E-03
490055932	polynucleotide phosphorylase	9.89E+00	1.16E+00	4.63E-05	-1.34E+00	3.44E-05	-2.50E+00	2.49E-06
497683755	formate dehydrogenase accessory protein FdhD	1.42E+01	1.14E+00	1.24E-01	-1.37E+00	9.23E-02	-2.50E+00	8.97E-03
497682296	pyrroline-5-carboxylate reductase	1.29E+01	7.98E-01	1.77E-01	-1.70E+00	2.17E-02	-2.50E+00	3.46E-03
490055717	proteasome subunit alpha	1.36E+01	-3.40E-01	5.53E-01	-2.84E+00	2.06E-03	-2.50E+00	3.45E-03
490058025	heme oxygenase	1.31E+01	2.40E-01	5.85E-01	-2.26E+00	1.70E-03	-2.50E+00	8.93E-04
490057783	metal-sulfur cluster biosynthesis protein	1.39E+01	-3.98E-01	7.73E-02	-2.89E+00	1.39E-05	-2.49E+00	1.97E-05
490052136	hydrolase	1.23E+01	2.69E+00	4.55E-04	2.00E-01	6.69E-01	-2.49E+00	9.00E-04
497682215	NADH dehydrogenase	1.37E+01	1.53E+00	2.32E-05	-9.46E-01	4.03E-04	-2.48E+00	3.82E-06
490056344	aspartate-semialdehyde dehydrogenase	1.26E+01	1.98E+00	1.46E-05	-5.06E-01	1.75E-02	-2.48E+00	6.40E-06
490055878	oligoribonuclease	1.46E+01	2.37E-01	2.33E-01	-2.24E+00	3.04E-05	-2.48E+00	1.49E-05
490057593	transposase IS150	1.29E+01	1.17E+00	2.08E-03	-1.31E+00	1.72E-03	-2.48E+00	5.33E-05

490057572	regulatory protein	1.34E+01	3.88E-01	4.78E-02	-2.09E+00	2.58E-05	-2.47E+00	9.23E-06
490058550	hypothetical protein	1.22E+01	1.32E+00	4.86E-04	-1.16E+00	1.43E-03	-2.47E+00	2.46E-05
490055318	D-alanine--D-alanine ligase	1.35E+01	1.00E+00	1.37E-04	-1.47E+00	3.13E-05	-2.47E+00	2.96E-06
490060346	Fe3+-hydroxamate ABC transporter	1.58E+01	1.17E+00	4.30E-04	-1.29E+00	3.87E-04	-2.47E+00	1.28E-05
497684123	putative DNA-binding protein	9.49E+00	-7.50E-02	8.06E-01	-2.54E+00	1.14E-04	-2.46E+00	1.10E-04
490059842	ATP-dependent DNA helicase RecQ	1.20E+01	5.46E-01	8.62E-03	-1.92E+00	2.54E-05	-2.46E+00	6.45E-06
497684176	dihydrouridine synthase	1.42E+01	-1.66E+00	1.58E-05	-4.12E+00	1.11E-06	-2.46E+00	3.82E-06
490051804	hypothetical protein	1.41E+01	-3.43E-01	2.45E-01	-2.80E+00	6.86E-05	-2.46E+00	1.11E-04
490055313	50S ribosomal protein L28	1.22E+01	1.36E+00	1.60E-02	-1.10E+00	5.01E-02	-2.46E+00	1.28E-03
490054139	30S ribosomal protein S8	1.13E+01	-2.43E-02	9.46E-01	-2.48E+00	1.52E-04	-2.46E+00	1.32E-04
490052184	acyl-CoA dehydrogenase	1.39E+01	-4.65E-01	3.32E-02	-2.92E+00	8.55E-06	-2.46E+00	1.38E-05
490057294	multidrug ABC transporter ATPase	1.25E+01	2.57E-01	3.64E-01	-2.20E+00	2.10E-04	-2.45E+00	9.91E-05
490054237	cystathionine gamma-lyase	1.30E+01	1.45E-01	6.73E-01	-2.30E+00	4.01E-04	-2.45E+00	2.53E-04
497681957	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	1.83E+01	1.60E+00	1.23E-04	-8.46E-01	4.65E-03	-2.44E+00	1.84E-05
490052934	GTP-binding protein YchF	1.35E+01	9.53E-01	1.01E-02	-1.49E+00	1.77E-03	-2.44E+00	1.14E-04
497685090	hypothetical protein	1.63E+01	1.37E+00	1.55E-04	-1.07E+00	8.38E-04	-2.44E+00	1.12E-05
490052186	citrate lyase beta chain	9.84E+00	6.56E-01	2.75E-02	-1.78E+00	3.56E-04	-2.44E+00	5.88E-05
497685198	pyridoxamine 5'-phosphate oxidase	1.47E+01	4.15E-01	1.40E-02	-2.02E+00	1.01E-05	-2.44E+00	3.82E-06
490054953	hypothetical protein	9.23E+00	3.13E+00	6.47E-06	7.00E-01	1.52E-02	-2.43E+00	2.68E-05
490047179	MerR-family transcriptional regulator	1.03E+01	-3.17E-02	9.63E-01	-2.45E+00	3.27E-03	-2.42E+00	3.06E-03
497682186	hypothetical protein	1.53E+01	7.96E-01	1.74E-03	-1.62E+00	6.74E-05	-2.42E+00	8.44E-06
490059244	50S ribosomal protein L4	1.29E+01	5.76E-01	1.02E-02	-1.84E+00	4.67E-05	-2.42E+00	1.07E-05
497682615	acetyltransferase	1.42E+01	1.25E-01	7.47E-01	-2.29E+00	6.98E-04	-2.42E+00	4.61E-04
497685427	acyl-CoA dehydrogenase	1.19E+01	5.36E-01	2.06E-02	-1.88E+00	6.68E-05	-2.41E+00	1.65E-05
490055301	50S ribosomal protein L32	1.64E+01	-8.57E-01	1.21E-01	-3.27E+00	6.22E-04	-2.41E+00	2.61E-03
497682940	N-acetyltransferase GCN5	1.43E+01	5.26E-01	2.04E-01	-1.87E+00	2.94E-03	-2.40E+00	7.27E-04
490050023	acetate kinase	1.22E+01	1.74E+00	8.11E-06	-6.62E-01	1.55E-03	-2.40E+00	3.04E-06
497682938	putative guanyltransferase	1.17E+01	1.26E+00	5.87E-04	-1.13E+00	1.53E-03	-2.39E+00	2.78E-05
490058146	glycyl-tRNA synthetase	1.36E+01	-1.44E-01	5.46E-01	-2.54E+00	4.30E-05	-2.39E+00	4.61E-05
497682158	hypothetical protein	1.27E+01	1.00E+00	3.86E-02	-1.39E+00	1.50E-02	-2.39E+00	9.88E-04

497681398	ATPase	1.29E+01	1.70E-02	9.73E-01	-2.37E+00	1.18E-03	-2.39E+00	1.01E-03
490054698	glyceraldehyde-3-phosphate dehydrogenase	1.05E+01	1.21E+00	8.41E-05	-1.18E+00	1.39E-04	-2.39E+00	4.56E-06
490052654	phosphoribosylaminoimidazole synthetase	1.40E+01	-1.37E-01	5.08E-01	-2.52E+00	2.38E-05	-2.39E+00	2.38E-05
490058694	acetyltransferase	1.28E+01	9.79E-01	3.76E-04	-1.40E+00	8.78E-05	-2.38E+00	6.07E-06
490051025	ABC transporter ATP-binding protein	1.23E+01	7.08E-01	2.68E-03	-1.67E+00	5.02E-05	-2.38E+00	7.86E-06
490054802	molecular chaperone GroES	1.00E+01	1.52E+00	2.11E-05	-8.59E-01	5.67E-04	-2.38E+00	3.92E-06
490051497	RNA polymerase sigma factor SigB	1.11E+01	9.76E-01	7.37E-03	-1.40E+00	1.92E-03	-2.38E+00	1.04E-04
497681016	glucosamine-6-phosphate deaminase	8.64E+00	1.28E+00	2.08E-03	-1.09E+00	6.76E-03	-2.37E+00	1.09E-04
490054261	ABC transporter permease	1.13E+01	1.36E+00	1.90E-04	-1.01E+00	1.36E-03	-2.37E+00	1.49E-05
490055240	alcohol dehydrogenase	1.10E+01	1.44E+00	3.36E-04	-9.28E-01	4.71E-03	-2.37E+00	3.31E-05
490060159	potassium transporter TrkA	1.33E+01	6.65E-01	8.63E-03	-1.70E+00	1.16E-04	-2.37E+00	1.90E-05
497683441	dihydrofolate reductase	9.83E+00	8.74E-01	1.01E-02	-1.49E+00	1.15E-03	-2.36E+00	8.83E-05
490054428	UDP-glucose 6-dehydrogenase	1.24E+01	2.97E-04	9.99E-01	-2.36E+00	7.24E-05	-2.36E+00	5.99E-05
490058175	leucyl-tRNA synthetase	1.33E+01	1.18E+00	1.96E-04	-1.18E+00	2.89E-04	-2.36E+00	8.14E-06
497681919	ACP S-malonyltransferase	1.02E+01	3.17E+00	7.78E-05	8.18E-01	6.06E-02	-2.36E+00	4.61E-04
490053499	protein-L-isoaspartate O-methyltransferase	1.06E+01	1.65E+00	2.88E-02	-7.08E-01	3.13E-01	-2.35E+00	8.45E-03
497685037	hypothetical protein	1.37E+01	1.95E-01	1.56E-01	-2.16E+00	7.09E-06	-2.35E+00	3.82E-06
497683714	GntR family transcriptional regulator	1.31E+01	2.23E-01	1.18E-01	-2.12E+00	7.83E-06	-2.34E+00	4.06E-06
490052926	malonic semialdehyde reductase	1.09E+01	1.01E+00	2.30E-02	-1.33E+00	1.03E-02	-2.34E+00	5.59E-04
490051798	hydrolase	1.18E+01	1.10E+00	5.26E-03	-1.24E+00	4.46E-03	-2.34E+00	1.44E-04
490050763	methyltransferase type 11	1.34E+01	2.23E+00	1.23E-05	-1.16E-01	5.39E-01	-2.34E+00	1.20E-05
490058538	glycerol acyltransferase	1.58E+01	1.22E+00	6.42E-05	-1.12E+00	1.53E-04	-2.34E+00	4.22E-06
490059080	phosphoserine aminotransferase	1.05E+01	2.37E-01	6.94E-02	-2.10E+00	5.50E-06	-2.34E+00	2.78E-06
490055329	isopropylmalate isomerase	1.28E+01	-1.28E-02	9.40E-01	-2.35E+00	6.80E-06	-2.34E+00	5.23E-06
497682932	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	1.28E+01	4.06E-01	2.30E-01	-1.93E+00	9.26E-04	-2.34E+00	2.95E-04
490057486	ATPase AAA	1.31E+01	9.82E-01	4.50E-04	-1.35E+00	1.30E-04	-2.33E+00	7.86E-06
490061076	NUDIX hydrolase	1.25E+01	1.82E+00	4.69E-06	-5.09E-01	4.10E-03	-2.33E+00	2.62E-06
490053230	histidine kinase	1.22E+01	-7.87E-02	7.33E-01	-2.41E+00	4.12E-05	-2.33E+00	3.92E-05
497683638	glycosyl transferase	1.29E+01	4.20E-02	7.95E-01	-2.28E+00	9.86E-06	-2.32E+00	6.74E-06
490053869	conserved hypothetical protein	1.25E+01	4.32E-01	2.27E-01	-1.88E+00	1.40E-03	-2.31E+00	4.20E-04

497681172	putative ferrodoxin oxidoreductase alpha subunit, partial	1.38E+01	-2.37E+00	4.41E-04	-4.68E+00	2.30E-05	-2.31E+00	6.57E-04
490051254	GTP cyclohydrolase	1.27E+01	-1.05E+00	9.41E-04	-3.36E+00	5.79E-06	-2.31E+00	2.11E-05
490059784	ribosome maturation protein RimP	1.22E+01	1.66E+00	4.30E-04	-6.54E-01	4.50E-02	-2.31E+00	9.71E-05
490056313	serine hydroxymethyltransferase	1.43E+01	-2.39E-01	2.36E-01	-2.54E+00	1.91E-05	-2.30E+00	2.27E-05
497682305	hypothetical protein	1.34E+01	-3.28E-01	1.80E-02	-2.63E+00	2.56E-06	-2.30E+00	2.57E-06
497681999	hypothetical protein	1.24E+01	2.36E+00	1.50E-03	6.09E-02	9.09E-01	-2.30E+00	2.25E-03
490054097	carbamoyl phosphate synthase small subunit	1.46E+01	1.06E+00	4.18E-04	-1.22E+00	2.99E-04	-2.28E+00	1.13E-05
490056700	cytochrome P450	8.68E+00	-2.87E-01	3.96E-01	-2.57E+00	2.33E-04	-2.28E+00	3.75E-04
490053048	2-oxoisovalerate dehydrogenase subunit beta	1.09E+01	1.36E+00	1.94E-02	-9.17E-01	1.02E-01	-2.28E+00	2.40E-03
490052652	valine dehydrogenase	1.42E+01	-6.55E-01	8.57E-03	-2.93E+00	8.89E-06	-2.28E+00	2.10E-05
490056071	argininosuccinate synthase	9.79E+00	-4.47E-01	2.70E-02	-2.73E+00	7.83E-06	-2.28E+00	1.28E-05
490059268	inosine 5'-monophosphate dehydrogenase	1.22E+01	1.35E+00	1.30E-04	-9.29E-01	1.30E-03	-2.28E+00	1.20E-05
490055113	cytochrome P450	1.27E+01	-3.15E-02	8.03E-01	-2.31E+00	4.31E-06	-2.28E+00	3.05E-06
490058894	LuxR family transcriptional regulator	1.50E+01	9.10E-01	2.18E-04	-1.37E+00	4.24E-05	-2.28E+00	3.85E-06
490061079	acetyltransferase	1.58E+01	1.09E+00	1.77E-04	-1.18E+00	1.79E-04	-2.27E+00	6.37E-06
490056013	peroxiredoxin	1.21E+01	6.31E-01	1.90E-02	-1.64E+00	2.75E-04	-2.27E+00	4.32E-05
490054876	conserved hypothetical protein	1.10E+01	2.42E-01	1.64E-01	-2.03E+00	2.44E-05	-2.27E+00	1.12E-05
490055493	MarR family transcriptional regulator	1.44E+01	-3.44E-01	3.60E-02	-2.61E+00	5.07E-06	-2.27E+00	5.80E-06
490050084	F0F1 ATP synthase subunit gamma	1.45E+01	1.75E-01	2.37E-01	-2.09E+00	1.19E-05	-2.26E+00	6.07E-06
490051417	MarR family transcriptional regulator	1.43E+01	-5.68E-01	1.79E-02	-2.83E+00	1.23E-05	-2.26E+00	2.46E-05
497683221	aminotransferase AlaT	1.16E+01	2.71E+00	8.57E-05	4.46E-01	2.04E-01	-2.26E+00	2.72E-04
490056454	ribosome-associated protein IOJAP	1.44E+01	1.17E+00	4.87E-04	-1.09E+00	1.03E-03	-2.26E+00	2.14E-05
490058535	REX family transcriptional regulator	1.26E+01	1.38E+00	4.17E-04	-8.76E-01	6.13E-03	-2.26E+00	4.11E-05
497681281	dolichol-phosphate mannosyltransferase	1.16E+01	7.31E-01	1.03E-02	-1.53E+00	4.05E-04	-2.26E+00	4.51E-05
490059734	5-hydroxymethyluracil DNA glycosylase	1.23E+01	1.05E+00	1.09E-04	-1.21E+00	7.69E-05	-2.26E+00	3.95E-06
490053662	2-methylcitrate dehydratase	1.32E+01	1.07E+00	1.41E-01	-1.18E+00	1.33E-01	-2.24E+00	1.40E-02
490057536	isocitrate dehydrogenase	1.13E+01	1.57E+00	4.16E-05	-6.75E-01	4.57E-03	-2.24E+00	9.31E-06
490055666	membrane protein	1.33E+01	-4.69E-01	6.17E-03	-2.71E+00	3.04E-06	-2.24E+00	4.05E-06
490058298	cell division protein FtsK	1.15E+01	9.60E-02	5.11E-01	-2.14E+00	1.09E-05	-2.24E+00	6.56E-06
490054741	transcriptional regulator	1.33E+01	1.80E+00	4.34E-06	-4.35E-01	7.05E-03	-2.24E+00	2.62E-06

490055854	sulfate ABC transporter permease	1.10E+01	2.92E-01	2.88E-01	-1.94E+00	3.17E-04	-2.23E+00	1.28E-04
490056667	diadenosine tetraphosphatase	1.20E+01	1.13E+00	6.24E-03	-1.11E+00	9.75E-03	-2.23E+00	2.54E-04
490055528	ketol-acid reductoisomerase	1.27E+01	3.41E-01	1.66E-01	-1.89E+00	1.82E-04	-2.23E+00	6.45E-05
490059197	hypothetical protein	1.22E+01	1.29E+00	9.54E-04	-9.37E-01	6.95E-03	-2.23E+00	7.13E-05
490056356	acyl-ACP desaturase	1.07E+01	3.16E-01	1.60E-01	-1.91E+00	1.08E-04	-2.23E+00	4.09E-05
490053936	DNA mismatch repair protein MutT	9.09E+00	5.59E-03	9.85E-01	-2.22E+00	1.14E-04	-2.22E+00	9.37E-05
497681131	hypothetical protein	1.39E+01	1.84E-01	2.10E-01	-2.04E+00	1.25E-05	-2.22E+00	6.22E-06
490053371	radical SAM protein	1.43E+01	1.82E-01	3.90E-01	-2.04E+00	6.96E-05	-2.22E+00	3.80E-05
490052490	molybdenum cofactor biosynthesis protein MoaD	1.34E+01	-2.17E+00	5.51E-04	-4.38E+00	2.49E-05	-2.22E+00	6.42E-04
490059516	molecular chaperone GroES	1.23E+01	-2.36E-01	5.08E-01	-2.45E+00	3.88E-04	-2.22E+00	5.73E-04
490051121	trehalose phosphatase	1.47E+01	-5.75E-01	3.29E-03	-2.79E+00	3.42E-06	-2.21E+00	5.57E-06
490054699	phosphoglycerate kinase	8.99E+00	8.25E-01	1.08E-03	-1.39E+00	1.10E-04	-2.21E+00	9.50E-06
490055902	thiazole synthase	1.42E+01	-1.24E+00	1.34E-02	-3.45E+00	1.26E-04	-2.21E+00	1.11E-03
490051175	asparaginase	1.39E+01	7.42E-01	6.20E-03	-1.47E+00	3.00E-04	-2.21E+00	3.14E-05
490054165	50S ribosomal protein L10	1.51E+01	-8.03E-01	1.83E-02	-3.01E+00	4.24E-05	-2.20E+00	1.69E-04
497681623	tellurium resistance protein TerC	1.32E+01	1.89E+00	4.46E-05	-3.11E-01	1.56E-01	-2.20E+00	2.59E-05
490058194	dihydrofolate synthase	1.34E+01	-1.24E+00	3.49E-04	-3.44E+00	5.07E-06	-2.20E+00	2.31E-05
490057426	Antagonist of KipI	1.31E+01	1.88E-01	1.56E-01	-2.01E+00	7.74E-06	-2.20E+00	4.18E-06
490055076	hypothetical protein	1.41E+01	8.70E-02	6.74E-01	-2.11E+00	4.79E-05	-2.20E+00	3.24E-05
490052921	hypothetical protein	1.13E+01	-3.64E-01	3.49E-01	-2.56E+00	4.75E-04	-2.19E+00	9.36E-04
490057452	3,4-dihydroxy-2-butanone 4-phosphate synthase	1.21E+01	7.94E-02	6.27E-01	-2.11E+00	1.78E-05	-2.19E+00	1.10E-05
497681752	hypothetical protein	1.50E+01	-1.18E+00	7.88E-04	-3.37E+00	7.74E-06	-2.19E+00	4.08E-05
490059904	inositol-phosphate phosphatase	1.24E+01	-6.54E-01	5.25E-02	-2.84E+00	7.89E-05	-2.19E+00	2.57E-04
497681216	adenylosuccinate lyase	1.36E+01	-2.09E-01	3.53E-01	-2.39E+00	4.28E-05	-2.19E+00	5.43E-05
490054877	hypothetical protein	1.25E+01	2.59E-01	4.03E-01	-1.92E+00	6.63E-04	-2.18E+00	2.98E-04
490053055	hypothetical protein	1.25E+01	7.81E-01	2.01E-03	-1.40E+00	1.48E-04	-2.18E+00	1.39E-05
490059915	phosphatase	1.34E+01	8.18E-01	3.74E-03	-1.36E+00	4.23E-04	-2.18E+00	3.24E-05
497682237	transcriptional regulator	1.18E+01	1.48E+00	1.64E-04	-6.86E-01	1.12E-02	-2.17E+00	2.97E-05
497683373	ATP synthase subunit beta	1.27E+01	2.31E-01	1.94E-01	-1.94E+00	3.43E-05	-2.17E+00	1.62E-05
490057740	phosphate transporter	8.50E+00	1.41E+00	8.49E-03	-7.60E-01	1.09E-01	-2.17E+00	1.37E-03
497681422	LuxR family transcriptional regulator	1.18E+01	4.68E-01	3.73E-02	-1.70E+00	1.22E-04	-2.16E+00	3.01E-05

490060088	acyl-peptide hydrolase	1.26E+01	-1.01E+00	1.53E-03	-3.17E+00	8.60E-06	-2.16E+00	3.79E-05
497683083	lysyl-tRNA synthetase	1.35E+01	9.27E-01	1.25E-03	-1.24E+00	4.18E-04	-2.16E+00	2.10E-05
490057686	transcriptional regulator	1.31E+01	5.10E-01	9.20E-03	-1.65E+00	3.92E-05	-2.16E+00	8.94E-06
490059961	glycogen debranching protein	8.50E+00	1.60E+00	4.90E-04	-5.59E-01	7.31E-02	-2.16E+00	1.31E-04
490059395	sugar transporter	9.44E+00	8.22E-01	3.31E-03	-1.34E+00	4.10E-04	-2.16E+00	3.03E-05
497683163	phosphoribosylglycinamide formyltransferase	1.29E+01	1.46E+00	3.08E-04	-7.00E-01	1.63E-02	-2.16E+00	5.06E-05
497683082	delta-aminolevulinic acid dehydratase	1.13E+01	-4.14E-01	5.27E-01	-2.57E+00	6.53E-03	-2.16E+00	1.31E-02
490054160	30S ribosomal protein S7	1.27E+01	-5.03E-02	7.78E-01	-2.20E+00	1.86E-05	-2.15E+00	1.56E-05
490054094	uracil phosphoribosyltransferase	1.37E+01	3.99E-02	8.35E-01	-2.11E+00	2.73E-05	-2.15E+00	2.00E-05
497682120	alanine glycine permease	1.19E+01	2.71E+00	4.08E-04	5.59E-01	2.38E-01	-2.15E+00	1.76E-03
497682123	ATP-dependent Clp protease ClpS	1.19E+01	1.79E+00	4.85E-05	-3.60E-01	9.66E-02	-2.15E+00	2.42E-05
490059585	homoserine dehydrogenase	1.23E+01	-8.84E-03	9.68E-01	-2.16E+00	2.07E-05	-2.15E+00	1.59E-05
490059782	kinase	1.28E+01	8.95E-01	4.21E-04	-1.25E+00	1.14E-04	-2.14E+00	7.10E-06
490057574	5'-3' exonuclease	1.42E+01	1.31E+00	3.76E-05	-8.28E-01	5.86E-04	-2.14E+00	5.23E-06
490054116	50S ribosomal protein L17	1.10E+01	1.56E+00	1.45E-03	-5.79E-01	1.11E-01	-2.14E+00	3.69E-04
490052950	ABC transporter	1.43E+01	9.55E-01	9.95E-04	-1.18E+00	4.90E-04	-2.14E+00	2.09E-05
490059730	methyltransferase	1.38E+01	1.10E+00	3.34E-05	-1.04E+00	6.68E-05	-2.13E+00	2.59E-06
490051382	transferase	1.31E+01	8.54E-01	4.28E-03	-1.27E+00	8.84E-04	-2.12E+00	5.08E-05
490054931	alpha/beta hydrolase	1.50E+01	-4.04E-01	1.39E-02	-2.52E+00	4.52E-06	-2.12E+00	5.57E-06
497681489	CTP synthetase	1.30E+01	3.43E-01	1.16E-01	-1.77E+00	1.21E-04	-2.12E+00	4.07E-05
490050759	hypothetical protein	1.42E+01	2.08E-01	3.97E-01	-1.91E+00	2.12E-04	-2.12E+00	1.04E-04
490059259	peptidase M22	1.03E+01	-1.76E-01	4.72E-01	-2.29E+00	8.29E-05	-2.11E+00	1.04E-04
497682822	RNA helicase	1.34E+01	1.54E-01	3.34E-01	-1.96E+00	2.28E-05	-2.11E+00	1.22E-05
490060315	sugar phosphotransferase	1.39E+01	-2.52E-01	1.34E-01	-2.36E+00	1.01E-05	-2.11E+00	1.26E-05
490058441	dynein regulation protein LC7	1.48E+01	8.38E-01	1.04E-03	-1.27E+00	1.81E-04	-2.11E+00	1.24E-05
497682609	aminotransferase	1.33E+01	3.14E-01	9.87E-02	-1.79E+00	5.53E-05	-2.11E+00	2.10E-05
497682425	alpha/beta hydrolase	1.31E+01	1.10E+00	1.18E-04	-1.00E+00	2.82E-04	-2.11E+00	6.42E-06
497681388	hypothetical protein	1.29E+01	1.15E+00	2.26E-03	-9.56E-01	8.05E-03	-2.11E+00	1.26E-04
490055862	phosphoadenosine phosphosulfate reductase	1.17E+01	-8.92E-01	2.56E-02	-3.00E+00	1.09E-04	-2.10E+00	5.89E-04
490057421	membrane protein	1.05E+01	5.48E-01	1.10E-02	-1.56E+00	9.17E-05	-2.10E+00	1.75E-05
497681680	indole-3-glycerol-phosphate synthase	1.04E+01	2.02E+00	6.33E-06	-8.83E-02	5.51E-01	-2.10E+00	6.61E-06

497681065	hyaluronate lyase	1.51E+01	3.89E-01	1.32E-01	-1.71E+00	3.58E-04	-2.10E+00	1.04E-04
497683296	hypothetical protein	1.20E+01	1.43E+00	2.47E-03	-6.66E-01	7.95E-02	-2.10E+00	4.55E-04
490057973	acetyltransferase	1.21E+01	1.82E+00	2.86E-03	-2.79E-01	5.37E-01	-2.10E+00	1.83E-03
497683948	hypothetical protein	1.42E+01	-4.49E-01	3.11E-01	-2.54E+00	9.50E-04	-2.09E+00	2.24E-03
490051625	peptide deformylase	1.30E+01	5.08E-01	2.92E-03	-1.59E+00	1.64E-05	-2.09E+00	3.92E-06
490054134	50S ribosomal protein L15	7.86E+00	5.70E-01	8.88E-03	-1.52E+00	9.76E-05	-2.09E+00	1.71E-05
490056072	argininosuccinate lyase	1.17E+01	3.49E-01	5.69E-01	-1.74E+00	2.58E-02	-2.09E+00	1.10E-02
497682040	aminopeptidase N	1.25E+01	1.19E+00	5.29E-05	-8.96E-01	3.36E-04	-2.09E+00	5.20E-06
490057736	ABC transporter	1.37E+01	2.39E-01	3.46E-01	-1.84E+00	2.87E-04	-2.08E+00	1.28E-04
490059014	XRE family transcriptional regulator	1.23E+01	1.57E+00	3.97E-04	-5.10E-01	8.01E-02	-2.08E+00	1.15E-04
490054208	inositol-3-phosphate synthase	1.26E+01	-1.67E-02	9.04E-01	-2.09E+00	6.67E-06	-2.07E+00	5.23E-06
497682020	rod shape-determining protein Mbl	1.19E+01	9.81E-01	2.69E-04	-1.09E+00	2.35E-04	-2.07E+00	8.57E-06
490054099	diguanylate cyclase	1.21E+01	3.98E-01	8.62E-02	-1.67E+00	2.07E-04	-2.07E+00	5.67E-05
497683627	ATPase	1.09E+01	1.18E+00	4.63E-05	-8.89E-01	2.89E-04	-2.07E+00	4.61E-06
497681732	phospho-2-dehydro-3-deoxyheptonate aldolase	1.33E+01	1.61E-01	3.30E-01	-1.90E+00	2.91E-05	-2.07E+00	1.57E-05
490059371	DUF255 domain-containing protein	1.08E+01	8.78E-01	7.76E-04	-1.18E+00	2.51E-04	-2.06E+00	1.32E-05
490057871	ribokinase	1.44E+01	7.26E-01	6.93E-04	-1.33E+00	4.72E-05	-2.06E+00	5.57E-06
490058395	phosphatase	1.08E+01	7.92E-02	8.77E-01	-1.97E+00	5.00E-03	-2.05E+00	3.66E-03
490054376	UDP-diphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	1.40E+01	1.10E+00	6.28E-02	-9.56E-01	1.19E-01	-2.05E+00	6.64E-03
490055502	branched-chain amino acid aminotransferase	1.31E+01	4.00E-01	2.49E-01	-1.65E+00	2.37E-03	-2.05E+00	6.87E-04
490055605	enoyl-ACP reductase	1.32E+01	1.49E+00	5.09E-04	-5.60E-01	5.88E-02	-2.05E+00	1.23E-04
490054095	aspartate carbamoyltransferase	1.25E+01	9.25E-01	4.96E-02	-1.12E+00	3.39E-02	-2.05E+00	2.05E-03
497681714	ATPase	9.79E+00	-1.11E+00	1.33E-03	-3.15E+00	1.24E-05	-2.04E+00	7.03E-05
490051147	RNA methyltransferase	1.50E+01	9.56E-01	9.65E-02	-1.09E+00	8.35E-02	-2.04E+00	6.81E-03
490054113	ABC transporter	1.15E+01	1.20E+00	9.57E-05	-8.38E-01	9.13E-04	-2.04E+00	8.94E-06
490053090	hypothetical protein	1.40E+01	3.92E-01	1.19E-01	-1.65E+00	3.65E-04	-2.04E+00	1.01E-04
490051483	UTP--glucose-1-phosphate uridylyltransferase	1.69E+01	1.58E+00	2.12E-05	-4.53E-01	1.57E-02	-2.04E+00	8.28E-06
497681559	amidohydrolase	1.21E+01	1.10E-01	3.91E-01	-1.92E+00	9.79E-06	-2.03E+00	5.81E-06
490052576	biotin carboxyl carrier protein	1.26E+01	1.08E+00	2.56E-04	-9.56E-01	7.08E-04	-2.03E+00	1.33E-05
490054893	iron ABC transporter ATP-binding protein	1.19E+01	6.84E-01	1.06E-02	-1.35E+00	5.69E-04	-2.03E+00	5.68E-05

490059514	hypothetical protein	1.35E+01	1.49E+00	1.02E-05	-5.38E-01	2.58E-03	-2.03E+00	3.80E-06
490058049	ketohydroxyglutarate aldolase	1.48E+01	7.25E-01	9.17E-03	-1.30E+00	7.71E-04	-2.03E+00	6.51E-05
490056330	malate dehydrogenase	1.32E+01	3.21E-01	3.86E-02	-1.70E+00	2.15E-05	-2.02E+00	7.45E-06
497681705	cell division protein DivIVA	1.41E+01	5.40E-01	1.30E-01	-1.48E+00	3.94E-03	-2.02E+00	7.10E-04
490059894	potassium transporter TrkA	8.69E+00	5.12E-01	2.25E-02	-1.51E+00	1.81E-04	-2.02E+00	3.43E-05
497681989	2-nitropropane dioxygenase	1.15E+01	1.54E+00	2.55E-04	-4.78E-01	7.11E-02	-2.02E+00	7.88E-05
497683278	hydrolase	1.13E+01	-3.52E-01	9.25E-02	-2.37E+00	2.37E-05	-2.02E+00	3.97E-05
497685129	ArsR family transcriptional regulator	1.09E+01	-2.57E-01	6.16E-02	-2.27E+00	5.07E-06	-2.02E+00	5.57E-06
497681370	acetyltransferase	1.34E+01	4.30E-02	7.13E-01	-1.97E+00	5.79E-06	-2.01E+00	3.92E-06
490057830	ATP-grasp superfamily enzyme	1.21E+01	-1.13E+00	1.19E-04	-3.14E+00	2.70E-06	-2.01E+00	8.58E-06
490051755	hypothetical protein	1.60E+01	-7.39E-02	6.76E-01	-2.08E+00	2.49E-05	-2.01E+00	2.31E-05
490056617	transcriptional regulator	1.15E+01	-1.14E-01	7.77E-01	-2.12E+00	1.24E-03	-2.00E+00	1.46E-03
490055435	membrane protein	1.23E+01	3.74E-01	3.75E-02	-1.63E+00	4.95E-05	-2.00E+00	1.49E-05
490051148	cysteinyl-tRNA synthetase	1.33E+01	-3.87E-01	2.03E-02	-2.39E+00	5.79E-06	-2.00E+00	8.58E-06
490058512	acetyltransferase	1.32E+01	2.36E+00	2.48E-05	3.63E-01	1.39E-01	-2.00E+00	7.12E-05
490054199	thioredoxin reductase	1.05E+01	4.27E-01	1.76E-02	-1.57E+00	4.43E-05	-1.99E+00	1.17E-05
490058945	hypothetical protein	1.01E+01	7.58E-01	4.77E-03	-1.23E+00	6.10E-04	-1.99E+00	4.34E-05
490059828	tRNA delta(2)-isopentenylpyrophosphate transferase	1.47E+01	5.39E-01	5.13E-03	-1.45E+00	5.11E-05	-1.99E+00	9.38E-06
497683024	hypothetical protein	1.30E+01	1.47E-01	4.35E-01	-1.85E+00	6.57E-05	-1.99E+00	3.72E-05
490054494	Crp/Fnr family transcriptional regulator	1.23E+01	9.83E-02	6.20E-01	-1.89E+00	6.78E-05	-1.99E+00	4.32E-05
497682041	dynein regulation protein LC7	1.44E+01	8.92E-01	4.35E-03	-1.10E+00	2.35E-03	-1.99E+00	9.19E-05
490053064	magnesium or manganese-dependent protein phosphatase	1.35E+01	1.63E+00	1.58E-05	-3.52E-01	3.67E-02	-1.98E+00	7.91E-06
490051760	ATP/GTP-binding protein	8.10E+00	9.85E-01	4.76E-04	-9.94E-01	6.80E-04	-1.98E+00	1.79E-05
490055041	DNA-binding protein	1.33E+01	1.30E+00	2.15E-04	-6.71E-01	8.73E-03	-1.97E+00	3.24E-05
490055694	glutamine amidotransferase	1.12E+01	1.67E+00	7.31E-05	-2.95E-01	1.64E-01	-1.96E+00	3.92E-05
490054879	3-ketoacyl-ACP reductase	1.00E+01	-6.10E-01	1.83E-02	-2.57E+00	2.49E-05	-1.96E+00	7.43E-05
490055754	ATP phosphoribosyltransferase	1.28E+01	-8.83E-02	8.69E-01	-2.04E+00	5.16E-03	-1.95E+00	5.69E-03
490057379	oxidoreductase	1.24E+01	-2.62E-01	2.61E-01	-2.21E+00	6.89E-05	-1.95E+00	1.09E-04
497682172	S-adenosyl-L-homocysteine hydrolase	1.43E+01	-1.86E-01	3.28E-01	-2.14E+00	3.25E-05	-1.95E+00	4.02E-05
497682591	Xaa-Pro aminopeptidase	1.15E+01	2.11E+00	1.12E-05	1.65E-01	3.48E-01	-1.95E+00	2.01E-05

497682431	ATPase	9.10E+00	5.93E-01	3.76E-02	-1.35E+00	1.36E-03	-1.94E+00	1.75E-04
497683112	50S ribosomal protein L22	1.44E+01	3.81E-02	8.77E-01	-1.90E+00	1.41E-04	-1.94E+00	1.06E-04
490058681	adenylosuccinate synthetase	1.31E+01	9.75E-01	1.40E-03	-9.67E-01	2.17E-03	-1.94E+00	4.93E-05
490057884	anthranilate synthase subunit I	1.29E+01	-3.35E-01	7.35E-02	-2.28E+00	1.72E-05	-1.94E+00	2.61E-05
490056621	polyisoprenoid-binding protein	1.24E+01	1.22E+00	4.20E-03	-7.19E-01	5.35E-02	-1.94E+00	5.30E-04
490058986	alkaline D-peptidase	1.52E+01	1.00E+00	1.93E-04	-9.24E-01	4.39E-04	-1.93E+00	9.59E-06
490053896	geranylgeranyl pyrophosphate synthase	1.23E+01	1.49E-01	3.50E-01	-1.78E+00	3.50E-05	-1.93E+00	1.92E-05
490057208	peptidase M20	1.43E+01	3.25E-01	1.10E-01	-1.60E+00	1.41E-04	-1.92E+00	4.54E-05
497682254	hypothetical protein	1.38E+01	1.00E+00	1.19E-02	-9.17E-01	2.49E-02	-1.92E+00	6.73E-04
490059729	ATP-dependent DNA helicase RecG	1.14E+01	1.36E+00	6.14E-05	-5.56E-01	8.47E-03	-1.92E+00	1.44E-05
490056872	AsnC family transcriptional regulator	1.32E+01	-7.50E-01	1.10E-02	-2.67E+00	3.10E-05	-1.92E+00	1.29E-04
490053850	glutamate-1-semialdehyde aminotransferase	1.12E+01	8.14E-01	1.11E-03	-1.10E+00	3.43E-04	-1.92E+00	1.81E-05
490059720	IclR family transcriptional regulator	1.49E+01	8.09E-01	1.51E-02	-1.11E+00	5.43E-03	-1.91E+00	2.88E-04
497681453	MaoC family dehydratase	1.37E+01	-7.78E-01	1.17E-02	-2.69E+00	3.76E-05	-1.91E+00	1.74E-04
490050131	hypothetical protein	1.12E+01	3.49E-01	2.37E-01	-1.56E+00	1.38E-03	-1.91E+00	4.24E-04
490057602	glycerol-3-phosphate dehydrogenase	1.11E+01	6.00E-01	2.22E-02	-1.31E+00	8.40E-04	-1.91E+00	9.96E-05
490056767	PTS glucose transporter subunit IIA	9.90E+00	3.86E+00	1.67E-06	1.96E+00	3.03E-05	-1.91E+00	2.71E-05
490055603	GntR family transcriptional regulator	1.33E+01	9.18E-01	1.12E-03	-9.84E-01	1.17E-03	-1.90E+00	3.33E-05
490054119	30S ribosomal protein S11	1.34E+01	1.14E+00	1.92E-03	-7.63E-01	1.78E-02	-1.90E+00	1.74E-04
490053558	XRE family transcriptional regulator	9.14E+00	-7.75E-04	9.97E-01	-1.90E+00	1.11E-04	-1.90E+00	9.26E-05
497681532	stress protein	1.39E+01	3.37E+00	1.55E-05	1.47E+00	1.54E-03	-1.90E+00	3.51E-04
497683320	alpha-ketoglutarate decarboxylase	1.22E+01	9.86E-01	6.12E-05	-9.11E-01	1.36E-04	-1.90E+00	4.03E-06
490052515	preprotein translocase SecA	1.23E+01	-5.48E-01	7.26E-03	-2.44E+00	7.83E-06	-1.89E+00	1.84E-05
490056868	RpiR family transcriptional regulator	1.24E+01	2.35E-01	1.33E-01	-1.66E+00	3.44E-05	-1.89E+00	1.48E-05
490051193	LacI family transcriptional regulator	1.35E+01	-9.46E-01	2.79E-03	-2.84E+00	1.84E-05	-1.89E+00	1.00E-04
490054105	S-adenosylmethionine synthase	1.26E+01	1.12E-01	5.47E-01	-1.77E+00	7.11E-05	-1.89E+00	4.32E-05
490051556	TetR family transcriptional regulator	1.23E+01	2.83E-02	9.42E-01	-1.86E+00	1.02E-03	-1.89E+00	8.35E-04
497685093	1,4-dihydropyridine enantioselective esterase	1.04E+01	-2.43E+00	6.60E-04	-4.31E+00	5.24E-05	-1.89E+00	3.13E-03
490059833	ATP-binding protein	1.20E+01	8.62E-01	2.84E-04	-1.02E+00	1.82E-04	-1.88E+00	7.86E-06
490059732	metal-binding protein	1.27E+01	1.20E+00	3.06E-04	-6.83E-01	7.61E-03	-1.88E+00	3.81E-05
490059032	sugar isomerase	1.24E+01	-1.69E+00	6.23E-03	-3.57E+00	2.12E-04	-1.88E+00	4.97E-03

490054222	30S ribosomal protein S18	1.59E+01	1.02E+00	5.29E-02	-8.61E-01	1.13E-01	-1.88E+00	5.55E-03
497682032	ribose 5-phosphate isomerase	1.13E+01	7.16E-01	2.11E-03	-1.16E+00	2.64E-04	-1.88E+00	2.00E-05
490050088	ATP synthase subunit C	2.07E+01	1.86E+00	4.60E-06	-1.96E-02	8.80E-01	-1.88E+00	5.79E-06
497682601	ABC transporter	1.18E+01	1.88E-01	5.75E-01	-1.68E+00	1.92E-03	-1.87E+00	9.88E-04
490055581	hypothetical protein	1.40E+01	9.72E-01	1.21E-03	-8.98E-01	2.70E-03	-1.87E+00	5.06E-05
497681642	DNA polymerase I	1.12E+01	1.00E+00	3.06E-02	-8.68E-01	6.82E-02	-1.87E+00	2.48E-03
490059123	citrate synthase	1.01E+01	4.85E-01	2.90E-01	-1.38E+00	1.97E-02	-1.87E+00	4.69E-03
490052367	cold-shock protein	1.27E+01	-1.94E+00	7.81E-04	-3.80E+00	3.84E-05	-1.87E+00	1.26E-03
490050761	hypothetical protein	1.12E+01	-5.11E-01	5.83E-03	-2.37E+00	5.79E-06	-1.86E+00	1.13E-05
490055884	glutamine amidotransferase	1.28E+01	5.56E-01	4.34E-02	-1.30E+00	1.44E-03	-1.86E+00	1.94E-04
490054424	membrane dipeptidase	1.41E+01	4.21E-01	4.99E-03	-1.44E+00	1.80E-05	-1.86E+00	4.61E-06
490053239	dUTPase	1.36E+01	1.32E+00	3.09E-03	-5.30E-01	1.36E-01	-1.85E+00	7.42E-04
497683184	sugar ABC transporter ATPase	1.18E+01	9.28E-01	2.10E-04	-9.26E-01	3.17E-04	-1.85E+00	8.67E-06
490054626	ferritin	1.52E+01	2.21E+00	1.21E-04	3.56E-01	2.42E-01	-1.85E+00	3.81E-04
490058389	peptide chain release factor 2	1.43E+01	1.58E-01	3.20E-01	-1.69E+00	4.16E-05	-1.85E+00	2.17E-05
497682688	peptidyl-prolyl cis-trans isomerase	1.22E+01	-1.10E-01	5.55E-01	-1.96E+00	4.43E-05	-1.85E+00	4.75E-05
497683372	F0F1 ATP synthase subunit A	1.36E+01	5.71E-01	5.06E-03	-1.28E+00	1.27E-04	-1.85E+00	1.72E-05
490060951	acetyltransferase	1.29E+01	8.80E-01	1.09E-03	-9.68E-01	9.90E-04	-1.85E+00	3.03E-05
490052457	oxidoreductase	1.21E+01	5.05E-01	1.79E-02	-1.34E+00	2.26E-04	-1.85E+00	3.76E-05
490058039	MFS transporter	1.36E+01	1.55E+00	6.12E-05	-2.92E-01	1.32E-01	-1.85E+00	3.24E-05
490051608	histidinol-phosphatase	1.21E+01	3.08E-01	3.18E-01	-1.54E+00	1.96E-03	-1.84E+00	6.74E-04
497683144	FAD-dependent oxidoreductase	1.44E+01	1.22E+00	5.63E-04	-6.20E-01	2.10E-02	-1.84E+00	8.53E-05
497682960	endoribonuclease	9.90E+00	8.30E-01	3.43E-03	-1.01E+00	1.94E-03	-1.84E+00	7.33E-05
497683476	acylphosphatase	1.54E+01	1.25E+00	7.16E-05	-5.94E-01	4.64E-03	-1.84E+00	1.29E-05
497683556	diaminopimelate epimerase	1.44E+01	7.29E-01	1.34E-02	-1.11E+00	2.84E-03	-1.84E+00	1.78E-04
490060217	amino acid oxidase	1.07E+01	1.37E-01	3.03E-01	-1.70E+00	1.88E-05	-1.84E+00	9.91E-06
497681743	glycosyl transferase family 1	1.07E+01	-7.43E-02	8.00E-01	-1.91E+00	3.85E-04	-1.84E+00	4.13E-04
490057607	cysteine--1-D-myo-inosityl 2-amino-2-deoxy-alpha-D-glucopyranoside ligase	1.31E+01	1.26E+00	4.77E-05	-5.71E-01	4.10E-03	-1.83E+00	9.82E-06
490054298	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.31E+01	-2.61E-01	4.28E-01	-2.09E+00	5.98E-04	-1.83E+00	1.06E-03
490055585	HNH nuclease	1.33E+01	-6.31E-02	8.66E-01	-1.89E+00	1.24E-03	-1.82E+00	1.31E-03

490054315	transcriptional regulator	1.28E+01	5.07E-01	5.32E-02	-1.32E+00	1.14E-03	-1.82E+00	1.79E-04
490058210	hypothetical protein	1.48E+01	1.14E+00	4.80E-03	-6.84E-01	5.49E-02	-1.82E+00	5.90E-04
490058102	pyruvate dehydrogenase E1	1.38E+01	4.80E-01	3.80E-03	-1.34E+00	3.25E-05	-1.82E+00	6.43E-06
490054287	glutamine synthetase	1.12E+01	1.01E+00	1.24E-03	-8.10E-01	5.46E-03	-1.82E+00	7.35E-05
490054907	gamma-aminobutyraldehyde dehydrogenase	1.14E+01	1.18E+00	4.44E-02	-6.43E-01	2.59E-01	-1.82E+00	1.00E-02
490051256	hypoxanthine phosphoribosyltransferase	1.37E+01	8.06E-02	8.17E-01	-1.74E+00	1.55E-03	-1.82E+00	1.09E-03
490053874	ubiquinone/menaquinone biosynthesis methyltransferase	1.33E+01	4.56E-01	1.07E-02	-1.36E+00	6.89E-05	-1.81E+00	1.42E-05
497682013	putative bifunctional ribulose 5-phosphate reductase/CDP-ribitol pyrophosphorylase	1.26E+01	-1.06E-01	5.89E-01	-1.92E+00	6.14E-05	-1.81E+00	6.71E-05
490057930	glycine oxidase	1.14E+01	-4.07E-02	8.01E-01	-1.85E+00	2.45E-05	-1.81E+00	2.12E-05
490058107	LuxR family transcriptional regulator	1.25E+01	-8.07E-01	6.02E-02	-2.61E+00	4.37E-04	-1.81E+00	2.57E-03
497683061	NmrA family protein	1.21E+01	-9.51E-01	1.66E-03	-2.76E+00	1.39E-05	-1.81E+00	7.54E-05
490057306	TetR family transcriptional regulator	1.15E+01	-8.32E-01	1.18E-03	-2.64E+00	7.11E-06	-1.81E+00	2.78E-05
490060107	XRE family transcriptional regulator	1.33E+01	3.99E-01	4.45E-02	-1.41E+00	1.82E-04	-1.81E+00	4.19E-05
497683825	metallo-beta-lactamase	1.40E+01	3.20E-01	4.48E-02	-1.48E+00	4.65E-05	-1.80E+00	1.49E-05
490054120	30S ribosomal protein S13	1.40E+01	-6.65E-01	2.11E-01	-2.47E+00	2.65E-03	-1.80E+00	1.05E-02
490051407	ribose-phosphate pyrophosphokinase	1.10E+01	5.38E-01	1.32E-02	-1.25E+00	3.09E-04	-1.79E+00	4.10E-05
490057690	inorganic polyphosphate/ATP-NAD kinase	1.33E+01	3.11E-01	1.21E-01	-1.48E+00	2.01E-04	-1.79E+00	6.24E-05
497683089	hypothetical protein	1.32E+01	-1.25E-01	4.33E-01	-1.91E+00	2.51E-05	-1.79E+00	2.73E-05
490055919	cyclase	1.40E+01	3.37E-01	1.82E-01	-1.45E+00	8.40E-04	-1.79E+00	2.42E-04
490055328	isopropylmalate isomerase	1.25E+01	3.32E-01	5.48E-02	-1.46E+00	8.01E-05	-1.79E+00	2.41E-05
497683935	hypothetical protein	1.50E+01	5.45E-01	9.78E-02	-1.24E+00	5.80E-03	-1.78E+00	8.24E-04
490050097	50S ribosomal protein L31	1.86E+01	1.04E+00	1.39E-04	-7.45E-01	1.15E-03	-1.78E+00	1.20E-05
490058344	methionine ABC transporter ATP-binding protein	1.45E+01	-1.14E+00	3.06E-04	-2.92E+00	5.83E-06	-1.78E+00	3.87E-05
497682384	phosphoadenosine phosphosulfate reductase	1.39E+01	1.42E+00	2.64E-04	-3.58E-01	1.29E-01	-1.78E+00	1.04E-04
490053805	DNA topoisomerase IV subunit B	1.24E+01	6.83E-01	3.19E-03	-1.09E+00	4.34E-04	-1.78E+00	3.10E-05
497683116	methionine aminopeptidase	1.21E+01	4.10E-01	4.34E-01	-1.37E+00	3.73E-02	-1.78E+00	1.19E-02
490055927	hypothetical protein	1.49E+01	1.19E+00	9.77E-03	-5.79E-01	1.55E-01	-1.77E+00	1.95E-03
490054653	O-sialoglycoprotein endopeptidase	8.75E+00	6.30E-01	6.86E-03	-1.14E+00	5.19E-04	-1.77E+00	4.51E-05
490051829	LysR family transcriptional regulator	1.42E+01	-7.73E-01	1.06E-02	-2.54E+00	4.30E-05	-1.76E+00	2.31E-04
490054971	conserved hypothetical protein	8.15E+00	6.46E-03	9.79E-01	-1.75E+00	1.75E-04	-1.76E+00	1.43E-04

490054972	type 11 methyltransferase	1.43E+01	-1.14E-03	9.96E-01	-1.76E+00	6.44E-05	-1.76E+00	5.22E-05
490056183	glycerol kinase	1.25E+01	2.63E-01	2.01E-01	-1.49E+00	2.57E-04	-1.76E+00	9.33E-05
490056429	recombinase RecF	1.13E+01	4.98E-01	1.43E-02	-1.26E+00	2.24E-04	-1.76E+00	3.44E-05
497683103	UDP-N-acetylenolpyruvoylglucosamine reductase	1.39E+01	1.30E-01	4.57E-01	-1.63E+00	8.43E-05	-1.76E+00	4.66E-05
490054132	adenylate kinase	1.24E+01	-7.65E-02	4.97E-01	-1.83E+00	7.16E-06	-1.75E+00	6.14E-06
490053359	GntR family transcriptional regulator	1.33E+01	1.16E+00	2.11E-04	-5.93E-01	9.10E-03	-1.75E+00	3.24E-05
490058283	copper-binding protein	1.54E+01	-1.68E-01	4.03E-01	-1.92E+00	7.30E-05	-1.75E+00	9.73E-05
490059931	3-hydroxyacyl-CoA dehydrogenase	1.26E+01	9.97E-01	2.27E-04	-7.53E-01	1.45E-03	-1.75E+00	1.71E-05
490052615	ABC transporter substrate-binding protein	9.33E+00	1.36E+00	4.81E-03	-3.95E-01	3.02E-01	-1.75E+00	1.80E-03
497681974	UDP pyrophosphate synthase	1.28E+01	1.10E+00	9.44E-04	-6.53E-01	1.63E-02	-1.75E+00	1.05E-04
490051184	hypothetical protein	1.54E+01	1.42E+00	1.52E-02	-3.25E-01	5.25E-01	-1.75E+00	8.15E-03
490052183	phosphatidylserine decarboxylase	1.05E+01	-5.29E-03	9.76E-01	-1.75E+00	2.73E-05	-1.75E+00	2.17E-05
497682904	D-inositol 3-phosphate glycosyltransferase	1.18E+01	1.13E+00	1.39E-04	-6.15E-01	4.63E-03	-1.75E+00	1.98E-05
497682890	D-tyrosyl-tRNA(Tyr) deacylase	1.24E+01	3.50E-01	1.89E-02	-1.39E+00	3.30E-05	-1.74E+00	9.29E-06
490059900	deoxyuridine 5'-triphosphate nucleotidohydrolase	9.97E+00	-1.37E-01	4.03E-01	-1.88E+00	3.13E-05	-1.74E+00	3.61E-05
490054175	50S ribosomal protein L33	1.43E+01	7.99E-01	3.94E-02	-9.42E-01	2.94E-02	-1.74E+00	1.60E-03
497681888	membrane protein	1.41E+01	1.47E+00	1.43E-05	-2.69E-01	6.05E-02	-1.74E+00	8.07E-06
497681424	transferase	1.29E+01	8.54E-01	8.06E-04	-8.86E-01	1.01E-03	-1.74E+00	2.68E-05
490055229	FAD-binding dehydrogenase	9.06E+00	5.24E-01	3.95E-02	-1.22E+00	1.33E-03	-1.74E+00	1.77E-04
490054722	hypothetical protein	1.19E+01	-6.50E-01	1.97E-03	-2.39E+00	5.88E-06	-1.74E+00	1.70E-05
497681776	pyruvate dehydrogenase E1	1.43E+01	8.33E-01	7.13E-03	-9.02E-01	7.28E-03	-1.74E+00	2.31E-04
490057170	hypothetical protein	1.45E+01	7.76E-01	9.77E-03	-9.58E-01	5.49E-03	-1.73E+00	2.31E-04
490060087	hypothetical protein	1.18E+01	6.80E-01	5.32E-03	-1.05E+00	9.02E-04	-1.73E+00	5.67E-05
490055933	30S ribosomal protein S15	1.40E+01	1.13E+00	2.80E-03	-5.97E-01	5.81E-02	-1.73E+00	4.18E-04
490057508	class IV aminotransferase	1.36E+01	5.29E-01	5.57E-02	-1.20E+00	2.51E-03	-1.72E+00	3.27E-04
490053279	peptidase	1.36E+01	5.83E-01	7.71E-03	-1.14E+00	4.03E-04	-1.72E+00	4.06E-05
490051754	hypothetical protein	1.31E+01	8.78E-02	7.65E-01	-1.64E+00	9.06E-04	-1.72E+00	5.97E-04
490059611	hypothetical protein	1.36E+01	4.57E-01	3.46E-01	-1.27E+00	3.60E-02	-1.72E+00	9.22E-03
490052788	hypothetical protein	1.55E+01	6.16E-01	1.02E-01	-1.11E+00	1.74E-02	-1.72E+00	1.98E-03
490050944	radical SAM protein	1.02E+01	4.40E-01	2.35E-02	-1.28E+00	2.04E-04	-1.72E+00	3.79E-05

490051255	cell division protein FtsH	1.26E+01	-1.11E-01	3.47E-01	-1.83E+00	8.33E-06	-1.72E+00	8.07E-06
490055931	zinc protease	8.32E+00	6.08E-01	3.71E-02	-1.11E+00	4.12E-03	-1.72E+00	3.81E-04
490059673	membrane protein	1.55E+01	1.39E+00	4.77E-05	-3.27E-01	6.02E-02	-1.72E+00	2.10E-05
490050861	hypothetical protein	1.52E+01	1.32E-01	3.92E-01	-1.58E+00	5.25E-05	-1.71E+00	2.91E-05
490052969	ABC transporter substrate-binding protein	1.28E+01	9.54E-01	4.71E-04	-7.57E-01	2.34E-03	-1.71E+00	3.01E-05
490059859	phosphodiesterase	1.49E+01	5.65E-01	9.47E-03	-1.14E+00	4.28E-04	-1.71E+00	4.52E-05
490052553	ABC transporter	1.34E+01	-1.79E-01	3.37E-01	-1.88E+00	5.50E-05	-1.70E+00	7.44E-05
490054429	acyl-CoA dehydrogenase	1.40E+01	1.09E+00	9.18E-05	-6.08E-01	2.75E-03	-1.70E+00	1.28E-05
490056489	aspartokinase	1.32E+01	8.57E-01	1.33E-03	-8.41E-01	2.18E-03	-1.70E+00	4.82E-05
490054049	threonyl-tRNA synthetase	1.28E+01	2.78E-01	1.56E-01	-1.42E+00	2.45E-04	-1.70E+00	8.10E-05
490052502	peroxiredoxin	1.39E+01	8.14E-01	1.93E-03	-8.80E-01	1.95E-03	-1.69E+00	5.51E-05
490052143	cytochrome P450	1.13E+01	-2.39E+00	3.93E-06	-4.08E+00	1.24E-06	-1.69E+00	2.13E-05
490054158	elongation factor Tu	1.07E+01	1.14E+00	5.01E-05	-5.49E-01	3.19E-03	-1.69E+00	9.39E-06
497682038	aminopeptidase N	1.35E+01	7.84E-01	2.94E-02	-9.05E-01	2.36E-02	-1.69E+00	1.15E-03
490055531	acetolactate synthase	1.34E+01	3.08E-02	8.07E-01	-1.65E+00	1.46E-05	-1.68E+00	9.59E-06
490057142	regulatory protein	1.14E+01	-8.91E-03	9.61E-01	-1.69E+00	2.60E-05	-1.68E+00	2.10E-05
490057891	imidazole glycerol phosphate synthase	1.16E+01	8.36E-01	2.56E-03	-8.43E-01	3.68E-03	-1.68E+00	8.96E-05
490059304	phosphoesterase	1.65E+01	5.76E-01	9.59E-03	-1.10E+00	5.84E-04	-1.68E+00	5.56E-05
490055040	RNA methyltransferase	1.27E+01	7.19E-01	2.27E-03	-9.59E-01	7.86E-04	-1.68E+00	3.72E-05
490052149	glucokinase	1.19E+01	-3.71E-01	4.29E-02	-2.05E+00	2.06E-05	-1.68E+00	4.02E-05
490055732	preprotein translocase subunit SecA	1.35E+01	2.29E-02	8.65E-01	-1.65E+00	1.63E-05	-1.68E+00	1.12E-05
490053532	lysine decarboxylase	1.30E+01	3.90E-01	8.49E-03	-1.28E+00	3.32E-05	-1.67E+00	7.86E-06
490054926	prolyl-tRNA synthetase	1.15E+01	9.37E-01	5.25E-04	-7.36E-01	2.73E-03	-1.67E+00	3.39E-05
490056254	glycerol acyltransferase	1.47E+01	7.68E-01	7.78E-03	-9.03E-01	5.40E-03	-1.67E+00	2.00E-04
497682071	acyl-CoA dehydrogenase	1.28E+01	-1.97E-01	3.33E-01	-1.86E+00	8.89E-05	-1.66E+00	1.31E-04
490059462	ATP-binding protein	1.47E+01	-1.45E+00	3.94E-04	-3.11E+00	1.49E-05	-1.66E+00	2.49E-04
490053537	glutamyl-tRNA amidotransferase subunit C	1.18E+01	3.62E-01	6.06E-02	-1.30E+00	2.66E-04	-1.66E+00	6.24E-05
490054101	guanylate kinase	1.51E+01	-1.46E+00	6.46E-04	-3.12E+00	2.28E-05	-1.66E+00	4.40E-04
490051542	phosphoesterase	1.31E+01	9.08E-01	1.66E-03	-7.50E-01	6.29E-03	-1.66E+00	9.33E-05
490056264	ATPase AAA	1.16E+01	-7.50E-01	3.72E-03	-2.41E+00	1.81E-05	-1.66E+00	8.16E-05
490059788	translation initiation factor IF-2	1.30E+01	-3.57E-01	1.72E-02	-2.01E+00	7.11E-06	-1.65E+00	1.18E-05

490058409	bifunctional glucose-6-phosphate/mannose-6-phosphate isomerase	1.35E+01	-2.27E-02	9.35E-01	-1.67E+00	3.36E-04	-1.65E+00	3.10E-04
490055252	transferase	1.45E+01	8.19E-01	3.67E-04	-8.29E-01	5.15E-04	-1.65E+00	1.38E-05
490051170	hypothetical protein	8.78E+00	1.05E+00	2.52E-04	-5.93E-01	6.76E-03	-1.65E+00	3.24E-05
497683104	DNA-directed RNA polymerase subunit beta	1.24E+01	3.45E-01	1.62E-02	-1.30E+00	3.58E-05	-1.65E+00	9.50E-06
490057340	membrane protein	1.41E+01	2.43E-01	4.60E-01	-1.40E+00	4.56E-03	-1.65E+00	1.81E-03
490051790	hypothetical protein	1.26E+01	-8.45E-01	4.30E-04	-2.49E+00	5.07E-06	-1.64E+00	1.89E-05
497684131	hypothetical protein	1.33E+01	-1.92E+00	1.54E-05	-3.56E+00	2.70E-06	-1.64E+00	3.96E-05
490057429	ankyrin	1.30E+01	-8.43E-01	1.60E-03	-2.48E+00	1.25E-05	-1.64E+00	6.45E-05
490054145	50S ribosomal protein L29	1.45E+01	-1.16E+00	2.62E-02	-2.80E+00	6.12E-04	-1.64E+00	7.93E-03
490053375	glutamine synthetase	1.30E+01	4.83E-01	5.90E-02	-1.15E+00	2.04E-03	-1.64E+00	2.89E-04
490055001	SAM-dependent methyltransferase	9.06E+00	1.69E-01	4.45E-01	-1.47E+00	4.76E-04	-1.64E+00	2.34E-04
490057298	acyl-CoA thioesterase	1.53E+01	6.85E-01	6.44E-03	-9.51E-01	1.93E-03	-1.64E+00	9.86E-05
490060988	Isoform 2 of Ribosomal protein S6 modification B	8.67E+00	3.11E-02	8.79E-01	-1.60E+00	1.34E-04	-1.64E+00	1.02E-04
490058671	precorrin-4 C11-methyltransferase	1.38E+01	3.95E-01	1.84E-02	-1.24E+00	1.03E-04	-1.63E+00	2.16E-05
490058431	hypothetical protein	1.36E+01	2.35E-01	1.07E-01	-1.39E+00	5.18E-05	-1.63E+00	2.01E-05
490055070	hypothetical protein	1.09E+01	3.04E-01	5.18E-02	-1.32E+00	7.59E-05	-1.63E+00	2.27E-05
490060210	3-hydroxyacyl-CoA dehydrogenase	1.27E+01	-7.47E-01	1.47E-03	-2.38E+00	8.12E-06	-1.63E+00	3.39E-05
497683293	NAD-dependent dehydratase	1.43E+01	5.78E-01	3.78E-03	-1.05E+00	2.72E-04	-1.63E+00	2.46E-05
497684047	hypothetical protein	1.26E+01	-9.34E-01	6.89E-03	-2.56E+00	6.40E-05	-1.62E+00	5.71E-04
497681368	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1.30E+01	2.06E-01	1.63E-01	-1.42E+00	5.74E-05	-1.62E+00	2.43E-05
490050024	pyruvate kinase	1.25E+01	5.08E-01	9.23E-03	-1.12E+00	2.73E-04	-1.62E+00	3.38E-05
490054098	carbamoyl phosphate synthase large subunit	1.39E+01	8.61E-01	1.43E-03	-7.59E-01	4.03E-03	-1.62E+00	6.82E-05
490054170	aspartate aminotransferase	1.27E+01	-2.59E-01	8.17E-02	-1.88E+00	1.48E-05	-1.62E+00	2.13E-05
490053240	histidine kinase	1.43E+01	-4.68E-01	5.21E-02	-2.09E+00	6.86E-05	-1.62E+00	2.14E-04
490053383	porphobilinogen deaminase	1.18E+01	1.62E-01	3.83E-01	-1.46E+00	1.99E-04	-1.62E+00	9.61E-05
497683138	sulfurase	1.03E+01	8.40E-01	1.49E-02	-7.78E-01	2.89E-02	-1.62E+00	8.53E-04
497682044	mechanosensitive ion channel MscS	1.27E+01	1.45E+00	3.22E-05	-1.65E-01	2.83E-01	-1.62E+00	2.38E-05
490054890	50S rRNA methyltransferase	1.25E+01	2.35E-01	1.98E-01	-1.38E+00	2.06E-04	-1.62E+00	7.60E-05
490060115	oxidoreductase	1.39E+01	5.45E-01	1.84E-01	-1.07E+00	3.22E-02	-1.62E+00	4.99E-03
490056610	ABC transporter	1.02E+01	3.67E-01	4.51E-02	-1.24E+00	2.24E-04	-1.61E+00	4.90E-05

497681006	cyclase	1.09E+01	-4.42E-01	8.06E-02	-2.05E+00	1.10E-04	-1.61E+00	3.30E-04
497685154	regulatory protein	1.58E+01	3.41E-01	3.10E-01	-1.27E+00	7.49E-03	-1.61E+00	2.09E-03
490054062	glutamine amidotransferase	1.43E+01	7.86E-01	2.04E-03	-8.23E-01	2.42E-03	-1.61E+00	6.38E-05
490051432	16S rRNA methyltransferase	1.47E+01	-2.85E-01	1.93E-01	-1.89E+00	1.05E-04	-1.61E+00	2.06E-04
490051425	glycerophosphoryl diester phosphodiesterase	1.28E+01	-6.66E-01	4.09E-02	-2.27E+00	1.90E-04	-1.61E+00	1.01E-03
490060208	L-carnitine dehydratase	1.34E+01	-1.25E+00	1.42E-04	-2.85E+00	5.40E-06	-1.61E+00	4.68E-05
497683088	hypothetical protein	1.36E+01	-1.10E+00	2.11E-04	-2.70E+00	5.46E-06	-1.61E+00	3.80E-05
497681611	glmZ(sRNA)-inactivating NTPase	1.36E+01	-1.91E-01	3.37E-01	-1.79E+00	9.41E-05	-1.60E+00	1.39E-04
490052924	fructose 1,6-bisphosphatase	1.42E+01	2.35E+00	2.21E-05	7.52E-01	9.99E-03	-1.60E+00	1.96E-04
490053069	methionyl-tRNA synthetase	1.21E+01	7.87E-01	2.92E-03	-8.12E-01	3.77E-03	-1.60E+00	9.71E-05
490059485	hypothetical protein	1.10E+01	-5.81E-01	9.91E-03	-2.18E+00	2.27E-05	-1.60E+00	7.83E-05
490055137	transcriptional regulator	1.37E+01	-2.42E-01	3.25E-01	-1.84E+00	2.43E-04	-1.60E+00	4.39E-04
490056909	polyketide synthase	1.62E+01	1.23E+00	8.12E-05	-3.66E-01	3.81E-02	-1.59E+00	2.70E-05
490055283	trigger factor	1.30E+01	-9.41E-02	4.60E-01	-1.69E+00	1.77E-05	-1.59E+00	1.69E-05
490053511	serine hydroxymethyltransferase	1.30E+01	2.72E-01	1.20E-01	-1.32E+00	1.80E-04	-1.59E+00	5.65E-05
490055315	phosphomethylpyrimidine kinase	1.24E+01	8.40E-01	9.51E-03	-7.52E-01	2.17E-02	-1.59E+00	5.32E-04
490054111	50S ribosomal protein L13	1.21E+01	-5.16E-01	3.03E-02	-2.11E+00	5.15E-05	-1.59E+00	1.79E-04
497683929	serine/threonine protein kinase	1.02E+01	1.34E+00	8.24E-04	-2.46E-01	3.52E-01	-1.59E+00	4.51E-04
497682307	adenine glycosylase	1.24E+01	-5.05E-02	8.39E-01	-1.64E+00	3.43E-04	-1.58E+00	3.49E-04
497685323	methyltransferase type 11	8.63E+00	-6.95E-02	5.85E-01	-1.65E+00	1.81E-05	-1.58E+00	1.64E-05
490059704	pyridoxal-5'-phosphate-dependent protein subunit beta	1.27E+01	3.14E-01	5.36E-02	-1.27E+00	1.19E-04	-1.58E+00	3.24E-05
490055127	peptide ABC transporter ATP-binding protein	1.41E+01	3.70E-01	1.18E-01	-1.21E+00	1.32E-03	-1.58E+00	2.85E-04
490054166	50S ribosomal protein L1	1.17E+01	-2.89E-01	1.51E-01	-1.87E+00	6.72E-05	-1.58E+00	1.31E-04
490054721	Fe-S cluster assembly protein SufB	1.33E+01	7.30E-01	1.47E-02	-8.49E-01	1.10E-02	-1.58E+00	4.53E-04
490055201	hypothetical protein	1.26E+01	1.34E+00	1.50E-05	-2.36E-01	7.10E-02	-1.58E+00	8.67E-06
490054647	copper-binding protein	1.40E+01	5.22E-01	2.30E-02	-1.06E+00	1.30E-03	-1.58E+00	1.36E-04
497681272	hypothetical protein, partial	9.45E+00	6.44E-01	2.32E-02	-9.26E-01	7.07E-03	-1.57E+00	4.36E-04
490052673	phosphoribosylamine--glycine ligase	1.40E+01	-4.47E-01	1.33E-01	-2.02E+00	3.19E-04	-1.57E+00	1.04E-03
497683467	hydrolase	1.29E+01	-5.66E-01	9.46E-03	-2.13E+00	2.13E-05	-1.56E+00	7.28E-05
497681516	tyrosyl-tRNA synthetase	1.39E+01	-3.09E-01	9.11E-02	-1.87E+00	3.68E-05	-1.56E+00	7.22E-05

490055122	exopolyphosphatase	1.34E+01	-5.32E-02	8.78E-01	-1.61E+00	1.96E-03	-1.56E+00	2.05E-03
490053496	phosphoglycolate phosphatase	1.37E+01	-7.60E-02	8.27E-01	-1.64E+00	2.06E-03	-1.56E+00	2.30E-03
490050085	F0F1 ATP synthase subunit alpha	1.24E+01	5.21E-02	8.05E-01	-1.51E+00	2.46E-04	-1.56E+00	1.75E-04
490051909	deaminase reductase	1.35E+01	-2.02E+00	3.11E-05	-3.58E+00	5.07E-06	-1.55E+00	1.48E-04
490058547	dihydroxy-acid dehydratase	1.34E+01	1.07E+00	4.28E-03	-4.83E-01	1.19E-01	-1.55E+00	8.72E-04
490057003	iron ABC transporter substrate-binding protein	1.11E+01	1.17E+00	5.98E-05	-3.82E-01	2.14E-02	-1.55E+00	1.88E-05
490056978	acetyltransferase	1.49E+01	2.44E-01	1.30E-01	-1.31E+00	1.29E-04	-1.55E+00	4.46E-05
490054727	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase	1.46E+01	4.20E-01	3.32E-02	-1.13E+00	4.87E-04	-1.55E+00	7.95E-05
497682970	copper homeostasis protein CutC	1.24E+01	1.20E+00	1.99E-04	-3.48E-01	7.45E-02	-1.54E+00	6.67E-05
490059773	FAD-dependent oxidoreductase	1.35E+01	1.19E+00	2.46E-03	-3.52E-01	2.36E-01	-1.54E+00	8.72E-04
490058708	molecular chaperone DnaJ	1.48E+01	2.19E-01	3.31E-01	-1.32E+00	8.65E-04	-1.54E+00	3.35E-04
497681329	histidyl-tRNA synthetase	1.51E+01	8.96E-01	2.86E-03	-6.46E-01	1.84E-02	-1.54E+00	2.28E-04
490055374	hypothetical protein	1.13E+01	3.87E-01	6.73E-02	-1.15E+00	8.16E-04	-1.54E+00	1.52E-04
490052778	fructose-bisphosphate aldolase	1.01E+01	1.24E+00	3.03E-04	-2.99E-01	1.53E-01	-1.54E+00	1.25E-04
490051745	aldo/keto reductase	1.15E+01	-6.97E-01	6.11E-03	-2.23E+00	2.73E-05	-1.54E+00	1.39E-04
490055121	conserved hypothetical protein	1.17E+01	1.35E-01	5.11E-01	-1.40E+00	4.07E-04	-1.54E+00	2.18E-04
490057952	cysteine desulfurase	1.47E+01	1.42E+00	2.52E-03	-1.19E-01	7.32E-01	-1.53E+00	2.20E-03
490059504	ATPase	1.40E+01	8.97E-01	2.86E-03	-6.32E-01	2.02E-02	-1.53E+00	2.39E-04
490056047	O-methyltransferase	1.43E+01	-2.00E+00	3.30E-05	-3.53E+00	5.07E-06	-1.53E+00	1.65E-04
490059291	purine biosynthesis protein purH	1.31E+01	4.35E-01	6.09E-02	-1.09E+00	1.67E-03	-1.53E+00	2.54E-04
497683969	electron transfer flavoprotein subunit alpha	1.01E+01	9.96E-01	3.67E-04	-5.30E-01	1.21E-02	-1.53E+00	5.03E-05
490052935	hypothetical protein	1.23E+01	-1.77E-01	2.09E-01	-1.70E+00	2.27E-05	-1.53E+00	2.91E-05
497683712	dehydrogenase	1.63E+01	1.52E-01	4.46E-01	-1.37E+00	3.99E-04	-1.52E+00	1.96E-04
497682188	phosphoribosylaminoimidazole carboxylase	1.39E+01	1.07E+00	5.63E-05	-4.50E-01	6.87E-03	-1.52E+00	1.28E-05
490053370	octanoyltransferase	1.27E+01	2.37E-02	9.00E-01	-1.50E+00	1.19E-04	-1.52E+00	9.12E-05
490060516	hypothetical protein	1.20E+01	-1.17E+00	3.36E-04	-2.69E+00	9.26E-06	-1.52E+00	1.09E-04
490051101	hypothetical protein	1.39E+01	-6.18E-01	1.63E-02	-2.13E+00	5.47E-05	-1.51E+00	2.65E-04
490058659	metallophosphoesterase	1.19E+01	6.42E-01	1.27E-02	-8.72E-01	4.64E-03	-1.51E+00	2.38E-04
490060089	peptidase U61	9.01E+00	1.67E+00	3.67E-05	1.55E-01	3.82E-01	-1.51E+00	7.37E-05
490056886	chemotaxis protein CheY	1.29E+01	-4.04E-01	6.37E-03	-1.91E+00	5.79E-06	-1.51E+00	1.12E-05

490055449	metallo-beta-lactamase	1.07E+01	1.01E+00	1.27E-04	-4.96E-01	6.90E-03	-1.51E+00	2.12E-05
490056602	seryl-tRNA synthetase	1.22E+01	-1.12E+00	1.71E-02	-2.63E+00	4.07E-04	-1.51E+00	6.06E-03
490059785	transcription elongation factor NusA	1.29E+01	1.17E+00	5.04E-04	-3.43E-01	1.21E-01	-1.51E+00	1.71E-04
490052559	methionine sulfoxide reductase A	1.41E+01	4.94E-03	9.84E-01	-1.50E+00	2.87E-04	-1.51E+00	2.42E-04
490058303	guanidinobutyrase	1.54E+01	1.39E+00	4.82E-04	-1.13E-01	6.45E-01	-1.51E+00	4.22E-04
490054385	hypothetical protein	7.80E+00	9.40E-01	5.82E-02	-5.66E-01	2.51E-01	-1.51E+00	1.21E-02
497682424	transporter	1.21E+01	4.40E-01	2.62E-01	-1.06E+00	2.97E-02	-1.50E+00	6.16E-03
490059040	RpiR family transcriptional regulator	1.34E+01	-4.70E-01	9.60E-02	-1.97E+00	2.50E-04	-1.50E+00	9.01E-04
490060889	luciferase	1.03E+01	-1.68E+00	1.21E-04	-3.18E+00	9.05E-06	-1.50E+00	2.72E-04
490059808	membrane protein	9.93E+00	8.03E-01	2.26E-02	-6.98E-01	5.22E-02	-1.50E+00	1.66E-03
490056913	cytochrome P450	7.88E+00	5.28E-01	7.29E-02	-9.72E-01	9.65E-03	-1.50E+00	1.04E-03
497683217	hypothetical protein	8.43E+00	8.78E-01	3.45E-03	-6.22E-01	2.33E-02	-1.50E+00	2.91E-04
497683130	carbohydrate kinase	1.32E+01	7.67E-01	8.49E-04	-7.31E-01	1.63E-03	-1.50E+00	3.43E-05
490059741	cell division protein FtsY	8.98E+00	1.90E-02	9.12E-01	-1.48E+00	6.99E-05	-1.50E+00	5.41E-05
490056083	ABC transporter substrate-binding protein	1.44E+01	1.32E+00	6.04E-05	-1.72E-01	2.77E-01	-1.49E+00	4.02E-05
497681571	penicillin-binding protein	1.37E+01	9.79E-01	6.23E-04	-5.13E-01	2.00E-02	-1.49E+00	8.89E-05
490054710	transaldolase	1.29E+01	-2.90E-01	2.01E-01	-1.78E+00	1.73E-04	-1.49E+00	3.72E-04
497684175	hypothetical protein	1.40E+01	-1.52E+00	4.62E-04	-3.01E+00	2.37E-05	-1.49E+00	6.73E-04
490055116	transglycosylase	1.48E+01	8.50E-01	7.56E-02	-6.40E-01	1.91E-01	-1.49E+00	1.16E-02
497681563	MarR family transcriptional regulator	1.47E+01	4.56E-01	1.46E-02	-1.03E+00	4.01E-04	-1.49E+00	5.06E-05
490059251	pantothenate kinase	1.40E+01	6.10E-01	2.05E-03	-8.79E-01	4.67E-04	-1.49E+00	2.69E-05
490056578	nucleotide sugar-1-phosphate transferase	1.38E+01	-9.55E-02	6.92E-01	-1.58E+00	4.39E-04	-1.48E+00	5.34E-04
490058819	histidine kinase	1.38E+01	1.29E+00	1.23E-04	-1.94E-01	2.71E-01	-1.48E+00	7.30E-05
497683496	AsnC family transcriptional regulator	1.32E+01	7.81E-01	8.57E-04	-6.98E-01	2.28E-03	-1.48E+00	4.02E-05
490054063	transcriptional regulator	1.41E+01	-2.86E-01	4.34E-02	-1.76E+00	1.34E-05	-1.48E+00	2.15E-05
490052949	ABC transporter permease	1.53E+01	-8.65E-02	7.09E-01	-1.56E+00	3.77E-04	-1.48E+00	4.41E-04
490054173	MaoC family dehydratase	1.35E+01	-1.02E+00	1.15E-04	-2.50E+00	3.93E-06	-1.47E+00	2.25E-05
497683271	sodium:proton antiporter	1.40E+01	1.54E+00	9.13E-06	6.72E-02	5.82E-01	-1.47E+00	1.38E-05
490056262	helicase	1.37E+01	7.86E-01	6.19E-04	-6.85E-01	1.88E-03	-1.47E+00	3.14E-05
490052752	phosphoribosyltransferase	1.29E+01	9.17E-01	1.04E-02	-5.53E-01	9.18E-02	-1.47E+00	1.43E-03
490054854	glycine dehydrogenase subunit 1	1.29E+01	1.39E+00	1.37E-04	-7.51E-02	6.96E-01	-1.47E+00	1.29E-04

497682872	mycothiol acetyltransferase	1.04E+01	1.06E+00	4.04E-04	-4.04E-01	4.92E-02	-1.47E+00	9.60E-05
497681868	hypothetical protein	1.43E+01	-4.42E-01	3.51E-02	-1.91E+00	4.70E-05	-1.47E+00	1.48E-04
490053058	DNA-binding protein	1.48E+01	5.15E-01	1.69E-02	-9.51E-01	1.40E-03	-1.47E+00	1.25E-04
490054073	GTP pyrophosphokinase	1.24E+01	1.33E+00	8.82E-04	-1.35E-01	6.05E-01	-1.46E+00	7.02E-04
490057889	imidazole glycerol phosphate synthase	1.43E+01	2.73E-01	6.71E-02	-1.19E+00	1.12E-04	-1.46E+00	3.29E-05
490059790	ribosome-binding factor A	1.39E+01	8.01E-02	6.80E-01	-1.38E+00	2.91E-04	-1.46E+00	1.84E-04
490055866	acetyltransferase	1.33E+01	1.51E+00	3.19E-05	4.74E-02	7.65E-01	-1.46E+00	4.58E-05
490054410	histidinol dehydrogenase	1.16E+01	2.14E+00	2.29E-05	6.79E-01	1.06E-02	-1.46E+00	2.00E-04
497681710	16S rRNA methyltransferase	1.01E+01	6.94E-01	6.38E-03	-7.66E-01	5.93E-03	-1.46E+00	1.89E-04
490057128	NUDIX hydrolase	1.10E+01	-3.18E-01	1.15E-01	-1.77E+00	8.01E-05	-1.45E+00	1.87E-04
497683736	GntR family transcriptional regulator	1.22E+01	1.07E+00	2.57E-04	-3.83E-01	4.42E-02	-1.45E+00	6.58E-05
497682134	phosphotransferase	1.52E+01	2.83E-01	2.28E-01	-1.17E+00	1.89E-03	-1.45E+00	5.36E-04
490058675	4-phosphopantetheinyl transferase	1.23E+01	-7.30E-01	5.67E-04	-2.18E+00	5.46E-06	-1.45E+00	2.16E-05
490053398	type II citrate synthase	1.37E+01	5.41E-01	1.41E-02	-9.08E-01	1.82E-03	-1.45E+00	1.36E-04
490054117	DNA-directed RNA polymerase subunit alpha	1.40E+01	-7.79E-01	1.46E-03	-2.23E+00	1.33E-05	-1.45E+00	7.43E-05
490051220	hypothetical protein	9.45E+00	1.07E+00	2.86E-03	-3.76E-01	1.75E-01	-1.44E+00	8.17E-04
490055567	hypothetical protein	1.26E+01	5.11E-01	9.51E-02	-9.32E-01	1.48E-02	-1.44E+00	1.66E-03
497682458	hypothetical protein	1.31E+01	-2.66E-02	8.75E-01	-1.47E+00	8.01E-05	-1.44E+00	7.29E-05
497685238	hypothetical protein	1.65E+01	3.26E-01	3.77E-02	-1.11E+00	1.69E-04	-1.44E+00	3.81E-05
490059150	acetyltransferase	1.22E+01	8.98E-01	2.76E-03	-5.41E-01	3.61E-02	-1.44E+00	3.16E-04
497681797	peptidase	1.23E+01	2.48E-01	1.12E-01	-1.19E+00	1.66E-04	-1.44E+00	5.11E-05
490054357	maleylpyruvate isomerase	1.25E+01	-8.42E-03	9.71E-01	-1.45E+00	2.12E-04	-1.44E+00	1.84E-04
497681720	methyltransferase type 12	9.44E+00	4.17E-02	8.61E-01	-1.40E+00	5.69E-04	-1.44E+00	4.27E-04
490051253	hypothetical protein	1.47E+01	1.31E+00	2.66E-05	-1.31E-01	3.19E-01	-1.44E+00	2.10E-05
490055546	acetyltransferase	1.31E+01	6.24E-01	1.05E-01	-8.11E-01	6.05E-02	-1.43E+00	5.54E-03
490059968	sulfate adenylyltransferase subunit 2	1.29E+01	-7.41E-01	5.05E-02	-2.17E+00	5.61E-04	-1.43E+00	4.16E-03
490054901	gamma-aminobutyraldehyde dehydrogenase	1.44E+01	1.06E+00	6.59E-04	-3.59E-01	9.43E-02	-1.42E+00	1.85E-04
497681801	reductase	1.34E+01	-9.25E-01	1.29E-03	-2.35E+00	1.93E-05	-1.42E+00	1.77E-04
490056619	transferase	1.35E+01	-2.69E-01	3.61E-01	-1.68E+00	1.02E-03	-1.42E+00	2.17E-03
490052504	chaperonin	1.51E+01	6.17E-01	2.11E-03	-7.94E-01	8.79E-04	-1.41E+00	3.81E-05
497685124	hypothetical protein	9.64E+00	-1.14E-01	6.25E-01	-1.53E+00	4.75E-04	-1.41E+00	6.25E-04

490057353	hypothetical protein	1.24E+01	-2.68E-01	4.71E-01	-1.68E+00	3.46E-03	-1.41E+00	7.10E-03
490052962	peptidase S9	1.13E+01	-4.04E-01	6.11E-03	-1.81E+00	6.80E-06	-1.41E+00	1.46E-05
490053695	transcriptional regulator	1.32E+01	-3.07E-03	9.87E-01	-1.41E+00	1.09E-04	-1.41E+00	9.22E-05
490051097	N-acetylmuramic acid-6-phosphate etherase	1.30E+01	3.92E-01	1.66E-01	-1.01E+00	8.48E-03	-1.41E+00	1.53E-03
490059124	pyridoxamine 5'-phosphate oxidase	1.13E+01	-1.41E+00	1.27E-04	-2.82E+00	7.74E-06	-1.40E+00	1.61E-04
490051669	pyruvate phosphate dikinase	1.06E+01	1.05E+00	6.87E-03	-3.54E-01	2.72E-01	-1.40E+00	2.22E-03
490050290	hypothetical protein	8.65E+00	8.62E-01	1.35E-03	-5.41E-01	1.75E-02	-1.40E+00	1.36E-04
490054041	glyceraldehyde-3-phosphate dehydrogenase	1.14E+01	-8.74E-01	2.04E-03	-2.28E+00	2.49E-05	-1.40E+00	2.30E-04
490058297	hypothetical protein	1.32E+01	-3.40E-01	9.05E-02	-1.74E+00	8.14E-05	-1.40E+00	2.11E-04
490052209	ribonuclease H	1.28E+01	5.86E-01	1.12E-02	-8.10E-01	3.77E-03	-1.40E+00	1.94E-04
497681723	TetR family transcriptional regulator	1.37E+01	1.16E+00	1.09E-04	-2.37E-01	1.39E-01	-1.39E+00	5.04E-05
497683342	isopenicillin N synthase	1.23E+01	-1.24E+00	7.17E-04	-2.63E+00	2.49E-05	-1.39E+00	5.05E-04
490057674	1-acyl-sn-glycerol-3-phosphate acyltransferase	1.39E+01	-1.20E-01	4.63E-01	-1.51E+00	8.99E-05	-1.39E+00	1.13E-04
497683460	ATP-binding protein	1.11E+01	-8.44E-02	6.57E-01	-1.47E+00	1.98E-04	-1.38E+00	2.29E-04
490055741	initiation factor 2B subunit alpha	1.25E+01	2.16E+00	5.31E-05	7.86E-01	1.23E-02	-1.38E+00	7.13E-04
490058112	peptidase M28	1.35E+01	4.14E-01	1.19E-01	-9.57E-01	7.38E-03	-1.37E+00	1.11E-03
490055277	valyl-tRNA synthetase	1.30E+01	-1.31E-01	3.69E-01	-1.50E+00	5.10E-05	-1.37E+00	6.55E-05
497682074	phosphatase	1.30E+01	8.93E-01	4.69E-03	-4.75E-01	7.94E-02	-1.37E+00	7.26E-04
490055606	3-oxoacyl-ACP reductase	1.26E+01	1.58E+00	1.61E-04	2.10E-01	3.51E-01	-1.37E+00	4.36E-04
497683568	peptidase M16	1.17E+01	-1.82E-01	4.50E-01	-1.54E+00	5.67E-04	-1.36E+00	9.64E-04
497681577	putative transport associated protein	1.16E+01	6.07E-01	3.03E-02	-7.54E-01	1.79E-02	-1.36E+00	9.72E-04
490056760	oxidoreductase	1.44E+01	-5.75E-01	4.17E-02	-1.93E+00	2.10E-04	-1.36E+00	1.15E-03
490051191	transcriptional regulator	1.30E+01	-3.64E-01	3.28E-01	-1.72E+00	2.89E-03	-1.36E+00	8.09E-03
490061203	methyl-accepting chemotaxis protein	9.40E+00	5.67E-01	5.48E-02	-7.87E-01	2.24E-02	-1.35E+00	1.62E-03
490050778	lipid hydroperoxide peroxidase	1.26E+01	-2.40E+00	6.46E-04	-3.75E+00	9.70E-05	-1.35E+00	1.39E-02
490051635	sugar hydrolase	1.27E+01	8.38E-01	2.84E-04	-5.15E-01	5.08E-03	-1.35E+00	3.13E-05
497681983	phosphate starvation protein PhoH	1.23E+01	2.80E-01	1.26E-01	-1.07E+00	6.63E-04	-1.35E+00	1.70E-04
490054252	cytochrome C oxidase assembly protein	1.53E+01	1.09E+00	3.31E-03	-2.57E-01	3.64E-01	-1.35E+00	1.53E-03
490050021	6-phosphofructokinase	1.38E+01	8.57E-01	3.17E-04	-4.93E-01	7.57E-03	-1.35E+00	3.89E-05
490057932	serine/threonine protein kinase	9.92E+00	6.43E-01	1.97E-02	-7.07E-01	1.90E-02	-1.35E+00	7.71E-04
497684650	GCN5 family acetyltransferase	1.37E+01	7.44E-01	1.24E-02	-6.05E-01	3.99E-02	-1.35E+00	9.36E-04

490055203	ATPase	1.25E+01	9.76E-01	9.79E-04	-3.72E-01	8.30E-02	-1.35E+00	2.35E-04
497682657	DNA gyrase subunit B	1.47E+01	-6.05E-02	7.77E-01	-1.41E+00	3.77E-04	-1.35E+00	4.13E-04
497682856	hypothetical protein	1.35E+01	-4.12E+00	1.99E-06	-5.46E+00	1.64E-06	-1.35E+00	4.45E-04
490061297	cytochrome P450	1.12E+01	-3.17E+00	1.57E-06	-4.51E+00	8.46E-07	-1.35E+00	4.78E-05
497682015	ribonuclease E	1.35E+01	-4.61E-02	7.65E-01	-1.39E+00	7.47E-05	-1.35E+00	7.35E-05
497681284	AsnC family transcriptional regulator	1.29E+01	4.10E-01	1.30E-01	-9.35E-01	9.10E-03	-1.35E+00	1.38E-03
490052651	hypothetical protein	1.12E+01	2.57E-03	9.87E-01	-1.34E+00	6.89E-05	-1.34E+00	5.61E-05
490052751	deoxycytidine triphosphate deaminase	1.33E+01	1.06E+00	8.19E-05	-2.70E-01	6.66E-02	-1.33E+00	3.24E-05
490053265	F420-dependent oxidoreductase	1.38E+01	3.09E-01	1.14E-01	-1.02E+00	1.15E-03	-1.33E+00	2.53E-04
490056719	hypothetical protein	9.98E+00	8.08E-01	4.81E-03	-5.19E-01	4.37E-02	-1.33E+00	5.18E-04
497684412	hypothetical protein	1.49E+01	-2.92E+00	1.78E-05	-4.25E+00	5.83E-06	-1.33E+00	1.27E-03
490057659	hypothetical protein	1.27E+01	7.50E-01	1.87E-02	-5.75E-01	6.77E-02	-1.32E+00	1.75E-03
490060239	XRE family transcriptional regulator	1.31E+01	2.06E+00	1.32E-03	7.31E-01	1.19E-01	-1.32E+00	1.43E-02
490057834	ATP-dependent helicase	1.37E+01	7.93E-01	4.07E-04	-5.31E-01	4.65E-03	-1.32E+00	3.69E-05
497681220	GntR family transcriptional regulator	1.35E+01	8.34E-01	1.98E-02	-4.89E-01	1.47E-01	-1.32E+00	3.23E-03
490057772	1-aminocyclopropane-1-carboxylate deaminase	1.51E+01	-9.60E-01	5.95E-03	-2.28E+00	1.11E-04	-1.32E+00	1.63E-03
490053538	glutamyl-tRNA amidotransferase subunit A	1.30E+01	-4.19E-01	2.27E-01	-1.74E+00	1.79E-03	-1.32E+00	6.22E-03
497683195	aldehyde dehydrogenase	1.33E+01	2.81E-01	7.80E-02	-1.03E+00	3.43E-04	-1.31E+00	8.29E-05
497683820	protein tyrosine/serine phosphatase	1.56E+01	-4.68E-01	7.90E-02	-1.78E+00	2.93E-04	-1.31E+00	1.26E-03
490057983	molybdenum cofactor sulfurase	1.03E+01	6.25E-01	6.81E-03	-6.87E-01	6.41E-03	-1.31E+00	2.07E-04
490054205	RNA nucleotidyltransferase	1.43E+01	3.22E-01	2.65E-02	-9.90E-01	1.81E-04	-1.31E+00	3.61E-05
490050022	phosphate acetyltransferase	1.40E+01	5.77E-01	4.86E-02	-7.33E-01	2.75E-02	-1.31E+00	1.74E-03
497682786	DNA polymerase III subunit gamma/tau	1.34E+01	1.24E-01	6.16E-01	-1.19E+00	2.37E-03	-1.31E+00	1.26E-03
490054382	alanine racemase	1.30E+01	2.56E-01	1.40E-01	-1.05E+00	5.69E-04	-1.31E+00	1.57E-04
497682456	peptide hydrolase	1.51E+01	2.78E-01	7.23E-02	-1.03E+00	2.93E-04	-1.31E+00	7.16E-05
490055865	sulfite reductase	1.42E+01	-6.03E-02	7.13E-01	-1.37E+00	1.28E-04	-1.31E+00	1.35E-04
490054136	30S ribosomal protein S5	1.32E+01	-5.64E-01	2.53E-02	-1.87E+00	1.16E-04	-1.30E+00	6.51E-04
490052780	hypothetical protein	1.24E+01	1.01E+00	5.82E-04	-2.89E-01	1.40E-01	-1.30E+00	2.03E-04
490054531	cobaltochelatase subunit CobN	1.23E+01	5.73E-01	6.65E-03	-7.29E-01	3.13E-03	-1.30E+00	1.31E-04
490055700	FAD-binding protein	8.69E+00	7.14E-01	5.89E-02	-5.87E-01	1.32E-01	-1.30E+00	6.88E-03
497682479	tryptophan 2,3-dioxygenase	1.21E+01	1.36E+00	2.79E-04	6.27E-02	7.73E-01	-1.30E+00	4.64E-04

490052491	cysteine synthase	1.35E+01	-9.02E-01	3.58E-03	-2.20E+00	5.74E-05	-1.30E+00	7.49E-04
490056249	N-acetyltransferase GCN5	1.18E+01	9.89E-02	6.38E-01	-1.20E+00	9.63E-04	-1.30E+00	5.54E-04
490055136	membrane protein	8.75E+00	-1.31E+00	2.83E-03	-2.61E+00	1.25E-04	-1.30E+00	3.98E-03
490056669	aspartate aminotransferase	1.11E+01	2.62E-01	1.59E-01	-1.03E+00	9.67E-04	-1.29E+00	2.55E-04
490055242	Zn-dependent hydrolase	1.33E+01	8.87E-01	2.80E-03	-4.06E-01	8.97E-02	-1.29E+00	5.33E-04
490056091	hypothetical protein	1.03E+01	-1.47E+00	6.54E-04	-2.77E+00	4.04E-05	-1.29E+00	1.68E-03
490060225	transferase	1.23E+01	8.22E-01	2.44E-03	-4.70E-01	3.99E-02	-1.29E+00	3.09E-04
490052563	zinc-binding dehydrogenase	1.05E+01	-6.00E-01	6.02E-03	-1.89E+00	2.91E-05	-1.29E+00	1.58E-04
497681302	transcriptional regulator	1.19E+01	1.10E+00	3.67E-04	-1.91E-01	3.04E-01	-1.29E+00	2.03E-04
490055503	3-isopropylmalate dehydrogenase	1.29E+01	-2.38E-01	3.86E-01	-1.53E+00	1.16E-03	-1.29E+00	2.41E-03
490051570	molybdopterin biosynthesis MoeZ	1.28E+01	-2.57E-01	3.58E-01	-1.55E+00	1.20E-03	-1.29E+00	2.66E-03
490051029	DtxR family transcriptional regulator	1.42E+01	-1.25E+00	4.95E-04	-2.53E+00	2.28E-05	-1.29E+00	5.52E-04
490054080	30S ribosomal protein S4	1.46E+01	2.80E-01	5.68E-02	-1.00E+00	2.37E-04	-1.28E+00	5.54E-05
490054214	alanine racemase	1.27E+01	3.01E-01	1.23E-01	-9.83E-01	1.44E-03	-1.28E+00	3.11E-04
497681321	chorismate synthase	1.39E+01	8.80E-01	3.52E-04	-4.03E-01	2.20E-02	-1.28E+00	6.27E-05
490054167	50S ribosomal protein L11	1.31E+01	-4.74E-03	9.72E-01	-1.29E+00	3.09E-05	-1.28E+00	2.48E-05
490052433	cell division protein FtsE	1.29E+01	-1.16E+00	7.11E-03	-2.44E+00	2.51E-04	-1.28E+00	5.86E-03
490052765	protein disaggregation chaperone	1.27E+01	-8.25E-02	7.32E-01	-1.36E+00	9.34E-04	-1.28E+00	1.14E-03
490057218	sporulation protein	8.61E+00	-1.68E-01	4.10E-01	-1.44E+00	3.36E-04	-1.28E+00	5.53E-04
490057468	methionyl-tRNA formyltransferase	1.23E+01	2.13E-01	3.57E-01	-1.06E+00	3.13E-03	-1.28E+00	1.09E-03
490058843	preprotein translocase subunit YidC	1.52E+01	7.14E-01	1.62E-03	-5.60E-01	7.78E-03	-1.27E+00	1.03E-04
490054888	ribosome recycling factor	1.34E+01	-7.81E-01	1.73E-03	-2.06E+00	2.13E-05	-1.27E+00	1.76E-04
490056051	hypothetical protein	1.10E+01	9.63E-02	6.67E-01	-1.18E+00	1.43E-03	-1.27E+00	8.41E-04
497681728	5,10-methylenetetrahydrofolate reductase	1.54E+01	3.03E-01	2.81E-02	-9.69E-01	1.59E-04	-1.27E+00	3.33E-05
490054885	30S ribosomal protein S2	1.22E+01	-1.90E-01	4.49E-01	-1.46E+00	9.34E-04	-1.27E+00	1.67E-03
490059862	thiosulfate sulfurtransferase	1.27E+01	-1.61E-01	3.62E-01	-1.43E+00	1.69E-04	-1.27E+00	2.66E-04
490053036	NAD(P)H quinone oxidoreductase	1.43E+01	-1.42E+00	1.11E-03	-2.69E+00	6.14E-05	-1.27E+00	2.50E-03
497682195	ATP/GTP-binding protein	1.40E+01	8.80E-01	3.40E-03	-3.88E-01	1.11E-01	-1.27E+00	7.07E-04
490051665	arginine ABC transporter ATP-binding protein	1.44E+01	1.82E+00	2.44E-04	5.49E-01	7.51E-02	-1.27E+00	2.05E-03
490053282	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.17E+01	4.85E-01	1.51E-01	-7.83E-01	4.76E-02	-1.27E+00	5.97E-03

490055453	elongation factor 4	1.25E+01	8.37E-01	1.12E-03	-4.30E-01	3.36E-02	-1.27E+00	1.65E-04
490054068	Holliday junction DNA helicase RuvB	1.16E+01	-1.97E-01	1.91E-01	-1.46E+00	5.82E-05	-1.27E+00	1.01E-04
490058573	LuxR family transcriptional regulator	1.28E+01	-8.38E-01	4.13E-02	-2.10E+00	9.46E-04	-1.26E+00	1.02E-02
490058946	amidophosphoribosyltransferase	1.28E+01	-3.52E-01	2.57E-02	-1.62E+00	2.49E-05	-1.26E+00	6.45E-05
490052552	ABC transporter	1.05E+01	6.80E-01	7.50E-03	-5.83E-01	2.09E-02	-1.26E+00	4.48E-04
490051537	hypothetical protein	1.37E+01	1.28E+00	4.42E-03	2.18E-02	9.52E-01	-1.26E+00	6.41E-03
490056082	ABC transporter permease	9.08E+00	2.68E-01	2.63E-01	-9.91E-01	4.83E-03	-1.26E+00	1.29E-03
490055333	glutamyl-tRNA synthetase	1.35E+01	-3.51E-01	1.64E-01	-1.61E+00	4.69E-04	-1.26E+00	1.48E-03
490055879	AraC family transcriptional regulator	1.36E+01	-1.26E+00	8.85E-05	-2.52E+00	5.93E-06	-1.26E+00	1.09E-04
497682788	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.32E+01	3.15E-01	1.85E-01	-9.44E-01	5.36E-03	-1.26E+00	1.13E-03
490050027	thioredoxin	1.41E+01	1.98E-01	4.01E-01	-1.06E+00	3.48E-03	-1.26E+00	1.29E-03
490058363	hypothetical protein	1.41E+01	-1.80E-01	2.41E-01	-1.43E+00	7.25E-05	-1.26E+00	1.20E-04
490051185	thiosulfate sulfurtransferase	9.54E+00	1.85E-01	2.15E-01	-1.06E+00	2.89E-04	-1.25E+00	1.06E-04
497681225	hypothetical protein	1.53E+01	6.74E-01	7.07E-03	-5.71E-01	2.09E-02	-1.24E+00	4.32E-04
490051112	hypothetical protein	1.31E+01	4.54E-01	4.04E-02	-7.90E-01	5.68E-03	-1.24E+00	5.02E-04
490059144	D-alanine--D-alanine ligase	1.22E+01	-3.96E+00	9.13E-06	-5.20E+00	5.40E-06	-1.24E+00	4.06E-03
497684923	hypothetical protein	1.14E+01	-3.67E+00	3.63E-06	-4.91E+00	2.63E-06	-1.24E+00	8.68E-04
490054262	ABC transporter permease	1.36E+01	2.30E-01	2.75E-01	-1.01E+00	2.36E-03	-1.24E+00	7.23E-04
497682613	phosphomethylpyrimidine synthase	1.22E+01	-7.48E-01	7.02E-02	-1.99E+00	1.55E-03	-1.24E+00	1.35E-02
490054331	30S ribosomal protein S1	1.31E+01	-2.69E-01	8.06E-02	-1.51E+00	4.34E-05	-1.24E+00	9.65E-05
490054076	peptidylprolyl isomerase	1.32E+01	1.21E+00	2.67E-03	-2.25E-02	9.42E-01	-1.24E+00	3.19E-03
490054886	elongation factor Ts	1.40E+01	-6.78E-02	7.19E-01	-1.30E+00	3.34E-04	-1.24E+00	3.81E-04
497682153	signal peptide protein	1.18E+01	-4.96E-03	9.73E-01	-1.24E+00	5.27E-05	-1.23E+00	4.37E-05
490056793	MFS transporter	1.41E+01	-6.12E-02	6.89E-01	-1.29E+00	1.20E-04	-1.23E+00	1.28E-04
490056069	acetylornithine aminotransferase	1.22E+01	-3.59E-01	5.85E-02	-1.59E+00	8.43E-05	-1.23E+00	2.69E-04
490059917	ornithine carbamoyltransferase	1.56E+01	-5.61E-01	2.36E-02	-1.79E+00	1.27E-04	-1.23E+00	7.77E-04
497681429	GntR family transcriptional regulator	1.44E+01	-4.61E-01	1.73E-01	-1.69E+00	1.70E-03	-1.23E+00	7.27E-03
490057818	excinuclease ABC subunit B	1.37E+01	3.41E-01	1.73E-01	-8.84E-01	9.04E-03	-1.23E+00	1.65E-03
490057924	membrane protein	1.50E+01	1.19E+00	4.01E-05	-3.84E-02	7.68E-01	-1.23E+00	4.17E-05
490054881	lipoprotein oligopeptide binding protein	1.56E+01	-3.61E-01	1.99E-01	-1.58E+00	9.67E-04	-1.22E+00	3.17E-03
490059049	Hypothetical protein	1.12E+01	-1.79E-02	9.27E-01	-1.24E+00	2.75E-04	-1.22E+00	2.55E-04

490050050	ABC transporter ATP-binding protein	1.20E+01	-5.20E-01	1.26E-02	-1.74E+00	4.79E-05	-1.22E+00	2.48E-04
497682582	putative two-component system sensor kinase/response regulator, bifunctional protein	1.38E+01	3.45E-01	1.51E-01	-8.67E-01	7.95E-03	-1.21E+00	1.37E-03
497685379	DNA-binding protein	1.54E+01	1.18E-01	6.46E-01	-1.09E+00	4.16E-03	-1.21E+00	2.19E-03
490050144	deacetoxycephalosporin C synthetase	1.07E+01	-1.71E+00	3.30E-05	-2.92E+00	5.50E-06	-1.21E+00	2.50E-04
490054392	RNA pseudouridine synthase	1.32E+01	3.84E-01	1.12E-02	-8.26E-01	3.86E-04	-1.21E+00	4.51E-05
490055930	dihydrodipicolinate reductase	1.38E+01	-1.28E-01	3.28E-01	-1.34E+00	5.11E-05	-1.21E+00	6.94E-05
497683211	cystathionine gamma-synthase	1.11E+01	-1.33E+00	9.50E-04	-2.54E+00	5.22E-05	-1.21E+00	2.05E-03
497683091	acetyltransferase	1.46E+01	4.06E-01	3.73E-02	-8.01E-01	2.77E-03	-1.21E+00	2.89E-04
490061204	lipase	1.38E+01	-7.42E-01	3.49E-03	-1.95E+00	3.98E-05	-1.21E+00	3.85E-04
490059935	hypothetical protein	1.30E+01	7.68E-01	2.92E-03	-4.38E-01	4.62E-02	-1.21E+00	3.81E-04
497685275	GCN5 family acetyltransferase	1.22E+01	-5.73E-01	3.96E-02	-1.78E+00	2.96E-04	-1.21E+00	1.94E-03
490058627	hypothetical protein	1.25E+01	9.19E-01	4.30E-04	-2.86E-01	9.41E-02	-1.21E+00	1.32E-04
490050491	ABC transporter	1.36E+01	9.65E-01	1.25E-02	-2.38E-01	4.73E-01	-1.20E+00	6.18E-03
490050482	acetyltransferase	1.10E+01	2.81E-01	2.39E-01	-9.21E-01	6.57E-03	-1.20E+00	1.56E-03
490054061	pyridoxal biosynthesis lyase	1.32E+01	1.01E+00	2.30E-04	-1.91E-01	2.27E-01	-1.20E+00	1.17E-04
490053475	ABC transporter	1.53E+01	6.08E-01	3.19E-03	-5.90E-01	5.55E-03	-1.20E+00	1.25E-04
490058394	NAD-glutamate dehydrogenase	1.27E+01	1.19E-01	5.20E-01	-1.08E+00	9.13E-04	-1.20E+00	4.61E-04
490054153	50S ribosomal protein L3	1.35E+01	2.84E-03	9.88E-01	-1.19E+00	3.39E-04	-1.20E+00	2.88E-04
490053047	pyruvate dehydrogenase E1 subunit alpha	1.32E+01	2.99E-01	2.33E-01	-8.98E-01	9.20E-03	-1.20E+00	2.05E-03
497683461	dynein regulation protein LC7	1.68E+01	-9.29E-01	1.66E-03	-2.13E+00	3.74E-05	-1.20E+00	5.90E-04
490058352	nucleoside-triphosphate diphosphatase	1.28E+01	6.03E-01	8.29E-03	-5.92E-01	1.29E-02	-1.19E+00	3.55E-04
490054159	elongation factor G	1.22E+01	8.12E-01	1.88E-04	-3.82E-01	1.17E-02	-1.19E+00	3.29E-05
497683716	sugar ABC transporter substrate-binding protein	1.20E+01	1.16E+00	9.65E-05	-3.66E-02	8.06E-01	-1.19E+00	1.01E-04
490051515	succinyl-diaminopimelate desuccinylase	1.38E+01	3.39E-01	3.74E-02	-8.54E-01	7.97E-04	-1.19E+00	1.17E-04
490053991	hypothetical protein	1.39E+01	-3.04E-01	4.45E-02	-1.50E+00	3.53E-05	-1.19E+00	8.83E-05
497683179	beta-N-acetylglucosaminidase	1.48E+01	1.49E+00	2.04E-05	2.98E-01	5.81E-02	-1.19E+00	7.47E-05
490057664	acyl-CoA dehydrogenase	1.35E+01	-5.97E-01	1.03E-02	-1.79E+00	6.45E-05	-1.19E+00	4.50E-04
490058132	deoxyguanosinetriphosphate triphosphohydrolase	1.34E+01	6.90E-01	4.04E-04	-4.98E-01	3.22E-03	-1.19E+00	3.15E-05
497682617	beta-lactamase	1.31E+01	3.41E-01	7.17E-02	-8.47E-01	2.27E-03	-1.19E+00	3.43E-04
490053816	phosphocarrier protein HPr	1.11E+01	1.01E-01	4.76E-01	-1.09E+00	2.32E-04	-1.19E+00	1.22E-04

497683812	isopentenyl-diphosphate delta-isomerase	1.04E+01	-1.14E+00	7.41E-04	-2.33E+00	3.09E-05	-1.19E+00	8.00E-04
490058354	ribonuclease PH	1.34E+01	7.06E-01	9.61E-03	-4.78E-01	6.06E-02	-1.18E+00	1.03E-03
497683594	hypothetical protein	1.54E+01	3.78E-01	5.23E-02	-8.05E-01	3.07E-03	-1.18E+00	3.68E-04
490060366	TetR family transcriptional regulator	1.56E+01	3.13E-01	2.35E-02	-8.64E-01	2.68E-04	-1.18E+00	4.52E-05
490057415	dynein regulation protein LC7	1.34E+01	-1.88E+00	2.55E-04	-3.05E+00	3.37E-05	-1.18E+00	3.69E-03
490051741	PucR family transcriptional regulator	1.12E+01	-5.67E-01	2.83E-02	-1.74E+00	1.97E-04	-1.18E+00	1.32E-03
497685177	DNA primase	1.31E+01	4.15E-01	5.51E-02	-7.53E-01	7.11E-03	-1.17E+00	7.03E-04
490050197	DNA-binding protein	9.67E+00	-1.17E+00	9.20E-04	-2.34E+00	4.11E-05	-1.17E+00	1.24E-03
497683551	(dimethylallyl)adenosine tRNA methylthiotransferase	1.15E+01	1.69E+00	3.61E-05	5.26E-01	1.72E-02	-1.17E+00	3.10E-04
497684167	3-oxoacyl-ACP reductase	1.41E+01	7.39E-01	1.33E-02	-4.26E-01	1.20E-01	-1.17E+00	2.05E-03
490059603	radical SAM protein	1.31E+01	-2.10E+00	4.23E-04	-3.26E+00	6.61E-05	-1.16E+00	1.04E-02
490056765	conserved hypothetical protein	1.37E+01	-1.61E+00	1.50E-05	-2.77E+00	3.04E-06	-1.16E+00	9.03E-05
490054141	50S ribosomal protein L5	1.44E+01	7.63E-01	1.29E-03	-4.00E-01	3.45E-02	-1.16E+00	1.84E-04
490056854	hypothetical protein	1.46E+01	-7.76E-02	5.72E-01	-1.24E+00	9.51E-05	-1.16E+00	1.09E-04
490055924	ribonuclease	1.30E+01	7.77E-02	6.31E-01	-1.08E+00	4.22E-04	-1.16E+00	2.54E-04
490052729	conserved hypothetical protein	1.11E+01	5.31E-01	3.05E-02	-6.27E-01	2.23E-02	-1.16E+00	1.13E-03
490051024	DNA primase	1.20E+01	-7.30E-01	1.01E-03	-1.89E+00	1.48E-05	-1.16E+00	1.16E-04
490051626	ribonucleoside-diphosphate reductase	1.21E+01	6.77E-01	5.02E-02	-4.79E-01	1.67E-01	-1.16E+00	7.46E-03
497682351	protein-L-isoaspartate O-methyltransferase	1.28E+01	-1.90E+00	2.68E-04	-3.06E+00	3.74E-05	-1.16E+00	4.57E-03
497681079	hypothetical protein	1.74E+01	9.06E-01	1.14E-02	-2.48E-01	4.18E-01	-1.15E+00	5.06E-03
497683199	purine nucleoside phosphorylase	1.43E+01	5.89E-01	2.49E-03	-5.63E-01	4.65E-03	-1.15E+00	9.96E-05
490056523	30S ribosomal protein S6 modification enzyme RimK	1.27E+01	2.41E-01	1.27E-01	-9.10E-01	7.28E-04	-1.15E+00	1.83E-04
490057108	methylmalonyl-CoA mutase	1.38E+01	4.76E-01	8.11E-02	-6.73E-01	3.34E-02	-1.15E+00	2.80E-03
490053814	protease	1.32E+01	-8.50E-01	1.16E-03	-2.00E+00	2.40E-05	-1.15E+00	3.11E-04
490051594	hydrolase	1.13E+01	-3.39E-01	2.42E-01	-1.49E+00	1.61E-03	-1.15E+00	5.23E-03
490052772	hypothetical protein	1.01E+01	1.55E+00	8.17E-05	4.04E-01	6.07E-02	-1.15E+00	4.97E-04
490051743	beta-lactamase	1.09E+01	3.16E-01	2.53E-02	-8.27E-01	3.89E-04	-1.14E+00	6.13E-05
490055373	aminotransferase	1.51E+01	1.07E+00	1.70E-03	-7.71E-02	7.50E-01	-1.14E+00	1.57E-03
490056579	UDP-glucose 4-epimerase	1.32E+01	7.66E-01	2.16E-04	-3.75E-01	1.11E-02	-1.14E+00	3.56E-05
497681294	DeoR family transcriptional regulator	1.34E+01	3.79E-01	9.13E-02	-7.62E-01	9.04E-03	-1.14E+00	1.12E-03

490054150	50S ribosomal protein L2	1.36E+01	-5.18E-01	2.39E-02	-1.66E+00	1.28E-04	-1.14E+00	7.79E-04
490051801	O-methyltransferase	1.37E+01	1.61E-03	9.93E-01	-1.14E+00	3.43E-04	-1.14E+00	2.93E-04
490055926	FAD-dependent thymidylate synthase	1.46E+01	7.41E-01	2.79E-03	-3.97E-01	5.49E-02	-1.14E+00	4.04E-04
490052578	DeoR family transcripitonal regulator	8.23E+00	-9.72E-01	1.87E-03	-2.11E+00	5.35E-05	-1.14E+00	1.11E-03
490054162	DNA-directed RNA polymerase subunit beta'	1.26E+01	-2.66E-02	8.74E-01	-1.16E+00	2.51E-04	-1.14E+00	2.43E-04
490052582	phosphomannomutase	1.29E+01	5.65E-02	6.57E-01	-1.08E+00	1.22E-04	-1.14E+00	7.78E-05
490058185	membrane protein	1.17E+01	5.64E-01	9.10E-02	-5.69E-01	1.10E-01	-1.13E+00	8.21E-03
497681813	LacI family transcriptional regulator	1.68E+01	-2.29E-01	1.76E-01	-1.36E+00	1.46E-04	-1.13E+00	3.27E-04
490054387	isoleucyl-tRNA synthase	1.30E+01	-1.77E-01	2.34E-01	-1.31E+00	9.91E-05	-1.13E+00	1.76E-04
497685350	oxidoreductase	1.36E+01	-1.61E+00	2.05E-04	-2.74E+00	2.30E-05	-1.13E+00	1.66E-03
497682414	oxidoreductase	1.32E+01	3.20E-01	2.98E-02	-8.10E-01	5.70E-04	-1.13E+00	8.65E-05
490059221	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	1.43E+01	-4.84E-01	2.09E-02	-1.61E+00	8.76E-05	-1.13E+00	4.76E-04
490052907	alkyl hydroperoxide reductase	1.36E+01	7.46E-02	7.65E-01	-1.05E+00	3.77E-03	-1.13E+00	2.34E-03
490057549	phenylalanyl-tRNA synthetase subunit beta	1.26E+01	-1.80E-01	2.10E-01	-1.31E+00	8.21E-05	-1.13E+00	1.47E-04
490057784	iron ABC transporter ATP-binding protein	1.29E+01	-9.61E-02	7.02E-01	-1.22E+00	2.04E-03	-1.13E+00	2.71E-03
490057893	histidinol-phosphate aminotransferase	1.42E+01	3.68E-01	9.77E-03	-7.57E-01	4.07E-04	-1.12E+00	4.47E-05
490050636	conserved hypothetical protein	9.29E+00	-1.88E+00	1.28E-04	-3.00E+00	2.05E-05	-1.12E+00	2.32E-03
497685533	acyl-CoA dehydrogenase	8.70E+00	-3.22E-01	1.10E-01	-1.44E+00	2.23E-04	-1.12E+00	7.24E-04
490054423	phosphoribosylaminoimidazole carboxylase	1.29E+01	-1.35E-01	6.55E-01	-1.26E+00	4.66E-03	-1.12E+00	7.16E-03
490051512	ferredoxin	1.41E+01	1.42E-01	4.09E-01	-9.77E-01	1.07E-03	-1.12E+00	4.61E-04
490054284	glutamine-synthetase adenylyltransferase	1.35E+01	4.56E-01	3.34E-02	-6.63E-01	1.01E-02	-1.12E+00	6.87E-04
490057459	inosine 5'-monophosphate dehydrogenase	1.06E+01	4.88E-01	1.51E-01	-6.31E-01	9.53E-02	-1.12E+00	1.10E-02
497681677	prolipoprotein diacylglyceryl transferase	1.08E+01	7.55E-01	6.46E-04	-3.62E-01	2.92E-02	-1.12E+00	1.06E-04
490054142	50S ribosomal protein L24	1.35E+01	-1.06E-01	7.02E-01	-1.22E+00	3.37E-03	-1.12E+00	4.68E-03
497683782	DNA-binding protein	1.25E+01	3.06E-01	7.30E-02	-8.08E-01	1.73E-03	-1.11E+00	2.82E-04
490057189	heat shock protein 90	1.31E+01	-8.22E-01	1.62E-02	-1.93E+00	3.78E-04	-1.11E+00	5.58E-03
497682945	threonine synthase	1.20E+01	-1.08E+00	1.59E-04	-2.19E+00	8.55E-06	-1.11E+00	1.71E-04
490057753	2,4-diaminobutyric acid acetyltransferase	1.27E+01	3.64E-01	7.47E-02	-7.43E-01	6.31E-03	-1.11E+00	7.56E-04
490054221	single-stranded DNA-binding protein	1.23E+01	1.56E+00	4.63E-05	4.54E-01	2.75E-02	-1.11E+00	3.42E-04
490057550	phenylalanyl-tRNA synthetase subunit alpha	1.27E+01	8.48E-01	1.25E-03	-2.59E-01	1.67E-01	-1.11E+00	4.13E-04

497682483	hypothetical protein	1.00E+01	5.81E-01	1.93E-03	-5.25E-01	4.75E-03	-1.11E+00	8.83E-05
497681843	oxidoreductase	1.32E+01	-2.38E-03	9.87E-01	-1.11E+00	1.28E-04	-1.11E+00	1.08E-04
490052610	pyrimidine-nucleoside phosphorylase	1.22E+01	9.82E-01	6.97E-03	-1.23E-01	6.77E-01	-1.11E+00	5.35E-03
490059709	hypothetical protein	7.67E+00	1.22E+00	3.81E-04	1.18E-01	5.66E-01	-1.11E+00	8.50E-04
490708574	ligase	1.18E+01	4.88E-01	2.41E-03	-6.17E-01	1.10E-03	-1.11E+00	4.51E-05
490055961	chitinase	1.80E+01	1.37E+00	1.76E-04	2.67E-01	1.93E-01	-1.10E+00	7.00E-04
490059418	fumarate hydratase	1.27E+01	-1.25E-01	4.11E-01	-1.23E+00	1.74E-04	-1.10E+00	2.57E-04
490057793	glucose-6-phosphate 1-dehydrogenase	1.36E+01	6.39E-01	6.64E-03	-4.64E-01	3.59E-02	-1.10E+00	5.67E-04
490059459	DEAD/DEAH box helicase	1.26E+01	9.30E-01	2.39E-04	-1.72E-01	2.40E-01	-1.10E+00	1.24E-04
490055118	enolase	1.23E+01	9.12E-02	6.01E-01	-1.01E+00	8.94E-04	-1.10E+00	4.95E-04
497681812	alpha-glucosidase	1.37E+01	-5.18E-01	8.62E-03	-1.62E+00	4.28E-05	-1.10E+00	2.55E-04
497681088	UDP-N-acetylglucosamine 2-epimerase	1.30E+01	-1.97E+00	2.00E-05	-3.07E+00	5.34E-06	-1.10E+00	4.95E-04
497683618	1-deoxy-D-xylulose-5-phosphate synthase	1.34E+01	-6.60E-02	7.00E-01	-1.16E+00	3.60E-04	-1.10E+00	4.24E-04
490055452	AMP-dependent synthetase	1.26E+01	4.02E-01	1.25E-01	-6.97E-01	2.74E-02	-1.10E+00	3.23E-03
497682539	hypothetical protein	1.30E+01	5.36E-01	5.36E-03	-5.62E-01	6.32E-03	-1.10E+00	1.80E-04
497681436	hypothetical protein	1.44E+01	5.17E-01	1.52E-02	-5.77E-01	1.37E-02	-1.09E+00	5.30E-04
490060241	alpha-galactosidase	1.26E+01	7.63E-03	9.70E-01	-1.09E+00	4.26E-04	-1.09E+00	3.59E-04
490056603	hydrolase	1.67E+01	-2.03E-01	3.16E-01	-1.30E+00	5.39E-04	-1.09E+00	1.15E-03
490058279	Aldolase	1.25E+01	1.75E+00	8.97E-04	6.56E-01	8.27E-02	-1.09E+00	1.17E-02
497683895	hypothetical protein	1.35E+01	1.58E-01	3.72E-01	-9.31E-01	1.53E-03	-1.09E+00	5.94E-04
490708573	glutamine amidotransferase	1.40E+01	3.72E-02	8.16E-01	-1.05E+00	3.69E-04	-1.09E+00	2.64E-04
490058534	glutamyl-tRNA reductase	1.34E+01	-2.09E-01	2.97E-01	-1.29E+00	5.03E-04	-1.08E+00	1.11E-03
490052467	4-hydroxyphenylpyruvate dioxygenase	1.55E+01	8.62E-01	2.91E-03	-2.21E-01	3.12E-01	-1.08E+00	1.22E-03
497682218	type II restriction endonuclease subunit M	1.16E+01	1.92E-01	2.65E-01	-8.89E-01	1.59E-03	-1.08E+00	5.05E-04
490051580	NUDIX hydrolase	1.29E+01	8.99E-01	1.87E-03	-1.79E-01	3.86E-01	-1.08E+00	9.84E-04
497685265	LuxR family transcriptional regulator	1.04E+01	-1.61E+00	2.70E-05	-2.69E+00	5.34E-06	-1.08E+00	2.72E-04
490051505	acyl-CoA synthetase	1.06E+01	7.89E-01	4.42E-03	-2.86E-01	2.00E-01	-1.08E+00	1.26E-03
490050917	arginyl-tRNA synthetase	1.27E+01	1.02E-01	5.11E-01	-9.72E-01	6.25E-04	-1.07E+00	3.24E-04
490053384	N-acetyltransferase GCN5	1.46E+01	8.19E-01	6.83E-03	-2.55E-01	3.05E-01	-1.07E+00	2.41E-03
490051406	N-acetylglucosamine-1-phosphate uridyltransferase	1.31E+01	4.02E-01	1.56E-01	-6.70E-01	4.47E-02	-1.07E+00	5.78E-03

490058026	Phenazine biosynthesis PhzC/PhzF protein	1.54E+01	1.09E-01	5.17E-01	-9.60E-01	1.05E-03	-1.07E+00	5.22E-04
497684104	parB-like partition protein	1.23E+01	5.12E-02	8.04E-01	-1.02E+00	1.68E-03	-1.07E+00	1.15E-03
490052953	peptide ABC transporter ATPase	1.25E+01	3.66E-01	2.44E-01	-7.00E-01	5.92E-02	-1.07E+00	1.07E-02
490054398	DSBA oxidoreductase	1.44E+01	6.81E-01	4.23E-02	-3.84E-01	2.40E-01	-1.06E+00	8.95E-03
490059691	aminoglycoside 2'-N-acetyltransferase	1.32E+01	-8.98E-01	1.31E-02	-1.96E+00	4.28E-04	-1.06E+00	8.27E-03
497682009	gamma-glutamyl phosphate reductase	1.27E+01	-9.36E-01	3.94E-03	-2.00E+00	1.24E-04	-1.06E+00	2.79E-03
490059367	GlcNAc-PI de-N-acetylase	1.35E+01	-9.65E-01	1.43E-04	-2.02E+00	7.21E-06	-1.06E+00	1.11E-04
497683979	alpha/beta hydrolase	1.28E+01	-1.12E-02	9.69E-01	-1.07E+00	2.60E-03	-1.06E+00	2.39E-03
490057082	radical SAM protein	1.24E+01	-5.12E-01	1.65E-02	-1.57E+00	1.00E-04	-1.05E+00	6.73E-04
497681488	NUDIX hydrolase	1.43E+01	-3.39E-01	1.84E-01	-1.39E+00	1.09E-03	-1.05E+00	3.95E-03
490059421	polyphosphate glucokinase	1.27E+01	3.04E-01	1.40E-01	-7.44E-01	7.68E-03	-1.05E+00	1.27E-03
490056068	acetylglutamate kinase	1.45E+01	-1.20E+00	5.82E-04	-2.25E+00	3.73E-05	-1.05E+00	1.58E-03
490059789	hypothetical protein	1.30E+01	2.53E-01	1.92E-01	-7.92E-01	4.81E-03	-1.05E+00	1.06E-03
490053517	hypothetical protein	1.25E+01	-3.36E-01	2.25E-02	-1.38E+00	3.51E-05	-1.04E+00	1.13E-04
497682004	nicotinic acid mononucleotide adenylyltransferase	1.32E+01	5.44E-02	7.02E-01	-9.84E-01	3.33E-04	-1.04E+00	2.14E-04
490056421	DNA-binding protein	1.10E+01	-2.97E-01	1.40E-01	-1.33E+00	3.69E-04	-1.04E+00	1.20E-03
497681765	phage-shock protein	1.21E+01	-1.39E-01	3.23E-01	-1.17E+00	1.36E-04	-1.04E+00	2.23E-04
490053904	hypothetical protein	1.23E+01	1.33E+00	2.22E-04	2.98E-01	1.59E-01	-1.04E+00	1.09E-03
490060544	N-acetyltransferase GCN5	9.59E+00	7.61E-01	5.32E-03	-2.73E-01	2.21E-01	-1.03E+00	1.54E-03
490051136	hypothetical protein	1.23E+01	2.23E-01	7.90E-02	-8.09E-01	3.78E-04	-1.03E+00	9.04E-05
497683813	transferase	1.52E+01	4.52E-01	2.35E-02	-5.79E-01	1.19E-02	-1.03E+00	6.25E-04
490055126	ABC transporter	1.37E+01	4.32E-01	7.34E-03	-6.00E-01	2.24E-03	-1.03E+00	1.14E-04
490054363	plant-type carbonic anhydrase	1.58E+01	1.38E+00	1.24E-04	3.52E-01	8.31E-02	-1.03E+00	7.28E-04
490060702	SAM-dependent methyltransferase	1.67E+01	-3.46E-01	5.57E-02	-1.38E+00	1.34E-04	-1.03E+00	5.24E-04
497683243	ATP-binding protein	1.13E+01	-7.65E-01	1.30E-03	-1.79E+00	2.69E-05	-1.03E+00	3.63E-04
490058278	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase	1.46E+01	6.40E-01	4.01E-03	-3.88E-01	4.70E-02	-1.03E+00	4.76E-04
497682494	membrane protein	8.49E+00	3.43E-01	7.90E-02	-6.85E-01	7.48E-03	-1.03E+00	8.92E-04
497681460	C4-dicarboxylate ABC transporter substrate-binding protein	1.38E+01	-6.26E-01	1.82E-03	-1.65E+00	2.20E-05	-1.03E+00	1.81E-04
490051939	hypothetical protein	1.44E+01	-8.64E-01	5.55E-04	-1.89E+00	1.84E-05	-1.03E+00	2.96E-04
490057810	FeS-binding protein	1.14E+01	-4.21E-02	7.98E-01	-1.06E+00	4.00E-04	-1.02E+00	4.32E-04

490051633	sugar ABC transporter permease	1.26E+01	5.19E-01	3.22E-02	-5.02E-01	4.97E-02	-1.02E+00	2.04E-03
490058553	DNA integrity scanning protein disA	1.29E+01	3.05E-01	1.51E-01	-7.15E-01	1.07E-02	-1.02E+00	1.73E-03
490055760	riboflavin synthase subunit alpha	1.37E+01	-1.72E-01	2.97E-01	-1.19E+00	2.85E-04	-1.02E+00	5.56E-04
490050708	phosphopantetheine--protein transferase	1.36E+01	-3.89E-02	8.53E-01	-1.05E+00	1.35E-03	-1.01E+00	1.44E-03
490058177	phosphoglycerate mutase	1.24E+01	2.30E-01	4.12E-01	-7.77E-01	2.94E-02	-1.01E+00	9.07E-03
497683256	DNA mismatch repair protein MutT	1.33E+01	-3.28E-01	5.57E-02	-1.33E+00	1.22E-04	-1.00E+00	4.57E-04
490054297	membrane protein	1.42E+01	8.87E-01	6.01E-03	-1.17E-01	6.51E-01	-1.00E+00	4.42E-03
497682607	hydrolase	1.33E+01	-4.69E-01	1.16E-02	-1.47E+00	5.88E-05	-1.00E+00	3.61E-04
490054072	adenine phosphoribosyltransferase	1.35E+01	-7.66E-01	7.95E-04	-1.77E+00	1.94E-05	-1.00E+00	2.54E-04
490056426	DNA gyrase subunit A	1.36E+01	9.06E-01	5.22E-04	-9.58E-02	5.54E-01	-1.00E+00	4.08E-04
490058249	ABC transporter ATP-binding protein	1.33E+01	-3.67E-01	2.49E-02	-1.36E+00	6.39E-05	-9.94E-01	2.71E-04
497685232	short-chain dehydrogenase	8.76E+00	-1.32E+00	2.82E-03	-2.31E+00	2.37E-04	-9.93E-01	1.39E-02
490052461	hypothetical protein	1.68E+01	3.14E-01	1.55E-01	-6.79E-01	1.61E-02	-9.93E-01	2.45E-03
490053245	MFS transporter	1.15E+01	7.25E-01	1.01E-02	-2.66E-01	2.72E-01	-9.91E-01	3.07E-03
490054700	triosephosphate isomerase	1.24E+01	1.12E+00	1.90E-03	1.34E-01	6.03E-01	-9.90E-01	4.73E-03
490057483	alanyl-tRNA synthetase	1.34E+01	-2.03E-02	8.89E-01	-1.01E+00	2.59E-04	-9.89E-01	2.47E-04
490057356	3-ketoacyl-ACP reductase	1.26E+01	6.24E-01	9.91E-03	-3.65E-01	9.64E-02	-9.89E-01	1.42E-03
497684432	hypothetical protein	1.13E+01	-4.16E+00	1.15E-06	-5.15E+00	4.81E-07	-9.89E-01	2.57E-04
497681576	NAD-dependent dehydratase	1.08E+01	-4.75E-01	2.77E-02	-1.46E+00	1.91E-04	-9.87E-01	1.28E-03
490055954	amino acid deaminase	1.66E+01	9.30E-01	7.80E-04	-5.27E-02	7.71E-01	-9.83E-01	7.71E-04
490061312	alkylhydroperoxidase	1.06E+01	-2.58E+00	2.79E-06	-3.56E+00	1.81E-06	-9.83E-01	3.26E-04
490054702	electron transporter	1.19E+01	-1.23E-01	4.20E-01	-1.10E+00	3.03E-04	-9.82E-01	4.87E-04
490057744	magnesium chelatase	1.34E+01	3.05E-01	1.40E-01	-6.77E-01	1.20E-02	-9.82E-01	1.81E-03
490054708	oxppcycle protein	1.41E+01	-1.39E+00	3.29E-04	-2.37E+00	3.39E-05	-9.81E-01	2.57E-03
490059191	hypothetical protein	1.46E+01	-5.84E-01	1.36E-02	-1.56E+00	1.57E-04	-9.81E-01	1.53E-03
497683997	MarR family transcriptional regulator	1.38E+01	-8.66E-02	4.23E-01	-1.07E+00	6.29E-05	-9.80E-01	7.95E-05
490051055	fatty acid--CoA ligase	1.06E+01	5.61E-01	1.70E-02	-4.17E-01	6.92E-02	-9.79E-01	1.66E-03
497684454	hypothetical protein	1.14E+01	-4.10E+00	2.19E-06	-5.07E+00	2.14E-06	-9.77E-01	2.56E-03
490055557	hypothetical protein	1.17E+01	8.24E-01	1.86E-03	-1.52E-01	4.20E-01	-9.76E-01	1.04E-03
490057967	dihydrolipoamide acyltransferase	9.18E+00	7.09E-01	3.87E-02	-2.66E-01	4.10E-01	-9.75E-01	1.42E-02
490058130	DNA primase	1.16E+01	-7.33E-02	5.76E-01	-1.04E+00	1.81E-04	-9.68E-01	2.25E-04

490058906	RNA polymerase sigma factor	9.61E+00	-7.00E-01	8.32E-03	-1.67E+00	1.60E-04	-9.67E-01	2.30E-03
490057346	transcriptional regulator	1.01E+01	1.20E-01	6.24E-01	-8.47E-01	1.09E-02	-9.67E-01	5.43E-03
497681484	GTP-binding protein Der	1.19E+01	1.91E-01	4.11E-01	-7.75E-01	1.37E-02	-9.66E-01	4.57E-03
490058391	serine/threonine-protein kinase	1.12E+01	3.09E-01	1.74E-02	-6.52E-01	7.28E-04	-9.61E-01	8.19E-05
490056623	acyl carrier protein	1.15E+01	-3.16E+00	1.71E-05	-4.12E+00	8.33E-06	-9.60E-01	8.74E-03
490051655	deaminase	1.09E+01	-3.28E-01	2.41E-01	-1.28E+00	2.88E-03	-9.55E-01	1.04E-02
490050933	membrane protein	1.27E+01	2.22E-01	1.53E-01	-7.32E-01	2.21E-03	-9.55E-01	4.93E-04
490055447	molecular chaperone DnaJ	1.36E+01	2.74E-01	2.03E-01	-6.79E-01	1.53E-02	-9.53E-01	2.85E-03
490058277	methylmalonate-semialdehyde dehydrogenase	1.34E+01	-2.42E-01	1.50E-01	-1.19E+00	2.64E-04	-9.51E-01	7.51E-04
490055913	1-acyl-sn-glycerol-3-phosphate acyltransferase	1.40E+01	6.11E-01	2.81E-03	-3.35E-01	5.12E-02	-9.46E-01	3.90E-04
490053401	IolB protein	1.50E+01	3.28E-01	3.39E-02	-6.16E-01	3.17E-03	-9.44E-01	3.03E-04
490058041	XRE family transcriptional regulator	1.05E+01	-1.32E+00	1.75E-04	-2.26E+00	1.96E-05	-9.43E-01	1.30E-03
490057910	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	1.40E+01	-4.43E-01	3.06E-02	-1.38E+00	2.04E-04	-9.36E-01	1.33E-03
497681699	mechanosensitive ion channel protein	1.21E+01	2.68E+00	1.27E-05	1.75E+00	1.54E-04	-9.35E-01	3.36E-03
490051579	peptidase M20	1.30E+01	7.75E-02	5.16E-01	-8.55E-01	3.18E-04	-9.33E-01	1.73E-04
497683533	regulatory protein	1.47E+01	-7.38E-01	3.23E-03	-1.67E+00	7.51E-05	-9.31E-01	1.34E-03
490051756	chemical-damaging agent resistance protein C	1.23E+01	1.87E-01	3.69E-01	-7.43E-01	1.01E-02	-9.30E-01	3.13E-03
497683252	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	1.46E+01	-1.14E+00	5.91E-04	-2.07E+00	4.28E-05	-9.28E-01	2.20E-03
497681774	dihydrolipoamide dehydrogenase	1.16E+01	5.87E-01	9.53E-03	-3.40E-01	9.66E-02	-9.27E-01	1.38E-03
497682262	esterase	1.37E+01	-9.98E-01	1.43E-04	-1.92E+00	9.86E-06	-9.21E-01	2.73E-04
490055338	dynein regulation protein LC7	1.31E+01	-1.77E+00	1.49E-04	-2.69E+00	2.88E-05	-9.19E-01	5.58E-03
490054711	transketolase	1.17E+01	5.86E-01	1.66E-03	-3.30E-01	3.21E-02	-9.16E-01	2.12E-04
490050104	diaminopimelate decarboxylase	1.32E+01	-9.27E-02	5.22E-01	-1.01E+00	3.70E-04	-9.15E-01	5.32E-04
490058669	precorrin-3B C17-methyltransferase	1.57E+01	8.00E-01	1.83E-04	-1.12E-01	3.39E-01	-9.12E-01	1.15E-04
490053010	hypothetical protein	1.26E+01	-5.31E-01	8.85E-03	-1.44E+00	9.02E-05	-9.05E-01	8.58E-04
497682442	hypothetical protein	1.07E+01	-1.67E-01	5.16E-01	-1.07E+00	5.01E-03	-9.03E-01	9.87E-03
490051666	ABC transporter permease	1.14E+01	2.00E-02	9.30E-01	-8.75E-01	3.50E-03	-8.95E-01	2.74E-03
497681649	aminopeptidase N	1.32E+01	-3.38E-01	9.81E-03	-1.23E+00	2.49E-05	-8.95E-01	9.58E-05
490058867	para-aminobenzoate synthase	1.61E+01	6.09E-01	3.16E-03	-2.85E-01	9.11E-02	-8.94E-01	5.92E-04
490060391	hisitidine kinase	1.36E+01	4.63E-01	3.48E-02	-4.31E-01	6.04E-02	-8.94E-01	2.47E-03

490056008	hypothetical protein	1.33E+01	2.08E-01	2.65E-01	-6.86E-01	8.33E-03	-8.94E-01	2.05E-03
497684011	GDP-mannose 6-dehydrogenase	1.23E+01	-2.24E+00	7.36E-05	-3.13E+00	2.27E-05	-8.92E-01	9.80E-03
490057153	short-chain dehydrogenase	1.31E+01	6.71E-01	8.49E-03	-2.21E-01	3.03E-01	-8.92E-01	2.88E-03
490053914	LuxR family transcriptional regulator	1.37E+01	-1.33E+00	1.36E-04	-2.22E+00	1.81E-05	-8.91E-01	1.40E-03
490060667	cytochrome P450	1.28E+01	-7.41E-01	5.13E-03	-1.63E+00	1.40E-04	-8.89E-01	2.79E-03
490053861	radical SAM protein	1.35E+01	-7.78E-04	9.97E-01	-8.87E-01	1.51E-03	-8.87E-01	1.33E-03
490056431	DNA polymerase III subunit beta	1.17E+01	-2.39E-01	2.33E-01	-1.12E+00	1.02E-03	-8.85E-01	3.03E-03
490054251	cytochrome BD ubiquinol oxidase subunit I	1.28E+01	1.45E+00	7.98E-05	5.62E-01	1.29E-02	-8.84E-01	1.31E-03
497683562	RNA polymerase sigma factor	1.33E+01	6.66E-02	6.48E-01	-8.16E-01	1.05E-03	-8.83E-01	6.08E-04
490054878	3-ketoacyl-ACP reductase	1.24E+01	-1.34E-01	3.20E-01	-1.02E+00	2.26E-04	-8.83E-01	4.10E-04
497683249	hypothetical protein	1.44E+01	4.09E-01	1.20E-02	-4.73E-01	9.24E-03	-8.83E-01	3.61E-04
490059939	protoporphyrinogen oxidase	1.34E+01	-7.93E-01	2.09E-03	-1.67E+00	6.78E-05	-8.81E-01	1.61E-03
497681729	oxidoreductase	1.50E+01	3.88E-01	2.61E-02	-4.89E-01	1.45E-02	-8.77E-01	7.62E-04
490055580	hypothetical protein	1.31E+01	-1.34E-01	2.49E-01	-1.01E+00	1.08E-04	-8.77E-01	1.87E-04
490051410	peptidyl-tRNA hydrolase	1.26E+01	-3.69E-01	2.46E-02	-1.24E+00	1.02E-04	-8.75E-01	5.40E-04
490059515	malate dehydrogenase	1.43E+01	-4.88E-01	2.07E-02	-1.36E+00	2.13E-04	-8.74E-01	1.85E-03
490050032	MarR family transcriptional regulator	1.27E+01	1.40E-01	3.44E-01	-7.34E-01	2.03E-03	-8.73E-01	7.27E-04
490059940	hypothetical protein	1.46E+01	-4.35E-01	6.19E-02	-1.31E+00	6.78E-04	-8.72E-01	4.71E-03
497685246	hypothetical protein	1.39E+01	-1.80E+00	1.31E-04	-2.67E+00	2.83E-05	-8.71E-01	6.86E-03
490061346	AMP-dependent synthetase	1.50E+01	-1.64E-01	3.80E-01	-1.04E+00	1.19E-03	-8.71E-01	2.53E-03
490058166	coproporphyrinogen III oxidase	1.59E+01	5.38E-01	8.49E-03	-3.30E-01	7.59E-02	-8.68E-01	1.08E-03
490059520	hypothetical protein	1.43E+01	6.15E-01	2.64E-02	-2.48E-01	3.33E-01	-8.63E-01	8.32E-03
490054819	succinate-semialdehyde dehydrogenase	1.31E+01	-7.96E-01	1.89E-04	-1.66E+00	8.91E-06	-8.63E-01	1.58E-04
490057758	hypothetical protein	1.12E+01	1.68E-01	3.54E-01	-6.94E-01	7.25E-03	-8.62E-01	2.24E-03
497681547	hypothetical protein	1.32E+01	4.34E-01	2.62E-02	-4.25E-01	3.93E-02	-8.59E-01	1.51E-03
490061383	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1.02E+01	-3.12E+00	4.03E-06	-3.98E+00	3.04E-06	-8.59E-01	2.93E-03
490052437	single-stranded DNA-binding protein	1.49E+01	4.27E-01	1.28E-01	-4.29E-01	1.53E-01	-8.56E-01	1.46E-02
497682397	DNA topoisomerase I	1.42E+01	4.86E-01	2.28E-02	-3.68E-01	8.12E-02	-8.54E-01	2.29E-03
490050757	hypothetical protein	1.35E+01	-6.44E-01	5.83E-03	-1.50E+00	1.21E-04	-8.54E-01	1.92E-03
490057455	transcriptional regulator	1.00E+01	8.74E-02	5.61E-01	-7.64E-01	1.80E-03	-8.52E-01	9.12E-04
490051026	transporter	1.27E+01	1.75E-01	1.58E-01	-6.74E-01	1.06E-03	-8.49E-01	2.75E-04

490057691	cytochrome C peroxidase	1.35E+01	4.58E-01	2.82E-03	-3.87E-01	9.12E-03	-8.44E-01	1.53E-04
490055921	long-chain fatty acid--CoA ligase	1.42E+01	8.62E-01	2.81E-04	1.74E-02	9.01E-01	-8.44E-01	4.10E-04
497683640	acyl-CoA dehydrogenase	1.26E+01	6.20E-01	1.85E-03	-2.23E-01	1.37E-01	-8.42E-01	4.96E-04
497683816	dimethylallyltranstransferase	1.40E+01	8.87E-01	4.62E-04	4.56E-02	7.71E-01	-8.42E-01	8.02E-04
497681279	membrane protein	1.25E+01	-1.69E-01	3.37E-01	-1.01E+00	1.00E-03	-8.38E-01	2.24E-03
497682159	chemotaxis protein CheY	1.46E+01	-9.94E-01	8.43E-04	-1.83E+00	5.53E-05	-8.37E-01	2.66E-03
490059431	acetyltransferase	1.37E+01	-6.01E-01	8.57E-03	-1.44E+00	1.62E-04	-8.36E-01	2.30E-03
490051157	PhoU family transcriptional regulator	1.38E+01	-7.23E-01	1.23E-03	-1.56E+00	3.74E-05	-8.35E-01	7.69E-04
490054092	XRE family transcriptional regulator	1.52E+01	9.54E-01	1.15E-04	1.20E-01	3.46E-01	-8.34E-01	2.88E-04
497681684	phosphoribosyl-AMP cyclohydrolase	1.29E+01	9.48E-01	2.35E-03	1.18E-01	6.05E-01	-8.30E-01	5.94E-03
497682175	LytR family transcriptional regulator	1.01E+01	-2.28E-01	1.58E-01	-1.06E+00	4.04E-04	-8.30E-01	1.26E-03
490057424	hypothetical protein	1.06E+01	2.49E+00	3.76E-05	1.66E+00	4.44E-04	-8.28E-01	1.24E-02
490055584	hypothetical protein	1.31E+01	-6.45E-01	1.98E-02	-1.47E+00	5.69E-04	-8.26E-01	8.97E-03
497683068	hypothetical protein	1.45E+01	6.90E-01	1.22E-02	-1.36E-01	5.66E-01	-8.26E-01	7.31E-03
490051846	hypothetical protein	1.32E+01	-4.05E-01	6.38E-02	-1.23E+00	6.70E-04	-8.25E-01	4.54E-03
490056110	glycosyl transferase	1.30E+01	-1.08E+00	4.18E-04	-1.90E+00	3.56E-05	-8.25E-01	2.13E-03
490054198	thioredoxin	1.32E+01	-1.63E+00	1.87E-04	-2.45E+00	3.68E-05	-8.20E-01	7.91E-03
490050096	peptide chain release factor 1	1.15E+01	3.64E-01	7.04E-02	-4.55E-01	4.40E-02	-8.19E-01	3.17E-03
497682087	LuxAB-like protein (oxygenase)	1.21E+01	-8.00E-01	4.89E-04	-1.62E+00	2.29E-05	-8.18E-01	5.73E-04
490058809	membrane protein	1.26E+01	3.23E-01	3.17E-02	-4.94E-01	7.59E-03	-8.17E-01	5.41E-04
497682249	tetrapyrrole methylase	1.32E+01	3.74E-01	1.43E-02	-4.42E-01	1.00E-02	-8.16E-01	4.21E-04
490053868	cold-shock protein	1.12E+01	7.51E-03	9.63E-01	-8.08E-01	5.70E-04	-8.16E-01	4.76E-04
490059669	DNA ligase	1.29E+01	3.62E-01	1.59E-02	-4.53E-01	8.67E-03	-8.16E-01	4.05E-04
497682167	membrane protein	1.35E+01	-3.62E-02	8.42E-01	-8.51E-01	2.02E-03	-8.15E-01	2.21E-03
490060991	acetyltransferase	1.27E+01	-9.25E-01	3.01E-03	-1.74E+00	1.81E-04	-8.12E-01	7.46E-03
497681617	excinuclease ABC subunit A	1.25E+01	-3.15E-02	8.71E-01	-8.39E-01	2.76E-03	-8.07E-01	2.92E-03
497682842	hydroxyglutarate oxidase	1.15E+01	-4.45E-01	4.96E-02	-1.25E+00	6.92E-04	-8.02E-01	5.70E-03
490058574	histidine kinase	1.25E+01	1.65E-01	3.45E-01	-6.37E-01	8.96E-03	-8.01E-01	2.65E-03
497683601	thioesterase	1.68E+01	5.18E-01	5.00E-02	-2.83E-01	2.74E-01	-8.01E-01	1.17E-02
490050285	short-chain dehydrogenase	1.38E+01	-5.86E-01	3.39E-03	-1.39E+00	6.34E-05	-8.00E-01	9.40E-04
490050132	DNA-binding protein	1.34E+01	-4.75E-01	1.96E-02	-1.27E+00	2.44E-04	-8.00E-01	2.35E-03

490059527	Lon protease	1.30E+01	-1.98E+00	5.73E-05	-2.78E+00	1.84E-05	-7.96E-01	7.67E-03
490051605	hydrogen peroxide sensitive repressor	1.74E+01	6.57E-01	8.01E-03	-1.38E-01	4.99E-01	-7.95E-01	4.34E-03
497681971	metal ABC transporter substrate-binding protein	1.07E+01	-6.72E-01	4.86E-03	-1.47E+00	1.38E-04	-7.95E-01	2.84E-03
490055856	sulfate ABC transporter substrate-binding protein	1.45E+01	-7.59E-01	9.12E-04	-1.55E+00	3.68E-05	-7.91E-01	9.76E-04
490057476	dihydroorotase	1.32E+01	4.32E-01	1.37E-02	-3.58E-01	4.07E-02	-7.90E-01	1.01E-03
490051413	phosphoenolpyruvate carboxylase	1.27E+01	-7.39E-01	5.51E-04	-1.52E+00	2.30E-05	-7.85E-01	5.30E-04
490052695	XRE family transcriptional regulator	1.24E+01	-2.17E-01	3.07E-01	-9.99E-01	2.61E-03	-7.83E-01	7.55E-03
497682035	amino acid transporter	1.57E+01	1.12E+00	5.44E-05	3.39E-01	2.70E-02	-7.81E-01	4.51E-04
490059245	50S ribosomal protein L23	1.38E+01	-8.76E-01	1.18E-03	-1.66E+00	6.67E-05	-7.80E-01	2.75E-03
497681789	membrane protein	1.33E+01	-2.97E-01	1.36E-01	-1.07E+00	1.07E-03	-7.75E-01	4.90E-03
497683590	hypothetical protein	1.39E+01	-8.14E-01	6.20E-04	-1.59E+00	3.21E-05	-7.75E-01	1.06E-03
490052455	dehydrogenase	1.36E+01	5.72E-01	5.74E-03	-2.01E-01	2.36E-01	-7.73E-01	1.72E-03
490059969	adenylylsulfate kinase	1.24E+01	5.39E-01	1.86E-02	-2.33E-01	2.63E-01	-7.72E-01	5.00E-03
497681332	preprotein translocase subunit SecD	1.40E+01	-6.10E-01	1.30E-02	-1.36E+00	3.75E-04	-7.55E-01	6.63E-03
490055887	hypothetical protein	1.22E+01	5.49E-01	9.48E-03	-2.06E-01	2.55E-01	-7.54E-01	2.75E-03
497683636	DNA polymerase III subunit epsilon	1.20E+01	1.22E+00	4.52E-05	4.71E-01	8.29E-03	-7.54E-01	7.10E-04
490051219	phosphate transport regulator	1.64E+01	7.94E-01	6.94E-04	4.04E-02	7.89E-01	-7.54E-01	1.20E-03
497683989	SAM-dependent methyltransferase	1.31E+01	-2.32E+00	1.08E-05	-3.08E+00	5.79E-06	-7.53E-01	4.12E-03
490054720	ArsR family transcriptional regulator	1.31E+01	6.78E-01	6.83E-03	-7.47E-02	7.14E-01	-7.53E-01	5.55E-03
490052148	sugar ABC transporter ATP-binding protein	1.36E+01	8.64E-01	5.80E-04	1.12E-01	4.77E-01	-7.51E-01	1.56E-03

[a] Identification is based on annotation by NCBI. **[b]** Description is based on NCBI annotation of protein similarity by BLAST. **[c]** Average normalized expression in the WT strain. **[d]** Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. **[e]** Adjusted P-value in *ΔbldG* as compared to the WT strain. **[f]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. **[g]** Adjusted P-value in *ΔbldA* as compared to the WT strain. **[h]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and **[i]** Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Table A.1.7: Proteins determined to be expressed similarly (P = 0.01) between the *ΔbldG* and the WT strains of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G -WT[e]	logFC A -WT[f]	adj.P.Val A-WT[g]	logFC A -G[h]	adj.P.Val A -G[i]
490060210	3-hydroxyacyl-CoA dehydrogenase	1.27E+01	-7.47E-01	1.47E-03	-2.38E+00	8.12E-06	-1.63E+00	3.39E-05
490061204	Lipase	1.38E+01	-7.42E-01	3.49E-03	-1.95E+00	3.98E-05	-1.21E+00	3.85E-04
490060667	cytochrome P450	1.28E+01	-7.41E-01	5.13E-03	-1.63E+00	1.40E-04	-8.89E-01	2.79E-03
490050336	hypothetical protein	1.56E+01	-7.40E-01	1.12E-02	-4.56E-01	9.11E-02	2.85E-01	2.60E-01
490051413	phosphoenolpyruvate carboxylase	1.27E+01	-7.39E-01	5.51E-04	-1.52E+00	2.30E-05	-7.85E-01	5.30E-04
497683533	regulatory protein	1.47E+01	-7.38E-01	3.23E-03	-1.67E+00	7.51E-05	-9.31E-01	1.34E-03
490056120	pseudouridine synthase	1.40E+01	-7.37E-01	2.23E-03	-5.91E-01	9.33E-03	1.46E-01	4.05E-01
490052685	hypothetical protein	1.43E+01	-7.35E-01	1.16E-02	-4.26E-01	1.10E-01	3.09E-01	2.23E-01
490058296	hypothetical protein	1.44E+01	-7.31E-01	3.04E-03	1.75E-01	3.47E-01	9.06E-01	1.37E-03
490051024	DNA primase	1.20E+01	-7.30E-01	1.01E-03	-1.89E+00	1.48E-05	-1.16E+00	1.16E-04
490058675	4-phosphopantetheinyl transferase	1.23E+01	-7.30E-01	5.67E-04	-2.18E+00	5.46E-06	-1.45E+00	2.16E-05
490057127	regulator	1.05E+01	-7.29E-01	4.47E-04	2.15E-01	1.13E-01	9.44E-01	1.48E-04
490059326	amidohydrolase	1.23E+01	-7.28E-01	8.31E-03	-9.58E-01	3.37E-03	-2.30E-01	3.15E-01
490051157	PhoU family transcriptional regulator	1.38E+01	-7.23E-01	1.23E-03	-1.56E+00	3.74E-05	-8.35E-01	7.69E-04
490055583	sporulation protein	1.42E+01	-7.20E-01	5.02E-03	-1.46E+00	2.07E-04	-7.43E-01	5.74E-03
497681599	glucose-6-phosphate isomerase	1.27E+01	-7.17E-01	1.25E-02	-5.39E-01	5.30E-02	1.78E-01	4.70E-01
497682075	biotin carboxyl carrier protein	1.12E+01	-7.06E-01	1.43E-02	7.23E-01	1.85E-02	1.43E+00	6.20E-04
490058906	RNA polymerase sigma factor	9.61E+00	-7.00E-01	8.32E-03	-1.67E+00	1.60E-04	-9.67E-01	2.30E-03
490051745	aldo/keto reductase	1.15E+01	-6.97E-01	6.11E-03	-2.23E+00	2.73E-05	-1.54E+00	1.39E-04
490061097	DNA primase	1.14E+01	-6.96E-01	3.92E-03	1.40E+00	1.67E-04	2.10E+00	1.89E-05
490057948	RNA-binding protein	1.22E+01	-6.95E-01	2.42E-03	-3.14E-01	8.53E-02	3.80E-01	4.35E-02
490058372	FAD-linked oxidase	1.19E+01	-6.93E-01	7.81E-04	-9.98E-01	1.79E-04	-3.05E-01	4.30E-02
490051385	anti-sigma regulatory factor	1.36E+01	-6.92E-01	1.57E-03	-7.06E-03	9.64E-01	6.85E-01	2.17E-03
497681631	acyltransferase	1.24E+01	-6.86E-01	5.60E-03	-1.18E+00	5.61E-04	-4.90E-01	3.13E-02
497682488	regulatory protein	1.40E+01	-6.82E-01	7.17E-03	-7.82E-01	5.58E-03	-1.00E-01	6.23E-01
490051650	anti-sigma regulatory factor	1.33E+01	-6.78E-01	2.13E-03	-5.45E-01	8.94E-03	1.33E-01	4.04E-01
497681971	metal ABC transporter substrate-binding	1.07E+01	-6.72E-01	4.86E-03	-1.47E+00	1.38E-04	-7.95E-01	2.84E-03

	protein							
490057617	ATP-dependent exoDNAse Exonuclease V , alpha subunit/helicase superfamily I member	1.13E+01	-6.70E-01	4.04E-04	-1.43E-01	2.23E-01	5.27E-01	1.81E-03
490051811	hypothetical protein	1.27E+01	-6.68E-01	1.71E-03	-5.41E-01	7.05E-03	1.27E-01	4.01E-01
497683030	regulator	1.37E+01	-6.56E-01	2.58E-03	-1.01E+00	4.12E-04	-3.58E-01	4.62E-02
490052652	valine dehydrogenase	1.42E+01	-6.55E-01	8.57E-03	-2.93E+00	8.89E-06	-2.28E+00	2.10E-05
490054722	hypothetical protein	1.19E+01	-6.50E-01	1.97E-03	-2.39E+00	5.88E-06	-1.74E+00	1.70E-05
490056565	ATP-dependent Clp protease ATP-binding protein	1.20E+01	-6.46E-01	9.95E-04	-1.30E+00	4.20E-05	-6.56E-01	1.21E-03
490050757	hypothetical protein	1.35E+01	-6.44E-01	5.83E-03	-1.50E+00	1.21E-04	-8.54E-01	1.92E-03
490058053	hypothetical protein	1.46E+01	-6.43E-01	1.45E-03	-4.25E-01	1.50E-02	2.19E-01	1.35E-01
490054035	molybdenum metabolism regulator	1.36E+01	-6.41E-01	2.45E-03	-5.37E-01	8.41E-03	1.04E-01	5.00E-01
497683388	hypothetical protein	1.41E+01	-6.40E-01	2.89E-03	-4.53E-01	2.01E-02	1.87E-01	2.50E-01
490051521	DNA-3-methyladenine glycosylase	1.42E+01	-6.30E-01	1.33E-02	3.26E-04	9.99E-01	6.30E-01	1.76E-02
490054040	hypothetical protein	1.08E+01	-6.26E-01	8.71E-03	-1.08E+00	8.91E-04	-4.56E-01	4.13E-02
497681460	C4-dicarboxylate ABC transporter substrate-binding protein	1.38E+01	-6.26E-01	1.82E-03	-1.65E+00	2.20E-05	-1.03E+00	1.81E-04
490050511	ATPase	1.36E+01	-6.14E-01	1.45E-03	-4.25E-01	1.23E-02	1.89E-01	1.72E-01
497681332	preprotein translocase subunit SecD	1.40E+01	-6.10E-01	1.30E-02	-1.36E+00	3.75E-04	-7.55E-01	6.63E-03
490051489	5'-methylthioadenosine phosphorylase	1.23E+01	-6.06E-01	4.23E-03	-9.70E-01	5.85E-04	-3.64E-01	4.72E-02
490059431	acetyltransferase	1.37E+01	-6.01E-01	8.57E-03	-1.44E+00	1.62E-04	-8.36E-01	2.30E-03
490052563	zinc-binding dehydrogenase	1.05E+01	-6.00E-01	6.02E-03	-1.89E+00	2.91E-05	-1.29E+00	1.58E-04
490057664	acyl-CoA dehydrogenase	1.35E+01	-5.97E-01	1.03E-02	-1.79E+00	6.45E-05	-1.19E+00	4.50E-04
490050285	short-chain dehydrogenase	1.38E+01	-5.86E-01	3.39E-03	-1.39E+00	6.34E-05	-8.00E-01	9.40E-04
497681405	glutamate--ammonia ligase	1.65E+01	-5.85E-01	1.23E-03	-1.02E+00	1.03E-04	-4.37E-01	6.80E-03
490059191	hypothetical protein	1.46E+01	-5.84E-01	1.36E-02	-1.56E+00	1.57E-04	-9.81E-01	1.53E-03
490059485	hypothetical protein	1.10E+01	-5.81E-01	9.91E-03	-2.18E+00	2.27E-05	-1.60E+00	7.83E-05
490060147	xylose isomerase	1.30E+01	-5.78E-01	6.89E-03	-2.95E-02	8.67E-01	5.49E-01	1.16E-02
490054452	glycosyl transferase family 2	1.38E+01	-5.77E-01	1.03E-02	-5.02E-01	2.63E-02	7.43E-02	6.93E-01
490051121	trehalose phosphatase	1.47E+01	-5.75E-01	3.29E-03	-2.79E+00	3.42E-06	-2.21E+00	5.57E-06
497683467	hydrolase	1.29E+01	-5.66E-01	9.46E-03	-2.13E+00	2.13E-05	-1.56E+00	7.28E-05
490057507	acetyltransferase	1.46E+01	-5.62E-01	4.81E-03	-5.92E-01	5.57E-03	-3.05E-02	8.42E-01
490057929	hypothetical protein	1.22E+01	-5.57E-01	1.02E-02	-4.21E-01	4.41E-02	1.36E-01	4.58E-01

497681263	signal peptide protein	1.38E+01	-5.57E-01	2.79E-03	-1.10E+00	1.27E-04	-5.42E-01	4.20E-03
497683603	hypothetical protein	1.16E+01	-5.55E-01	6.83E-03	-8.85E-01	1.02E-03	-3.30E-01	6.84E-02
490054923	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1.32E+01	-5.54E-01	2.97E-03	-5.17E-01	6.16E-03	3.67E-02	7.90E-01
490054828	LuxR family transcriptional regulator	1.57E+01	-5.52E-01	7.05E-03	-1.04E+00	4.41E-04	-4.87E-01	1.62E-02
490058959	hypothetical protein	1.47E+01	-5.49E-01	8.84E-03	-5.97E-01	8.79E-03	-4.83E-02	7.80E-01
490053060	butyryl-CoA dehydrogenase	1.38E+01	-5.48E-01	8.68E-03	3.23E-01	8.66E-02	8.72E-01	1.20E-03
490052515	preprotein translocase SecA	1.23E+01	-5.48E-01	7.26E-03	-2.44E+00	7.83E-06	-1.89E+00	1.84E-05
490053010	hypothetical protein	1.26E+01	-5.31E-01	8.85E-03	-1.44E+00	9.02E-05	-9.05E-01	8.58E-04
497683911	transcriptional regulator	1.27E+01	-5.29E-01	5.87E-03	-8.89E-01	6.52E-04	-3.60E-01	3.87E-02
490059781	zinc metalloprotease	1.44E+01	-5.23E-01	9.26E-03	-6.64E-01	4.54E-03	-1.41E-01	4.02E-01
490050050	ABC transporter ATP-binding protein	1.20E+01	-5.20E-01	1.26E-02	-1.74E+00	4.79E-05	-1.22E+00	2.48E-04
497681812	alpha-glucosidase	1.37E+01	-5.18E-01	8.62E-03	-1.62E+00	4.28E-05	-1.10E+00	2.55E-04
497682435	esterase	1.10E+01	-5.12E-01	9.62E-03	-1.10E+00	3.18E-04	-5.91E-01	6.63E-03
490050761	hypothetical protein	1.12E+01	-5.11E-01	5.83E-03	-2.37E+00	5.79E-06	-1.86E+00	1.13E-05
490054192	single-stranded DNA-binding protein	1.50E+01	-5.11E-01	1.67E-03	-6.91E-01	5.27E-04	-1.80E-01	1.32E-01
497683176	hypothetical protein	1.44E+01	-5.07E-01	1.15E-02	-3.14E+00	3.94E-06	-2.63E+00	5.14E-06
490056611	membrane protein	1.81E+01	-5.07E-01	2.35E-03	-5.40E-01	2.56E-03	-3.29E-02	7.84E-01
490056814	acetyltransferase	1.22E+01	-5.06E-01	9.66E-03	-3.25E+00	3.04E-06	-2.75E+00	3.79E-06
497682081	helicase	1.23E+01	-4.97E-01	4.73E-03	-1.88E-01	1.88E-01	3.09E-01	4.53E-02
490053484	calcium-binding protein	1.23E+01	-4.96E-01	6.74E-03	-1.26E-01	3.96E-01	3.70E-01	3.06E-02
490054499	hypothetical protein	1.27E+01	-4.84E-01	6.11E-03	-2.73E-01	7.86E-02	2.11E-01	1.51E-01
490058652	beta-lactamase	1.21E+01	-4.83E-01	9.46E-03	-2.55E-03	9.87E-01	4.80E-01	1.28E-02
490053302	AsnC family transcriptional regulator	1.56E+01	-4.72E-01	4.97E-03	-8.42E-01	3.99E-04	-3.70E-01	1.94E-02
490057811	sugar kinase	1.46E+01	-4.71E-01	1.37E-02	8.25E-02	6.18E-01	5.53E-01	8.95E-03
490055666	membrane protein	1.33E+01	-4.69E-01	6.17E-03	-2.71E+00	3.04E-06	-2.24E+00	4.05E-06
497682607	hydrolase	1.33E+01	-4.69E-01	1.16E-02	-1.47E+00	5.88E-05	-1.00E+00	3.61E-04
497681054	sporulation protein	1.24E+01	-4.68E-01	6.20E-03	1.03E+00	1.74E-04	1.50E+00	2.18E-05
490054109	phosphoglucosamine mutase	1.42E+01	-4.61E-01	1.08E-02	-8.57E-01	7.97E-04	-3.95E-01	2.72E-02
490055707	preprotein translocase subunit TatA	1.24E+01	-4.60E-01	1.09E-02	-6.38E-01	3.57E-03	-1.78E-01	2.54E-01
490052577	TetR family transcriptional regulator	1.51E+01	-4.56E-01	8.36E-03	-2.61E-01	9.16E-02	1.95E-01	1.85E-01
497683188	dienelactone hydrolase	1.20E+01	-4.49E-01	1.04E-02	-1.03E+00	2.54E-04	-5.80E-01	4.24E-03

497685294	transcriptional regulator	1.21E+01	-4.24E-01	4.05E-03	-1.90E-01	1.18E-01	2.34E-01	6.07E-02
490052962	peptidase S9	1.13E+01	-4.04E-01	6.11E-03	-1.81E+00	6.80E-06	-1.41E+00	1.46E-05
490056886	chemotaxis protein CheY	1.29E+01	-4.04E-01	6.37E-03	-1.91E+00	5.79E-06	-1.51E+00	1.12E-05
490054931	alpha/beta hydrolase	1.50E+01	-4.04E-01	1.39E-02	-2.52E+00	4.52E-06	-2.12E+00	5.57E-06
490056644	6-phospho-beta-glucosidase	9.75E+00	-4.03E-01	1.32E-02	-3.11E+00	2.23E-06	-2.71E+00	2.49E-06
497683303	GntR family transcriptional regulator	1.26E+01	-3.74E-01	6.74E-03	-7.66E-01	2.72E-04	-3.92E-01	7.15E-03
497681649	aminopeptidase N	1.32E+01	-3.38E-01	9.81E-03	-1.23E+00	2.49E-05	-8.95E-01	9.58E-05
490057893	histidinol-phosphate aminotransferase	1.42E+01	3.68E-01	9.77E-03	-7.57E-01	4.07E-04	-1.12E+00	4.47E-05
497682249	tetrapyrrole methylase	1.32E+01	3.74E-01	1.43E-02	-4.42E-01	1.00E-02	-8.16E-01	4.21E-04
490054392	RNA pseudouridine synthase	1.32E+01	3.84E-01	1.12E-02	-8.26E-01	3.86E-04	-1.21E+00	4.51E-05
490053532	lysine decarboxylase	1.30E+01	3.90E-01	8.49E-03	-1.28E+00	3.32E-05	-1.67E+00	7.86E-06
497683478	chromosome segregation protein SMC	1.27E+01	3.97E-01	9.12E-03	2.98E-01	4.13E-02	-9.97E-02	4.32E-01
490055736	ribosomal subunit interface protein	1.55E+01	4.09E-01	4.69E-03	6.16E-01	9.06E-04	2.07E-01	8.78E-02
497683249	hypothetical protein	1.44E+01	4.09E-01	1.20E-02	-4.73E-01	9.24E-03	-8.83E-01	3.61E-04
497685198	pyridoxamine 5'-phosphate oxidase	1.47E+01	4.15E-01	1.40E-02	-2.02E+00	1.01E-05	-2.44E+00	3.82E-06
490054811	inosine-5`-monophosphate dehydrogenase	1.32E+01	4.17E-01	9.60E-03	-1.91E-01	1.75E-01	-6.08E-01	2.09E-03
490050062	3-hydroxybutyryl-CoA dehydrogenase	8.99E+00	4.18E-01	1.32E-02	2.83E+00	3.04E-06	2.41E+00	3.85E-06
490054424	membrane dipeptidase	1.41E+01	4.21E-01	4.99E-03	-1.44E+00	1.80E-05	-1.86E+00	4.61E-06
490055126	ABC transporter	1.37E+01	4.32E-01	7.34E-03	-6.00E-01	2.24E-03	-1.03E+00	1.14E-04
490057476	dihydroorotase	1.32E+01	4.32E-01	1.37E-02	-3.58E-01	4.07E-02	-7.90E-01	1.01E-03
490053313	cystathionine beta-lyase	1.60E+01	4.47E-01	8.26E-03	2.12E-01	1.48E-01	-2.35E-01	1.11E-01
497681563	MarR family transcriptional regulator	1.47E+01	4.56E-01	1.46E-02	-1.03E+00	4.01E-04	-1.49E+00	5.06E-05
490053874	ubiquinone/menaquinone biosynthesis methyltransferase	1.33E+01	4.56E-01	1.07E-02	-1.36E+00	6.89E-05	-1.81E+00	1.42E-05
490057691	cytochrome C peroxidase	1.35E+01	4.58E-01	2.82E-03	-3.87E-01	9.12E-03	-8.44E-01	1.53E-04
497683507	ATP-binding protein	1.10E+01	4.63E-01	9.65E-03	9.27E-01	4.67E-04	4.63E-01	1.28E-02
490056236	MarR family transcriptional regulator	1.42E+01	4.67E-01	9.69E-03	1.05E-01	4.87E-01	-3.61E-01	3.63E-02
490050094	hypothetical protein	1.42E+01	4.75E-01	1.09E-02	-3.22E+00	2.82E-06	-3.69E+00	1.57E-06
490059042	hypothetical protein	1.01E+01	4.78E-01	9.47E-03	-2.06E+00	1.21E-05	-2.54E+00	3.92E-06
490058102	pyruvate dehydrogenase E1	1.38E+01	4.80E-01	3.80E-03	-1.34E+00	3.25E-05	-1.82E+00	6.43E-06
490052503	membrane protein	1.69E+01	4.86E-01	2.27E-03	1.74E-01	1.53E-01	-3.13E-01	2.24E-02

490708574	ligase	1.18E+01	4.88E-01	2.41E-03	-6.17E-01	1.10E-03	-1.11E+00	4.51E-05
490050038	MarR family transcriptional regulator	1.08E+01	4.89E-01	1.09E-02	-2.43E+00	7.49E-06	-2.92E+00	2.96E-06
490056429	recombinase RecF	1.13E+01	4.98E-01	1.43E-02	-1.26E+00	2.24E-04	-1.76E+00	3.44E-05
490058999	Hypothetical protein	1.31E+01	4.98E-01	1.04E-02	2.27E-01	1.84E-01	-2.71E-01	1.18E-01
490057338	glyoxalase	1.37E+01	4.98E-01	1.44E-02	2.89E-01	1.24E-01	-2.09E-01	2.47E-01
490051625	peptide deformylase	1.30E+01	5.08E-01	2.92E-03	-1.59E+00	1.64E-05	-2.09E+00	3.92E-06
490050024	pyruvate kinase	1.25E+01	5.08E-01	9.23E-03	-1.12E+00	2.73E-04	-1.62E+00	3.38E-05
497683289	ATP-dependent DNA helicase	1.24E+01	5.09E-01	3.32E-03	-2.82E+00	2.50E-06	-3.33E+00	1.17E-06
490057686	transcriptional regulator	1.31E+01	5.10E-01	9.20E-03	-1.65E+00	3.92E-05	-2.16E+00	8.94E-06
497683131	ATP-binding protein	1.19E+01	5.16E-01	1.28E-02	4.56E-01	2.99E-02	-5.95E-02	7.37E-01
490054189	ribonuclease P	1.37E+01	5.25E-01	7.82E-03	-2.60E+00	5.79E-06	-3.13E+00	2.49E-06
490055906	bacterioferritin	1.42E+01	5.29E-01	8.99E-03	6.63E-01	4.67E-03	1.33E-01	4.29E-01
497682271	5-formyltetrahydrofolate cyclo-ligase	1.15E+01	5.32E-01	7.49E-03	4.23E-01	2.81E-02	-1.09E-01	5.02E-01
490058154	2-isopropylmalate synthase	1.33E+01	5.34E-01	1.36E-02	-2.27E+00	1.84E-05	-2.80E+00	5.57E-06
497682539	hypothetical protein	1.30E+01	5.36E-01	5.36E-03	-5.62E-01	6.32E-03	-1.10E+00	1.80E-04
490051407	ribose-phosphate pyrophosphokinase	1.10E+01	5.38E-01	1.32E-02	-1.25E+00	3.09E-04	-1.79E+00	4.10E-05
490061042	glycosyl transferase	1.57E+01	5.38E-01	4.20E-03	-6.82E-02	6.38E-01	-6.06E-01	3.08E-03
490058166	coproporphyrinogen III oxidase	1.59E+01	5.38E-01	8.49E-03	-3.30E-01	7.59E-02	-8.68E-01	1.08E-03
490059828	tRNA delta(2)-isopentenylpyrophosphate transferase	1.47E+01	5.39E-01	5.13E-03	-1.45E+00	5.11E-05	-1.99E+00	9.38E-06
490053398	type II citrate synthase	1.37E+01	5.41E-01	1.41E-02	-9.08E-01	1.82E-03	-1.45E+00	1.36E-04
490059842	ATP-dependent DNA helicase RecQ	1.20E+01	5.46E-01	8.62E-03	-1.92E+00	2.54E-05	-2.46E+00	6.45E-06
490057421	membrane protein	1.05E+01	5.48E-01	1.10E-02	-1.56E+00	9.17E-05	-2.10E+00	1.75E-05
490055887	hypothetical protein	1.22E+01	5.49E-01	9.48E-03	-2.06E-01	2.55E-01	-7.54E-01	2.75E-03
490054474	phosphomannomutase	1.39E+01	5.57E-01	1.02E-03	-2.62E+00	1.85E-06	-3.18E+00	8.19E-07
490059859	phosphodiesterase	1.49E+01	5.65E-01	9.47E-03	-1.14E+00	4.28E-04	-1.71E+00	4.52E-05
490057941	glucokinase	1.44E+01	5.67E-01	1.09E-02	-2.32E+00	1.76E-05	-2.89E+00	5.23E-06
490055046	ABC transporter	1.24E+01	5.69E-01	1.44E-02	3.06E-01	1.51E-01	-2.63E-01	2.05E-01
490054456	acyl-CoA synthetase	1.38E+01	5.69E-01	5.91E-03	-2.32E+00	9.11E-06	-2.89E+00	3.20E-06
490054134	50S ribosomal protein L15	7.86E+00	5.70E-01	8.88E-03	-1.52E+00	9.76E-05	-2.09E+00	1.71E-05
497681682	membrane protein	1.53E+01	5.71E-01	2.74E-03	-1.18E-01	4.03E-01	-6.90E-01	1.39E-03

497683372	F0F1 ATP synthase subunit A	1.36E+01	5.71E-01	5.06E-03	-1.28E+00	1.27E-04	-1.85E+00	1.72E-05
490052455	dehydrogenase	1.36E+01	5.72E-01	5.74E-03	-2.01E-01	2.36E-01	-7.73E-01	1.72E-03
490054531	cobaltochelatase subunit CobN	1.23E+01	5.73E-01	6.65E-03	-7.29E-01	3.13E-03	-1.30E+00	1.31E-04
490059244	50S ribosomal protein L4	1.29E+01	5.76E-01	1.02E-02	-1.84E+00	4.67E-05	-2.42E+00	1.07E-05
490059304	phosphoesterase	1.65E+01	5.76E-01	9.59E-03	-1.10E+00	5.84E-04	-1.68E+00	5.56E-05
497683293	NAD-dependent dehydratase	1.43E+01	5.78E-01	3.78E-03	-1.05E+00	2.72E-04	-1.63E+00	2.46E-05
497682483	hypothetical protein	1.00E+01	5.81E-01	1.93E-03	-5.25E-01	4.75E-03	-1.11E+00	8.83E-05
490053279	peptidase	1.36E+01	5.83E-01	7.71E-03	-1.14E+00	4.03E-04	-1.72E+00	4.06E-05
490055235	L-asparagine permease	1.48E+01	5.84E-01	6.18E-03	9.55E-01	7.96E-04	3.72E-01	5.04E-02
490054711	transketolase	1.17E+01	5.86E-01	1.66E-03	-3.30E-01	3.21E-02	-9.16E-01	2.12E-04
490052209	ribonuclease H	1.28E+01	5.86E-01	1.12E-02	-8.10E-01	3.77E-03	-1.40E+00	1.94E-04
497681774	dihydrolipoamide dehydrogenase	1.16E+01	5.87E-01	9.53E-03	-3.40E-01	9.66E-02	-9.27E-01	1.38E-03
490054839	mannose-6-phosphate isomerase	1.38E+01	5.88E-01	8.26E-03	-7.76E-02	6.72E-01	-6.65E-01	6.15E-03
497683199	purine nucleoside phosphorylase	1.43E+01	5.89E-01	2.49E-03	-5.63E-01	4.65E-03	-1.15E+00	9.96E-05
497681448	TetR family transcriptional regulator	1.32E+01	5.98E-01	8.42E-03	2.78E-01	1.57E-01	-3.19E-01	1.08E-01
490055160	cell division protein FtsW	1.28E+01	6.00E-01	1.36E-02	-4.96E-02	8.15E-01	-6.50E-01	1.28E-02
490058352	nucleoside-triphosphate diphosphatase	1.28E+01	6.03E-01	8.29E-03	-5.92E-01	1.29E-02	-1.19E+00	3.55E-04
497681311	guanylate kinase	1.15E+01	6.06E-01	1.01E-02	-2.05E+00	3.56E-05	-2.65E+00	8.58E-06
497681192	DEAD/DEAH box helicase	1.28E+01	6.06E-01	7.14E-03	-2.25E+00	1.76E-05	-2.86E+00	4.84E-06
490053475	ABC transporter	1.53E+01	6.08E-01	3.19E-03	-5.90E-01	5.55E-03	-1.20E+00	1.25E-04
490058867	para-aminobenzoate synthase	1.61E+01	6.09E-01	3.16E-03	-2.85E-01	9.11E-02	-8.94E-01	5.92E-04
490059251	pantothenate kinase	1.40E+01	6.10E-01	2.05E-03	-8.79E-01	4.67E-04	-1.49E+00	2.69E-05
490055913	1-acyl-sn-glycerol-3-phosphate acyltransferase	1.40E+01	6.11E-01	2.81E-03	-3.35E-01	5.12E-02	-9.46E-01	3.90E-04
497683472	phosphopantetheine adenylyltransferase	1.27E+01	6.16E-01	6.86E-03	8.04E-03	9.66E-01	-6.08E-01	9.63E-03
490052504	chaperonin	1.51E+01	6.17E-01	2.11E-03	-7.94E-01	8.79E-04	-1.41E+00	3.81E-05
497683567	DNA topoisomerase IV subunit A	1.28E+01	6.20E-01	3.63E-03	-2.44E+00	7.29E-06	-3.06E+00	2.57E-06
497683640	acyl-CoA dehydrogenase	1.26E+01	6.20E-01	1.85E-03	-2.23E-01	1.37E-01	-8.42E-01	4.96E-04
497681908	hypothetical protein	1.32E+01	6.21E-01	8.13E-04	-3.37E+00	1.11E-06	-3.99E+00	4.00E-07
490051030	hypothetical protein	1.47E+01	6.22E-01	2.41E-03	1.25E+00	1.01E-04	6.26E-01	3.04E-03
490057356	3-ketoacyl-ACP reductase	1.26E+01	6.24E-01	9.91E-03	-3.65E-01	9.64E-02	-9.89E-01	1.42E-03

490055254	50S ribosomal protein L27	1.32E+01	6.24E-01	5.83E-03	-2.56E+00	8.89E-06	-3.19E+00	3.06E-06
490057983	molybdenum cofactor sulfurase	1.03E+01	6.25E-01	6.81E-03	-6.87E-01	6.41E-03	-1.31E+00	2.07E-04
490054653	O-sialoglycoprotein endopeptidase	8.75E+00	6.30E-01	6.86E-03	-1.14E+00	5.19E-04	-1.77E+00	4.51E-05
490057785	Rieske (2Fe-2S) protein	1.27E+01	6.31E-01	3.72E-03	3.96E-01	3.91E-02	-2.34E-01	1.72E-01
490051738	acyl carrier protein	1.46E+01	6.35E-01	1.09E-02	8.61E-01	4.03E-03	2.25E-01	2.92E-01
497683725	DNA polymerase subunit beta	1.31E+01	6.39E-01	1.22E-02	-3.14E+00	8.55E-06	-3.77E+00	3.34E-06
490057793	glucose-6-phosphate 1-dehydrogenase	1.36E+01	6.39E-01	6.64E-03	-4.64E-01	3.59E-02	-1.10E+00	5.67E-04
490058278	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase	1.46E+01	6.40E-01	4.01E-03	-3.88E-01	4.70E-02	-1.03E+00	4.76E-04
490058659	metallophosphoesterase	1.19E+01	6.42E-01	1.27E-02	-8.72E-01	4.64E-03	-1.51E+00	2.38E-04
497683621	uroporphyrinogen decarboxylase	1.35E+01	6.46E-01	1.08E-02	-9.33E-02	6.64E-01	-7.40E-01	7.88E-03
497681485	chromosome partitioning protein	1.28E+01	6.50E-01	2.26E-03	-2.32E+00	7.22E-06	-2.98E+00	2.49E-06
490054100	orotidine 5'-phosphate decarboxylase	1.45E+01	6.55E-01	3.04E-03	-2.04E+00	1.75E-05	-2.69E+00	4.06E-06
490054384	cell division protein SepF	1.42E+01	6.55E-01	6.77E-03	1.75E-01	3.74E-01	-4.80E-01	3.28E-02
490051605	hydrogen peroxide sensitive repressor	1.74E+01	6.57E-01	8.01E-03	-1.38E-01	4.99E-01	-7.95E-01	4.34E-03
490060159	potassium transporter TrkA	1.33E+01	6.65E-01	8.63E-03	-1.70E+00	1.16E-04	-2.37E+00	1.90E-05
490057153	short-chain dehydrogenase	1.31E+01	6.71E-01	8.49E-03	-2.21E-01	3.03E-01	-8.92E-01	2.88E-03
497681225	hypothetical protein	1.53E+01	6.74E-01	7.07E-03	-5.71E-01	2.09E-02	-1.24E+00	4.32E-04
490059071	hypothetical protein	1.33E+01	6.75E-01	2.19E-03	5.96E-01	5.96E-03	-7.92E-02	6.16E-01
490054720	ArsR family transcriptional regulator	1.31E+01	6.78E-01	6.83E-03	-7.47E-02	7.14E-01	-7.53E-01	5.55E-03
490058051	ribonuclease	1.50E+01	6.78E-01	2.82E-03	9.25E-03	9.57E-01	-6.69E-01	3.98E-03
490052552	ABC transporter	1.05E+01	6.80E-01	7.50E-03	-5.83E-01	2.09E-02	-1.26E+00	4.48E-04
490060087	hypothetical protein	1.18E+01	6.80E-01	5.32E-03	-1.05E+00	9.02E-04	-1.73E+00	5.67E-05
490053805	DNA topoisomerase IV subunit B	1.24E+01	6.83E-01	3.19E-03	-1.09E+00	4.34E-04	-1.78E+00	3.10E-05
490054893	iron ABC transporter ATP-binding protein	1.19E+01	6.84E-01	1.06E-02	-1.35E+00	5.69E-04	-2.03E+00	5.68E-05
490057298	acyl-CoA thioesterase	1.53E+01	6.85E-01	6.44E-03	-9.51E-01	1.93E-03	-1.64E+00	9.86E-05
490053057	aminopeptidase	1.30E+01	6.85E-01	3.39E-03	5.75E-01	1.12E-02	-1.10E-01	5.32E-01
490058132	deoxyguanosinetriphosphate triphosphohydrolase	1.34E+01	6.90E-01	4.04E-04	-4.98E-01	3.22E-03	-1.19E+00	3.15E-05
497683068	hypothetical protein	1.45E+01	6.90E-01	1.22E-02	-1.36E-01	5.66E-01	-8.26E-01	7.31E-03
490051238	MarR family transcriptional regulator	1.17E+01	6.92E-01	1.12E-03	-4.10E+00	1.11E-06	-4.79E+00	4.00E-07
497681690	hypothetical protein	1.24E+01	6.93E-01	2.36E-03	9.11E-02	5.84E-01	-6.01E-01	6.22E-03

497681710	16S rRNA methyltransferase	1.01E+01	6.94E-01	6.38E-03	-7.66E-01	5.93E-03	-1.46E+00	1.89E-04
490051472	exodeoxyribonuclease III	1.57E+01	7.02E-01	4.27E-03	7.50E-01	4.64E-03	4.80E-02	7.98E-01
490058354	ribonuclease PH	1.34E+01	7.06E-01	9.61E-03	-4.78E-01	6.06E-02	-1.18E+00	1.03E-03
490051025	ABC transporter ATP-binding protein	1.23E+01	7.08E-01	2.68E-03	-1.67E+00	5.02E-05	-2.38E+00	7.86E-06
490057335	biotin synthase	1.33E+01	7.11E-01	6.43E-03	8.60E-01	3.88E-03	1.49E-01	4.78E-01
490058843	preprotein translocase subunit YidC	1.52E+01	7.14E-01	1.62E-03	-5.60E-01	7.78E-03	-1.27E+00	1.03E-04
497682032	ribose 5-phosphate isomerase	1.13E+01	7.16E-01	2.11E-03	-1.16E+00	2.64E-04	-1.88E+00	2.00E-05
490055040	RNA methyltransferase	1.27E+01	7.19E-01	2.27E-03	-9.59E-01	7.86E-04	-1.68E+00	3.72E-05
490054918	aldehyde dehydrogenase	1.32E+01	7.22E-01	1.16E-02	5.38E-01	5.14E-02	-1.84E-01	4.50E-01
490060228	techoic acid ABC transporter ATP-binding protein	1.18E+01	7.22E-01	9.89E-03	-2.39E+00	3.86E-05	-3.11E+00	9.00E-06
490058049	ketohydroxyglutarate aldolase	1.48E+01	7.25E-01	9.17E-03	-1.30E+00	7.71E-04	-2.03E+00	6.51E-05
490053245	MFS transporter	1.15E+01	7.25E-01	1.01E-02	-2.66E-01	2.72E-01	-9.91E-01	3.07E-03
490057871	ribokinase	1.44E+01	7.26E-01	6.93E-04	-1.33E+00	4.72E-05	-2.06E+00	5.57E-06
490055743	acyl-CoA dehydrogenase	1.45E+01	7.27E-01	1.76E-03	2.32E-01	1.76E-01	-4.95E-01	1.43E-02
490053856	membrane protein	1.50E+01	7.28E-01	3.87E-03	7.84E-02	6.85E-01	-6.49E-01	8.78E-03
497683556	diaminopimelate epimerase	1.44E+01	7.29E-01	1.34E-02	-1.11E+00	2.84E-03	-1.84E+00	1.78E-04
490054721	Fe-S cluster assembly protein SufB	1.33E+01	7.30E-01	1.47E-02	-8.49E-01	1.10E-02	-1.58E+00	4.53E-04
497681281	dolichol-phosphate mannosyltransferase	1.16E+01	7.31E-01	1.03E-02	-1.53E+00	4.05E-04	-2.26E+00	4.51E-05
497684167	3-oxoacyl-ACP reductase	1.41E+01	7.39E-01	1.33E-02	-4.26E-01	1.20E-01	-1.17E+00	2.05E-03
490055926	FAD-dependent thymidylate synthase	1.46E+01	7.41E-01	2.79E-03	-3.97E-01	5.49E-02	-1.14E+00	4.04E-04
490051175	asparaginase	1.39E+01	7.42E-01	6.20E-03	-1.47E+00	3.00E-04	-2.21E+00	3.14E-05
497684650	GCN5 family acetyltransferase	1.37E+01	7.44E-01	1.24E-02	-6.05E-01	3.99E-02	-1.35E+00	9.36E-04
490053350	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1.26E+01	7.47E-01	1.10E-03	3.17E-02	8.40E-01	-7.15E-01	1.79E-03
490057132	membrane protein	1.32E+01	7.47E-01	8.49E-04	1.27E+00	8.25E-05	5.24E-01	6.63E-03
490052908	hydrogen peroxide-inducible protein	1.35E+01	7.50E-01	1.10E-03	-2.48E+00	5.79E-06	-3.23E+00	2.03E-06
490058552	DNA repair protein RadA	1.08E+01	7.55E-01	3.54E-04	-2.53E+00	2.83E-06	-3.28E+00	1.01E-06
497681677	prolipoprotein diacylglyceryl transferase	1.08E+01	7.55E-01	6.46E-04	-3.62E-01	2.92E-02	-1.12E+00	1.06E-04
490053470	globin	1.34E+01	7.56E-01	4.61E-03	-2.52E+00	1.84E-05	-3.28E+00	4.65E-06
490058945	hypothetical protein	1.01E+01	7.58E-01	4.77E-03	-1.23E+00	6.10E-04	-1.99E+00	4.34E-05
490060544	N-acetyltransferase GCN5	9.59E+00	7.61E-01	5.32E-03	-2.73E-01	2.21E-01	-1.03E+00	1.54E-03

490054141	50S ribosomal protein L5	1.44E+01	7.63E-01	1.29E-03	-4.00E-01	3.45E-02	-1.16E+00	1.84E-04
497681339	HIT family hydrolase	1.54E+01	7.63E-01	9.54E-04	2.74E-02	8.60E-01	-7.36E-01	1.51E-03
490056579	UDP-glucose 4-epimerase	1.32E+01	7.66E-01	2.16E-04	-3.75E-01	1.11E-02	-1.14E+00	3.56E-05
497683130	carbohydrate kinase	1.32E+01	7.67E-01	8.49E-04	-7.31E-01	1.63E-03	-1.50E+00	3.43E-05
490056254	glycerol acyltransferase	1.47E+01	7.68E-01	7.78E-03	-9.03E-01	5.40E-03	-1.67E+00	2.00E-04
490059935	hypothetical protein	1.30E+01	7.68E-01	2.92E-03	-4.38E-01	4.62E-02	-1.21E+00	3.81E-04
490057170	hypothetical protein	1.45E+01	7.76E-01	9.77E-03	-9.58E-01	5.49E-03	-1.73E+00	2.31E-04
490053055	hypothetical protein	1.25E+01	7.81E-01	2.01E-03	-1.40E+00	1.48E-04	-2.18E+00	1.39E-05
497683496	AsnC family transcriptional regulator	1.32E+01	7.81E-01	8.57E-04	-6.98E-01	2.28E-03	-1.48E+00	4.02E-05
490053061	hypothetical protein	9.44E+00	7.82E-01	1.09E-02	-1.74E+00	3.16E-04	-2.52E+00	3.96E-05
490055112	nucleoside triphosphate pyrophosphohydrolase	1.21E+01	7.84E-01	1.04E-03	-2.31E+00	8.33E-06	-3.09E+00	2.49E-06
490054062	glutamine amidotransferase	1.43E+01	7.86E-01	2.04E-03	-8.23E-01	2.42E-03	-1.61E+00	6.38E-05
490056262	helicase	1.37E+01	7.86E-01	6.19E-04	-6.85E-01	1.88E-03	-1.47E+00	3.14E-05
490053069	methionyl-tRNA synthetase	1.21E+01	7.87E-01	2.92E-03	-8.12E-01	3.77E-03	-1.60E+00	9.71E-05
490051505	acyl-CoA synthetase	1.06E+01	7.89E-01	4.42E-03	-2.86E-01	2.00E-01	-1.08E+00	1.26E-03
490057834	ATP-dependent helicase	1.37E+01	7.93E-01	4.07E-04	-5.31E-01	4.65E-03	-1.32E+00	3.69E-05
490051219	phosphate transport regulator	1.64E+01	7.94E-01	6.94E-04	4.04E-02	7.89E-01	-7.54E-01	1.20E-03
497682186	hypothetical protein	1.53E+01	7.96E-01	1.74E-03	-1.62E+00	6.74E-05	-2.42E+00	8.44E-06
490058669	precorrin-3B C17-methyltransferase	1.57E+01	8.00E-01	1.83E-04	-1.12E-01	3.39E-01	-9.12E-01	1.15E-04
490060226	dehydrogenase	9.34E+00	8.06E-01	4.28E-03	-2.84E+00	1.39E-05	-3.65E+00	3.82E-06
490056719	hypothetical protein	9.98E+00	8.08E-01	4.81E-03	-5.19E-01	4.37E-02	-1.33E+00	5.18E-04
490057320	tripeptidyl aminopeptidase	1.49E+01	8.10E-01	3.63E-03	-2.18E+00	3.72E-05	-2.99E+00	6.86E-06
490054159	elongation factor G	1.22E+01	8.12E-01	1.88E-04	-3.82E-01	1.17E-02	-1.19E+00	3.29E-05
490053850	glutamate-1-semialdehyde aminotransferase	1.12E+01	8.14E-01	1.11E-03	-1.10E+00	3.43E-04	-1.92E+00	1.81E-05
490052502	peroxiredoxin	1.39E+01	8.14E-01	1.93E-03	-8.80E-01	1.95E-03	-1.69E+00	5.51E-05
497681608	sporulation protein	1.16E+01	8.15E-01	1.46E-03	-2.06E+00	2.20E-05	-2.87E+00	4.16E-06
490059915	phosphatase	1.34E+01	8.18E-01	3.74E-03	-1.36E+00	4.23E-04	-2.18E+00	3.24E-05
490053384	N-acetyltransferase GCN5	1.46E+01	8.19E-01	6.83E-03	-2.55E-01	3.05E-01	-1.07E+00	2.41E-03
490055252	transferase	1.45E+01	8.19E-01	3.67E-04	-8.29E-01	5.15E-04	-1.65E+00	1.38E-05
490059395	sugar transporter	9.44E+00	8.22E-01	3.31E-03	-1.34E+00	4.10E-04	-2.16E+00	3.03E-05
490060225	transferase	1.23E+01	8.22E-01	2.44E-03	-4.70E-01	3.99E-02	-1.29E+00	3.09E-04

490055557	hypothetical protein	1.17E+01	8.24E-01	1.86E-03	-1.52E-01	4.20E-01	-9.76E-01	1.04E-03
497681245	50S rRNA methyltransferase	1.41E+01	8.24E-01	1.88E-04	4.50E-01	6.03E-03	-3.74E-01	1.27E-02
490054699	phosphoglycerate kinase	8.99E+00	8.25E-01	1.08E-03	-1.39E+00	1.10E-04	-2.21E+00	9.50E-06
490050102	threonine synthase	1.38E+01	8.26E-01	2.28E-03	-2.23E+00	2.39E-05	-3.06E+00	4.92E-06
497682960	endoribonuclease	9.90E+00	8.30E-01	3.43E-03	-1.01E+00	1.94E-03	-1.84E+00	7.33E-05
490060709	hypothetical protein	1.45E+01	8.30E-01	3.58E-03	-2.95E+00	1.10E-05	-3.78E+00	3.24E-06
497681776	pyruvate dehydrogenase E1	1.43E+01	8.33E-01	7.13E-03	-9.02E-01	7.28E-03	-1.74E+00	2.31E-04
490051375	DNA polymerase III subunit delta	1.35E+01	8.36E-01	8.47E-03	-2.25E+00	8.73E-05	-3.09E+00	1.55E-05
490057891	imidazole glycerol phosphate synthase	1.16E+01	8.36E-01	2.56E-03	-8.43E-01	3.68E-03	-1.68E+00	8.96E-05
490055453	elongation factor 4	1.25E+01	8.37E-01	1.12E-03	-4.30E-01	3.36E-02	-1.27E+00	1.65E-04
490057794	6-phosphogluconolactonase, partial	1.44E+01	8.38E-01	4.53E-04	-2.51E+00	5.07E-06	-3.34E+00	1.58E-06
490059712	hypothetical protein	8.12E+00	8.38E-01	3.35E-03	-1.04E+01	1.03E-07	-1.12E+01	4.46E-08
490058441	dynein regulation protein LC7	1.48E+01	8.38E-01	1.04E-03	-1.27E+00	1.81E-04	-2.11E+00	1.24E-05
490051635	sugar hydrolase	1.27E+01	8.38E-01	2.84E-04	-5.15E-01	5.08E-03	-1.35E+00	3.13E-05
490055315	phosphomethylpyrimidine kinase	1.24E+01	8.40E-01	9.51E-03	-7.52E-01	2.17E-02	-1.59E+00	5.32E-04
497683138	sulfurase	1.03E+01	8.40E-01	1.49E-02	-7.78E-01	2.89E-02	-1.62E+00	8.53E-04
497683509	PucR family transcriptional regulator	1.36E+01	8.44E-01	4.39E-04	-1.89E+00	1.39E-05	-2.74E+00	2.57E-06
490057550	phenylalanyl-tRNA synthetase subunit alpha	1.27E+01	8.48E-01	1.25E-03	-2.59E-01	1.67E-01	-1.11E+00	4.13E-04
497681424	transferase	1.29E+01	8.54E-01	8.06E-04	-8.86E-01	1.01E-03	-1.74E+00	2.68E-05
490051382	transferase	1.31E+01	8.54E-01	4.28E-03	-1.27E+00	8.84E-04	-2.12E+00	5.08E-05
490054402	hypothetical protein	9.95E+00	8.57E-01	4.20E-03	-1.72E+00	1.82E-04	-2.57E+00	2.02E-05
490050127	GntR family transcriptional regulator	1.54E+01	8.57E-01	4.72E-04	1.10E-01	4.66E-01	-7.47E-01	1.27E-03
490056489	aspartokinase	1.32E+01	8.57E-01	1.33E-03	-8.41E-01	2.18E-03	-1.70E+00	4.82E-05
490050021	6-phosphofructokinase	1.38E+01	8.57E-01	3.17E-04	-4.93E-01	7.57E-03	-1.35E+00	3.89E-05
490059052	haloacid dehalogenase	8.90E+00	8.61E-01	4.71E-03	-2.15E+00	6.73E-05	-3.01E+00	1.12E-05
490054098	carbamoyl phosphate synthase large subunit	1.39E+01	8.61E-01	1.43E-03	-7.59E-01	4.03E-03	-1.62E+00	6.82E-05
490054090	elongation factor P	1.87E+01	8.61E-01	1.23E-02	5.51E-01	8.65E-02	-3.10E-01	2.98E-01
490052467	4-hydroxyphenylpyruvate dioxygenase	1.55E+01	8.62E-01	2.91E-03	-2.21E-01	3.12E-01	-1.08E+00	1.22E-03
490055921	long-chain fatty acid--CoA ligase	1.42E+01	8.62E-01	2.81E-04	1.74E-02	9.01E-01	-8.44E-01	4.10E-04
490050290	hypothetical protein	8.65E+00	8.62E-01	1.35E-03	-5.41E-01	1.75E-02	-1.40E+00	1.36E-04
490059833	ATP-binding protein	1.20E+01	8.62E-01	2.84E-04	-1.02E+00	1.82E-04	-1.88E+00	7.86E-06

490052148	sugar ABC transporter ATP-binding protein	1.36E+01	8.64E-01	5.80E-04	1.12E-01	4.77E-01	-7.51E-01	1.56E-03
497683539	ribosomal protein S12 methylthiotransferase	1.05E+01	8.74E-01	5.39E-03	-3.01E+00	1.84E-05	-3.88E+00	4.84E-06
497683441	dihydrofolate reductase	9.83E+00	8.74E-01	1.01E-02	-1.49E+00	1.15E-03	-2.36E+00	8.83E-05
497683217	hypothetical protein	8.43E+00	8.78E-01	3.45E-03	-6.22E-01	2.33E-02	-1.50E+00	2.91E-04
490059371	DUF255 domain-containing protein	1.08E+01	8.78E-01	7.76E-04	-1.18E+00	2.51E-04	-2.06E+00	1.32E-05
497681321	chorismate synthase	1.39E+01	8.80E-01	3.52E-04	-4.03E-01	2.20E-02	-1.28E+00	6.27E-05
490060951	acetyltransferase	1.29E+01	8.80E-01	1.09E-03	-9.68E-01	9.90E-04	-1.85E+00	3.03E-05
497682195	ATP/GTP-binding protein	1.40E+01	8.80E-01	3.40E-03	-3.88E-01	1.11E-01	-1.27E+00	7.07E-04
490053871	radical SAM protein	1.21E+01	8.82E-01	2.43E-03	-2.17E+00	3.77E-05	-3.05E+00	6.41E-06
490055242	Zn-dependent hydrolase	1.33E+01	8.87E-01	2.80E-03	-4.06E-01	8.97E-02	-1.29E+00	5.33E-04
490054297	membrane protein	1.42E+01	8.87E-01	6.01E-03	-1.17E-01	6.51E-01	-1.00E+00	4.42E-03
497683816	dimethylallyltranstransferase	1.40E+01	8.87E-01	4.62E-04	4.56E-02	7.71E-01	-8.42E-01	8.02E-04
490053513	glycine cleavage system protein T	7.26E+00	8.88E-01	3.04E-03	-9.24E+00	1.87E-07	-1.01E+01	9.76E-08
497682225	transcription-repair coupling factor	1.30E+01	8.88E-01	2.92E-03	-1.63E+00	1.95E-04	-2.52E+00	1.89E-05
497682041	dynein regulation protein LC7	1.44E+01	8.92E-01	4.35E-03	-1.10E+00	2.35E-03	-1.99E+00	9.19E-05
497682074	phosphatase	1.30E+01	8.93E-01	4.69E-03	-4.75E-01	7.94E-02	-1.37E+00	7.26E-04
490059782	Kinase	1.28E+01	8.95E-01	4.21E-04	-1.25E+00	1.14E-04	-2.14E+00	7.10E-06
497681329	histidyl-tRNA synthetase	1.51E+01	8.96E-01	2.86E-03	-6.46E-01	1.84E-02	-1.54E+00	2.28E-04
490059504	ATPase	1.40E+01	8.97E-01	2.86E-03	-6.32E-01	2.02E-02	-1.53E+00	2.39E-04
490059150	acetyltransferase	1.22E+01	8.98E-01	2.76E-03	-5.41E-01	3.61E-02	-1.44E+00	3.16E-04
490051580	NUDIX hydrolase	1.29E+01	8.99E-01	1.87E-03	-1.79E-01	3.86E-01	-1.08E+00	9.84E-04
490059435	N-acetyl-1-D-myo-inosityl-2-amino-2	1.17E+01	9.01E-01	2.56E-04	-3.42E+00	1.68E-06	-4.32E+00	5.97E-07
497683726	hypothetical protein	1.52E+01	9.05E-01	2.69E-04	3.47E-01	3.61E-02	-5.58E-01	4.26E-03
497681079	hypothetical protein	1.74E+01	9.06E-01	1.14E-02	-2.48E-01	4.18E-01	-1.15E+00	5.06E-03
490056426	DNA gyrase subunit A	1.36E+01	9.06E-01	5.22E-04	-9.58E-02	5.54E-01	-1.00E+00	4.08E-04
490051542	phosphoesterase	1.31E+01	9.08E-01	1.66E-03	-7.50E-01	6.29E-03	-1.66E+00	9.33E-05
490059479	ABC transporter ATP-binding protein	9.53E+00	9.09E-01	4.66E-03	-3.03E+00	1.84E-05	-3.93E+00	4.72E-06
490058894	LuxR family transcriptional regulator	1.50E+01	9.10E-01	2.18E-04	-1.37E+00	4.24E-05	-2.28E+00	3.85E-06
490051506	uroporphyrin-III C-methyltransferase	1.28E+01	9.14E-01	7.07E-04	-1.63E+00	5.55E-05	-2.54E+00	5.86E-06
490052752	phosphoribosyltransferase	1.29E+01	9.17E-01	1.04E-02	-5.53E-01	9.18E-02	-1.47E+00	1.43E-03
490055603	GntR family transcriptional regulator	1.33E+01	9.18E-01	1.12E-03	-9.84E-01	1.17E-03	-1.90E+00	3.33E-05

490058627	hypothetical protein	1.25E+01	9.19E-01	4.30E-04	-2.86E-01	9.41E-02	-1.21E+00	1.32E-04
490059261	O-sialoglycoprotein endopeptidase	1.15E+01	9.19E-01	6.25E-04	-2.11E+00	1.66E-05	-3.03E+00	3.01E-06
497683083	lysyl-tRNA synthetase	1.35E+01	9.27E-01	1.25E-03	-1.24E+00	4.18E-04	-2.16E+00	2.10E-05
497683184	sugar ABC transporter ATPase	1.18E+01	9.28E-01	2.10E-04	-9.26E-01	3.17E-04	-1.85E+00	8.67E-06
490055954	amino acid deaminase	1.66E+01	9.30E-01	7.80E-04	-5.27E-02	7.71E-01	-9.83E-01	7.71E-04
490059459	DEAD/DEAH box helicase	1.26E+01	9.30E-01	2.39E-04	-1.72E-01	2.40E-01	-1.10E+00	1.24E-04
497683076	D-alanyl-D-alanine carboxypeptidase	1.34E+01	9.36E-01	6.60E-04	3.11E-01	9.92E-02	-6.25E-01	6.61E-03
490054926	prolyl-tRNA synthetase	1.15E+01	9.37E-01	5.25E-04	-7.36E-01	2.73E-03	-1.67E+00	3.39E-05
497681684	phosphoribosyl-AMP cyclohydrolase	1.29E+01	9.48E-01	2.35E-03	1.18E-01	6.05E-01	-8.30E-01	5.94E-03
490052952	peptide ABC transporter ATPase	1.26E+01	9.51E-01	7.82E-03	-2.98E+00	3.89E-05	-3.93E+00	8.62E-06
490051619	RNA polymerase sigma factor RpoE	1.31E+01	9.53E-01	7.17E-03	-1.75E+00	5.17E-04	-2.70E+00	4.58E-05
490052934	GTP-binding protein YchF	1.35E+01	9.53E-01	1.01E-02	-1.49E+00	1.77E-03	-2.44E+00	1.14E-04
490054092	XRE family transcriptional regulator	1.52E+01	9.54E-01	1.15E-04	1.20E-01	3.46E-01	-8.34E-01	2.88E-04
490052969	ABC transporter substrate-binding protein	1.28E+01	9.54E-01	4.71E-04	-7.57E-01	2.34E-03	-1.71E+00	3.01E-05
490052950	ABC transporter	1.43E+01	9.55E-01	9.95E-04	-1.18E+00	4.90E-04	-2.14E+00	2.09E-05
497682046	signal peptide protein	9.91E+00	9.61E-01	9.46E-03	-1.61E+00	1.13E-03	-2.58E+00	8.51E-05
490053269	methyltransferase type 12	1.30E+01	9.63E-01	5.02E-03	-2.17E+00	1.23E-04	-3.13E+00	1.69E-05
490050491	ABC transporter	1.36E+01	9.65E-01	1.25E-02	-2.38E-01	4.73E-01	-1.20E+00	6.18E-03
490055581	hypothetical protein	1.40E+01	9.72E-01	1.21E-03	-8.98E-01	2.70E-03	-1.87E+00	5.06E-05
490058681	adenylosuccinate synthetase	1.31E+01	9.75E-01	1.40E-03	-9.67E-01	2.17E-03	-1.94E+00	4.93E-05
490055203	ATPase	1.25E+01	9.76E-01	9.79E-04	-3.72E-01	8.30E-02	-1.35E+00	2.35E-04
490051497	RNA polymerase sigma factor SigB	1.11E+01	9.76E-01	7.37E-03	-1.40E+00	1.92E-03	-2.38E+00	1.04E-04
490058694	acetyltransferase	1.28E+01	9.79E-01	3.76E-04	-1.40E+00	8.78E-05	-2.38E+00	6.07E-06
490058571	NADP oxidoreductase coenzyme F420-dependent	1.37E+01	9.79E-01	2.26E-03	-2.33E+00	4.13E-05	-3.31E+00	6.56E-06
497681571	penicillin-binding protein	1.37E+01	9.79E-01	6.23E-04	-5.13E-01	2.00E-02	-1.49E+00	8.89E-05
497682020	rod shape-determining protein Mbl	1.19E+01	9.81E-01	2.69E-04	-1.09E+00	2.35E-04	-2.07E+00	8.57E-06
490057486	ATPase AAA	1.31E+01	9.82E-01	4.50E-04	-1.35E+00	1.30E-04	-2.33E+00	7.86E-06
490052610	pyrimidine-nucleoside phosphorylase	1.22E+01	9.82E-01	6.97E-03	-1.23E-01	6.77E-01	-1.11E+00	5.35E-03
490051760	ATP/GTP-binding protein	8.10E+00	9.85E-01	4.76E-04	-9.94E-01	6.80E-04	-1.98E+00	1.79E-05
497683320	alpha-ketoglutarate decarboxylase	1.22E+01	9.86E-01	6.12E-05	-9.11E-01	1.36E-04	-1.90E+00	4.03E-06

490053859	aromatic acid decarboxylase	1.35E+01	9.92E-01	2.58E-04	-2.00E+00	1.41E-05	-2.99E+00	2.49E-06
490060751	acetyltransferase	1.41E+01	9.93E-01	4.62E-04	-2.74E+00	6.05E-06	-3.73E+00	1.88E-06
497683969	electron transfer flavoprotein subunit alpha	1.01E+01	9.96E-01	3.67E-04	-5.30E-01	1.21E-02	-1.53E+00	5.03E-05
490059931	3-hydroxyacyl-CoA dehydrogenase	1.26E+01	9.97E-01	2.27E-04	-7.53E-01	1.45E-03	-1.75E+00	1.71E-05
490054507	conserved hypothetical protein	1.20E+01	1.00E+00	3.49E-03	2.16E+00	1.03E-04	1.16E+00	2.20E-03
490055318	D-alanine--D-alanine ligase	1.35E+01	1.00E+00	1.37E-04	-1.47E+00	3.13E-05	-2.47E+00	2.96E-06
490053288	aconitate hydratase	1.29E+01	1.00E+00	2.11E-04	-1.76E+00	2.12E-05	-2.76E+00	2.68E-06
490058986	alkaline D-peptidase	1.52E+01	1.00E+00	1.93E-04	-9.24E-01	4.39E-04	-1.93E+00	9.59E-06
497682254	hypothetical protein	1.38E+01	1.00E+00	1.19E-02	-9.17E-01	2.49E-02	-1.92E+00	6.73E-04
490059512	methyltransferase	1.06E+01	1.01E+00	7.55E-04	-2.20E+00	2.30E-05	-3.21E+00	3.82E-06
490054061	pyridoxal biosynthesis lyase	1.32E+01	1.01E+00	2.30E-04	-1.91E-01	2.27E-01	-1.20E+00	1.17E-04
490054287	glutamine synthetase	1.12E+01	1.01E+00	1.24E-03	-8.10E-01	5.46E-03	-1.82E+00	7.35E-05
490052780	hypothetical protein	1.24E+01	1.01E+00	5.82E-04	-2.89E-01	1.40E-01	-1.30E+00	2.03E-04
490055449	metallo-beta-lactamase	1.07E+01	1.01E+00	1.27E-04	-4.96E-01	6.90E-03	-1.51E+00	2.12E-05
490057512	nuclease PIN	1.22E+01	1.02E+00	9.40E-05	3.87E-01	1.63E-02	-6.34E-01	1.41E-03
497682319	diguanylate cyclase	1.26E+01	1.02E+00	4.30E-04	3.69E-01	6.05E-02	-6.53E-01	5.50E-03
490052169	N5,N10-methylene tetrahydromethanopterin reductase	1.04E+01	1.03E+00	3.76E-03	6.41E-01	3.99E-02	-3.84E-01	1.70E-01
490052171	inositol monophosphatase	1.03E+01	1.03E+00	5.87E-04	-3.22E+00	5.07E-06	-4.26E+00	1.64E-06
490050353	DEAD/DEAH box helicase	1.33E+01	1.04E+00	1.81E-04	-1.80E+00	1.92E-05	-2.83E+00	2.57E-06
490050097	50S ribosomal protein L31	1.86E+01	1.04E+00	1.39E-04	-7.45E-01	1.15E-03	-1.78E+00	1.20E-05
490055334	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	1.40E+01	1.04E+00	4.46E-05	-1.62E+00	9.05E-06	-2.67E+00	1.57E-06
490058358	ABC transporter ATP-binding protein	1.17E+01	1.05E+00	5.27E-05	-1.75E+00	7.83E-06	-2.80E+00	1.57E-06
490059734	5-hydroxymethyluracil DNA glycosylase	1.23E+01	1.05E+00	1.09E-04	-1.21E+00	7.69E-05	-2.26E+00	3.95E-06
490058231	hypothetical protein	1.59E+01	1.05E+00	1.79E-03	3.72E-01	1.40E-01	-6.79E-01	1.82E-02
490051669	pyruvate phosphate dikinase	1.06E+01	1.05E+00	6.87E-03	-3.54E-01	2.72E-01	-1.40E+00	2.22E-03
490051170	hypothetical protein	8.78E+00	1.05E+00	2.52E-04	-5.93E-01	6.76E-03	-1.65E+00	3.24E-05
490054097	carbamoyl phosphate synthase small subunit	1.46E+01	1.06E+00	4.18E-04	-1.22E+00	2.99E-04	-2.28E+00	1.13E-05
490054901	gamma-aminobutyraldehyde dehydrogenase	1.44E+01	1.06E+00	6.59E-04	-3.59E-01	9.43E-02	-1.42E+00	1.85E-04
490056167	conserved hypothetical protein	1.20E+01	1.06E+00	6.59E-04	-1.69E+00	9.02E-05	-2.76E+00	7.39E-06
490052751	deoxycytidine triphosphate deaminase	1.33E+01	1.06E+00	8.19E-05	-2.70E-01	6.66E-02	-1.33E+00	3.24E-05

497682872	mycothiol acetyltransferase	1.04E+01	1.06E+00	4.04E-04	-4.04E-01	4.92E-02	-1.47E+00	9.60E-05
490055373	aminotransferase	1.51E+01	1.07E+00	1.70E-03	-7.71E-02	7.50E-01	-1.14E+00	1.57E-03
490051220	hypothetical protein	9.45E+00	1.07E+00	2.86E-03	-3.76E-01	1.75E-01	-1.44E+00	8.17E-04
497683736	GntR family transcriptional regulator	1.22E+01	1.07E+00	2.57E-04	-3.83E-01	4.42E-02	-1.45E+00	6.58E-05
490058547	dihydroxy-acid dehydratase	1.34E+01	1.07E+00	4.28E-03	-4.83E-01	1.19E-01	-1.55E+00	8.72E-04
490058384	malate dehydrogenase	1.41E+01	1.07E+00	2.70E-03	-1.69E+00	3.86E-04	-2.77E+00	2.68E-05
497682188	phosphoribosylaminoimidazole carboxylase	1.39E+01	1.07E+00	5.63E-05	-4.50E-01	6.87E-03	-1.52E+00	1.28E-05
490053262	cell division protein SepF	9.78E+00	1.07E+00	9.94E-04	7.08E+00	6.87E-07	6.00E+00	8.19E-07
490052576	biotin carboxyl carrier protein	1.26E+01	1.08E+00	2.56E-04	-9.56E-01	7.08E-04	-2.03E+00	1.33E-05
490060090	adenosine deaminase	1.21E+01	1.08E+00	3.50E-04	-1.56E+00	7.92E-05	-2.64E+00	5.70E-06
490056250	glycerophosphoryl diester phosphodiesterase	8.63E+00	1.08E+00	4.94E-04	3.94E-01	6.42E-02	-6.87E-01	6.46E-03
497681275	GntR family transcriptional regulator	9.47E+00	1.08E+00	2.23E-04	-2.31E+00	9.05E-06	-3.39E+00	2.03E-06
490053510	serine dehydratase	1.44E+01	1.08E+00	5.43E-04	6.47E-01	1.01E-02	-4.35E-01	4.62E-02
490054429	acyl-CoA dehydrogenase	1.40E+01	1.09E+00	9.18E-05	-6.08E-01	2.75E-03	-1.70E+00	1.28E-05
490061079	acetyltransferase	1.58E+01	1.09E+00	1.77E-04	-1.18E+00	1.79E-04	-2.27E+00	6.37E-06
490054252	cytochrome C oxidase assembly protein	1.53E+01	1.09E+00	3.31E-03	-2.57E-01	3.64E-01	-1.35E+00	1.53E-03
497681974	UDP pyrophosphate synthase	1.28E+01	1.10E+00	9.44E-04	-6.53E-01	1.63E-02	-1.75E+00	1.05E-04
490059730	methyltransferase	1.38E+01	1.10E+00	3.34E-05	-1.04E+00	6.68E-05	-2.13E+00	2.59E-06
497681302	transcriptional regulator	1.19E+01	1.10E+00	3.67E-04	-1.91E-01	3.04E-01	-1.29E+00	2.03E-04
490051798	hydrolase	1.18E+01	1.10E+00	5.26E-03	-1.24E+00	4.46E-03	-2.34E+00	1.44E-04
490059511	hypothetical protein	1.39E+01	1.10E+00	2.55E-04	5.24E-01	1.45E-02	-5.78E-01	8.57E-03
497681590	nitrogen fixation protein NifU	1.10E+01	1.10E+00	6.38E-03	4.75E-01	1.63E-01	-6.29E-01	7.46E-02
497682425	alpha/beta hydrolase	1.31E+01	1.10E+00	1.18E-04	-1.00E+00	2.82E-04	-2.11E+00	6.42E-06
497682035	amino acid transporter	1.57E+01	1.12E+00	5.44E-05	3.39E-01	2.70E-02	-7.81E-01	4.51E-04
490054700	triosephosphate isomerase	1.24E+01	1.12E+00	1.90E-03	1.34E-01	6.03E-01	-9.90E-01	4.73E-03
490056667	diadenosine tetraphosphatase	1.20E+01	1.13E+00	6.24E-03	-1.11E+00	9.75E-03	-2.23E+00	2.54E-04
497682904	D-inositol 3-phosphate glycosyltransferase	1.18E+01	1.13E+00	1.39E-04	-6.15E-01	4.63E-03	-1.75E+00	1.98E-05
490055933	30S ribosomal protein S15	1.40E+01	1.13E+00	2.80E-03	-5.97E-01	5.81E-02	-1.73E+00	4.18E-04
490052653	hypothetical protein	1.42E+01	1.14E+00	1.63E-04	5.92E-01	6.51E-03	-5.43E-01	8.74E-03
490054119	30S ribosomal protein S11	1.34E+01	1.14E+00	1.92E-03	-7.63E-01	1.78E-02	-1.90E+00	1.74E-04
490058210	hypothetical protein	1.48E+01	1.14E+00	4.80E-03	-6.84E-01	5.49E-02	-1.82E+00	5.90E-04

490056193	hydrolase	1.35E+01	1.14E+00	9.70E-05	-1.79E+00	1.81E-05	-2.93E+00	2.24E-06
490054158	elongation factor Tu	1.07E+01	1.14E+00	5.01E-05	-5.49E-01	3.19E-03	-1.69E+00	9.39E-06
490054077	hypothetical protein	1.15E+01	1.14E+00	7.32E-04	5.23E-01	3.79E-02	-6.19E-01	1.82E-02
490061031	monooxygenase	1.27E+01	1.15E+00	1.87E-03	3.67E-01	1.81E-01	-7.83E-01	1.52E-02
497681388	hypothetical protein	1.29E+01	1.15E+00	2.26E-03	-9.56E-01	8.05E-03	-2.11E+00	1.26E-04

[a] Identification is based on annotation by NCBI. **[b]** Description is based on NCBI annotation of protein similarity by BLAST. **[c]** Average normalized expression in the WT strain. **[d]** Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. **[e]** Adjusted P-value in *ΔbldG* as compared to the WT strain. **[f]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. **[g]** Adjusted P-value in *ΔbldA* as compared to the WT strain. **[h]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and **[i]** Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Table A.1.8: Proteins determined to be similarly expressed (P = 0.01) between the *ΔbldA* and WT strains of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G -WT[e]	logFC A -WT[f]	adj.P.Val A-WT[g]	logFC A -G[h]	adj.P.Val A -G[i]
490051542	phosphoesterase	1.31E+01	9.08E-01	1.66E-03	-7.50E-01	6.29E-03	-1.66E+00	9.33E-05
490053540	aspartyl/glutamyl-tRNA amidotransferase subunit B	1.45E+01	-8.39E-01	3.00E-04	-7.48E-01	8.21E-04	9.08E-02	4.98E-01
490050097	50S ribosomal protein L31	1.86E+01	1.04E+00	1.39E-04	-7.45E-01	1.15E-03	-1.78E+00	1.20E-05
490050047	cellulose-binding protein	1.39E+01	-1.60E+00	1.55E-05	-7.45E-01	1.10E-03	8.58E-01	4.61E-04
490055708	membrane protein	1.31E+01	-8.63E-01	3.81E-04	-7.44E-01	1.22E-03	1.19E-01	4.13E-01
490059421	polyphosphate glucokinase	1.27E+01	3.04E-01	1.40E-01	-7.44E-01	7.68E-03	-1.05E+00	1.27E-03
490057753	2,4-diaminobutyric acid acetyltransferase	1.27E+01	3.64E-01	7.47E-02	-7.43E-01	6.31E-03	-1.11E+00	7.56E-04
490051756	chemical-damaging agent resistance protein C	1.23E+01	1.87E-01	3.69E-01	-7.43E-01	1.01E-02	-9.30E-01	3.13E-03
490059726	thiamine monophosphate kinase	1.45E+01	-3.41E-01	1.14E-01	-7.43E-01	8.90E-03	-4.02E-01	8.49E-02
497681415	ATPase AAA	1.42E+01	-1.36E+00	1.77E-04	-7.41E-01	5.72E-03	6.20E-01	1.17E-02
490059021	restriction endonuclease	1.11E+01	-8.20E-01	3.55E-03	-7.41E-01	8.48E-03	7.93E-02	7.10E-01
490056986	Putative dehydrogenase	1.23E+01	2.49E+00	6.27E-06	-7.40E-01	4.07E-03	-3.23E+00	3.06E-06
490061074	Telomere-associated protein	1.07E+01	2.79E+00	3.03E-06	-7.39E-01	2.84E-03	-3.53E+00	2.03E-06
490054926	prolyl-tRNA synthetase	1.15E+01	9.37E-01	5.25E-04	-7.36E-01	2.73E-03	-1.67E+00	3.39E-05
490050032	MarR family transcriptional regulator	1.27E+01	1.40E-01	3.44E-01	-7.34E-01	2.03E-03	-8.73E-01	7.27E-04
490050933	membrane protein	1.27E+01	2.22E-01	1.53E-01	-7.32E-01	2.21E-03	-9.55E-01	4.93E-04
490060993	esterase	1.49E+01	-2.00E+00	3.36E-05	-7.32E-01	8.00E-03	1.27E+00	4.54E-04
497683130	carbohydrate kinase	1.32E+01	7.67E-01	8.49E-04	-7.31E-01	1.63E-03	-1.50E+00	3.43E-05
490054531	cobaltochelatase subunit CobN	1.23E+01	5.73E-01	6.65E-03	-7.29E-01	3.13E-03	-1.30E+00	1.31E-04
490053315	chemotaxis protein CheY	8.47E+00	-3.94E-01	9.16E-02	-7.28E-01	1.32E-02	-3.34E-01	1.65E-01
490057896	Peptidase S16	1.04E+01	-4.61E-02	7.97E-01	-7.24E-01	4.53E-03	-6.78E-01	5.53E-03
497685343	hypothetical protein	1.54E+01	-2.63E+00	1.99E-06	-7.17E-01	1.28E-03	1.91E+00	8.05E-06
497681549	fuculose phosphate aldolase	1.40E+01	-3.61E-01	1.67E-02	-7.17E-01	9.58E-04	-3.55E-01	2.35E-02
490058553	DNA integrity scanning protein disA	1.29E+01	3.05E-01	1.51E-01	-7.15E-01	1.07E-02	-1.02E+00	1.73E-03
490058131	ferredoxin	1.31E+01	-1.40E+00	9.97E-05	-7.14E-01	4.56E-03	6.83E-01	5.03E-03
490055158	serine/threonine protein kinase	1.31E+01	4.61E-02	7.03E-01	-7.01E-01	8.52E-04	-7.48E-01	5.30E-04

490052035	short-chain dehydrogenase	1.36E+01	-3.82E+00	1.87E-06	-6.99E-01	7.34E-03	3.12E+00	4.39E-06
497683496	AsnC family transcriptional regulator	1.32E+01	7.81E-01	8.57E-04	-6.98E-01	2.28E-03	-1.48E+00	4.02E-05
490055769	carbon-nitrogen hydrolase	1.15E+01	3.89E+00	2.79E-06	-6.96E-01	1.47E-02	-4.58E+00	2.23E-06
490057758	hypothetical protein	1.12E+01	1.68E-01	3.54E-01	-6.94E-01	7.25E-03	-8.62E-01	2.24E-03
490054192	single-stranded DNA-binding protein	1.50E+01	-5.11E-01	1.67E-03	-6.91E-01	5.27E-04	-1.80E-01	1.32E-01
490057983	molybdenum cofactor sulfurase	1.03E+01	6.25E-01	6.81E-03	-6.87E-01	6.41E-03	-1.31E+00	2.07E-04
497682237	transcriptional regulator	1.18E+01	1.48E+00	1.64E-04	-6.86E-01	1.12E-02	-2.17E+00	2.97E-05
490056008	hypothetical protein	1.33E+01	2.08E-01	2.65E-01	-6.86E-01	8.33E-03	-8.94E-01	2.05E-03
497682494	membrane protein	8.49E+00	3.43E-01	7.90E-02	-6.85E-01	7.48E-03	-1.03E+00	8.92E-04
490056262	helicase	1.37E+01	7.86E-01	6.19E-04	-6.85E-01	1.88E-03	-1.47E+00	3.14E-05
490054468	integral membrane regulatory protein	1.26E+01	-7.88E-01	1.12E-03	-6.84E-01	3.40E-03	1.04E-01	5.22E-01
490059732	metal-binding protein	1.27E+01	1.20E+00	3.06E-04	-6.83E-01	7.61E-03	-1.88E+00	3.81E-05
490057393	PadR family transcriptional regulator	1.28E+01	2.52E-02	8.75E-01	-6.83E-01	3.10E-03	-7.08E-01	2.25E-03
490056017	UDP-N-acetylmuramate--alanine ligase	1.30E+01	-8.05E-02	6.16E-01	-6.77E-01	4.36E-03	-5.97E-01	7.08E-03
490057744	magnesium chelatase	1.34E+01	3.05E-01	1.40E-01	-6.77E-01	1.20E-02	-9.82E-01	1.81E-03
490057536	isocitrate dehydrogenase	1.13E+01	1.57E+00	4.16E-05	-6.75E-01	4.57E-03	-2.24E+00	9.31E-06
490051026	transporter	1.27E+01	1.75E-01	1.58E-01	-6.74E-01	1.06E-03	-8.49E-01	2.75E-04
497682482	aminotransferase	1.49E+01	-1.43E+00	1.80E-05	-6.71E-01	1.23E-03	7.58E-01	5.75E-04
490055041	DNA-binding protein	1.33E+01	1.30E+00	2.15E-04	-6.71E-01	8.73E-03	-1.97E+00	3.24E-05
497683596	hypothetical protein	9.33E+00	2.20E+00	6.08E-06	-6.67E-01	3.50E-03	-2.87E+00	2.96E-06
490059781	zinc metalloprotease	1.44E+01	-5.23E-01	9.26E-03	-6.64E-01	4.54E-03	-1.41E-01	4.02E-01
490054284	glutamine-synthetase adenylyltransferase	1.35E+01	4.56E-01	3.34E-02	-6.63E-01	1.01E-02	-1.12E+00	6.87E-04
490050023	acetate kinase	1.22E+01	1.74E+00	8.11E-06	-6.62E-01	1.55E-03	-2.40E+00	3.04E-06
490055475	methionyl-tRNA formyltransferase	1.18E+01	-1.88E+00	5.01E-05	-6.58E-01	1.38E-02	1.22E+00	5.97E-04
490058537	RNA polymerase subunit sigma-24	1.13E+01	-3.42E+00	3.40E-06	-6.56E-01	1.41E-02	2.77E+00	9.80E-06
490056677	30S ribosomal protein S16	1.30E+01	-1.13E-01	5.71E-01	-6.53E-01	1.41E-02	-5.41E-01	2.84E-02
490058391	serine/threonine-protein kinase	1.12E+01	3.09E-01	1.74E-02	-6.52E-01	7.28E-04	-9.61E-01	8.19E-05
490060633	hypothetical protein	1.51E+01	-2.55E+00	4.16E-06	-6.50E-01	5.31E-03	1.90E+00	1.95E-05
497684087	helicase	1.41E+01	-1.20E-01	4.08E-01	-6.46E-01	3.73E-03	-5.26E-01	8.79E-03
490055150	urocanate hydratase	1.10E+01	-3.41E-01	4.22E-02	-6.41E-01	4.17E-03	-3.01E-01	7.97E-02
497683970	electron transfer flavoprotein subunit beta	1.42E+01	-1.45E-01	4.56E-01	-6.40E-01	1.48E-02	-4.95E-01	3.84E-02

497683687	ATP-binding protein	9.36E+00	-2.11E+00	1.30E-05	-6.39E-01	7.62E-03	1.47E+00	9.39E-05
490058782	magnesium transporter CorA	1.30E+01	-1.33E+00	1.79E-04	-6.38E-01	1.01E-02	6.88E-01	6.54E-03
490055707	preprotein translocase subunit TatA	1.24E+01	-4.60E-01	1.09E-02	-6.38E-01	3.57E-03	-1.78E-01	2.54E-01
490058574	histidine kinase	1.25E+01	1.65E-01	3.45E-01	-6.37E-01	8.96E-03	-8.01E-01	2.65E-03
497681613	excinuclease ABC subunit C	1.15E+01	5.41E-02	7.66E-01	-6.36E-01	9.02E-03	-6.90E-01	5.59E-03
490051214	phosphate ABC transporter substrate-binding protein	1.38E+01	-1.43E+00	5.40E-05	-6.32E-01	5.20E-03	7.97E-01	1.43E-03
490053516	hypothetical protein	1.43E+01	-1.01E+00	7.00E-04	-6.32E-01	1.01E-02	3.76E-01	6.95E-02
490052572	methylmalonyl-CoA carboxyltransferase	1.10E+01	1.17E-01	4.84E-01	-6.24E-01	8.42E-03	-7.41E-01	3.31E-03
490708574	Ligase	1.18E+01	4.88E-01	2.41E-03	-6.17E-01	1.10E-03	-1.11E+00	4.51E-05
490053401	IolB protein	1.50E+01	3.28E-01	3.39E-02	-6.16E-01	3.17E-03	-9.44E-01	3.03E-04
497682904	D-inositol 3-phosphate glycosyltransferase	1.18E+01	1.13E+00	1.39E-04	-6.15E-01	4.63E-03	-1.75E+00	1.98E-05
490052584	membrane protein	1.32E+01	2.07E+00	1.78E-05	-6.15E-01	1.11E-02	-2.69E+00	6.58E-06
497683069	permease	1.36E+01	-3.63E+00	1.15E-06	-6.14E-01	3.38E-03	3.01E+00	2.03E-06
490054223	50S ribosomal protein L9	1.21E+01	-2.93E-01	5.07E-02	-6.09E-01	3.34E-03	-3.16E-01	4.95E-02
490054429	acyl-CoA dehydrogenase	1.40E+01	1.09E+00	9.18E-05	-6.08E-01	2.75E-03	-1.70E+00	1.28E-05
490052918	aspartate ammonia-lyase	1.29E+01	-2.50E-01	1.79E-01	-6.07E-01	1.29E-02	-3.57E-01	8.52E-02
490055030	methyltransferase	1.38E+01	-1.67E+00	1.40E-05	-6.03E-01	3.51E-03	1.06E+00	1.61E-04
490059902	membrane protein	1.50E+01	-9.82E-01	3.93E-04	-6.00E-01	6.93E-03	3.83E-01	4.12E-02
490055126	ABC transporter	1.37E+01	4.32E-01	7.34E-03	-6.00E-01	2.24E-03	-1.03E+00	1.14E-04
490057935	LuxR family transcriptional regulator	1.51E+01	-1.05E+00	6.12E-05	-6.00E-01	1.61E-03	4.47E-01	6.15E-03
490055831	hypothetical protein	1.25E+01	-2.43E-01	1.05E-01	-5.99E-01	4.48E-03	-3.56E-01	3.78E-02
490058959	hypothetical protein	1.47E+01	-5.49E-01	8.84E-03	-5.97E-01	8.79E-03	-4.83E-02	7.80E-01
497682588	protease	1.39E+01	-9.62E-01	2.96E-04	-5.96E-01	5.07E-03	3.66E-01	3.71E-02
497683476	acylphosphatase	1.54E+01	1.25E+00	7.16E-05	-5.94E-01	4.64E-03	-1.84E+00	1.29E-05
490051170	hypothetical protein	8.78E+00	1.05E+00	2.52E-04	-5.93E-01	6.76E-03	-1.65E+00	3.24E-05
490053359	GntR family transcriptional regulator	1.33E+01	1.16E+00	2.11E-04	-5.93E-01	9.10E-03	-1.75E+00	3.24E-05
497683444	3-phosphoglycerate dehydrogenase	1.18E+01	-6.07E-03	9.68E-01	-5.92E-01	1.78E-03	-5.86E-01	1.64E-03
490057507	acetyltransferase	1.46E+01	-5.62E-01	4.81E-03	-5.92E-01	5.57E-03	-3.05E-02	8.42E-01
490058352	nucleoside-triphosphate diphosphatase	1.28E+01	6.03E-01	8.29E-03	-5.92E-01	1.29E-02	-1.19E+00	3.55E-04
490056120	pseudouridine synthase	1.40E+01	-7.37E-01	2.23E-03	-5.91E-01	9.33E-03	1.46E-01	4.05E-01
497683267	hypothetical protein	1.23E+01	1.21E-01	4.03E-01	-5.90E-01	5.58E-03	-7.12E-01	1.96E-03

490055202	GntR family transcriptional regulator	1.28E+01	-3.55E-01	3.39E-02	-5.90E-01	5.63E-03	-2.36E-01	1.47E-01
490053475	ABC transporter	1.53E+01	6.08E-01	3.19E-03	-5.90E-01	5.55E-03	-1.20E+00	1.25E-04
490050764	conserved hypothetical protein	1.41E+01	-2.63E+00	4.60E-06	-5.89E-01	1.09E-02	2.04E+00	1.89E-05
497683535	histidine kinase	1.27E+01	-1.31E-01	2.80E-01	-5.88E-01	2.21E-03	-4.57E-01	6.76E-03
497681945	hypothetical protein	1.55E+01	-9.61E-02	4.11E-01	-5.86E-01	2.03E-03	-4.90E-01	4.41E-03
490054344	pseudouridine-5'-phosphate glycosidase	1.35E+01	-2.10E+00	2.79E-06	-5.82E-01	1.88E-03	1.52E+00	1.27E-05
497682796	phosphoribosylformylglycinamidine synthase	1.21E+01	-5.32E-02	7.16E-01	-5.82E-01	5.54E-03	-5.28E-01	7.80E-03
497683813	transferase	1.52E+01	4.52E-01	2.35E-02	-5.79E-01	1.19E-02	-1.03E+00	6.25E-04
497681436	hypothetical protein	1.44E+01	5.17E-01	1.52E-02	-5.77E-01	1.37E-02	-1.09E+00	5.30E-04
490052939	hypothetical protein	1.44E+01	-2.71E+00	1.86E-06	-5.77E-01	3.36E-03	2.13E+00	4.84E-06
490057278	histidine kinase	1.24E+01	-1.48E+00	3.69E-05	-5.77E-01	6.63E-03	9.08E-01	5.97E-04
490058111	hypothetical protein	1.48E+01	2.12E+00	7.16E-06	-5.71E-01	7.47E-03	-2.69E+00	3.79E-06
490057607	cysteine--1-D-myo-inosityl 2-amino-2-deoxy-alpha-D-glucopyranoside ligase	1.31E+01	1.26E+00	4.77E-05	-5.71E-01	4.10E-03	-1.83E+00	9.82E-06
497682315	hypothetical protein	1.39E+01	-1.01E+00	1.41E-04	-5.69E-01	3.94E-03	4.40E-01	1.17E-02
490060489	hypothetical protein	1.39E+01	-1.02E+00	3.19E-04	-5.66E-01	9.10E-03	4.58E-01	2.08E-02
497683199	purine nucleoside phosphorylase	1.43E+01	5.89E-01	2.49E-03	-5.63E-01	4.65E-03	-1.15E+00	9.96E-05
497682539	hypothetical protein	1.30E+01	5.36E-01	5.36E-03	-5.62E-01	6.32E-03	-1.10E+00	1.80E-04
490058843	preprotein translocase subunit YidC	1.52E+01	7.14E-01	1.62E-03	-5.60E-01	7.78E-03	-1.27E+00	1.03E-04
490055874	conserved hypothetical protein	1.42E+01	2.08E+00	4.44E-06	-5.58E-01	4.53E-03	-2.64E+00	2.57E-06
490059729	ATP-dependent DNA helicase RecG	1.14E+01	1.36E+00	6.14E-05	-5.56E-01	8.47E-03	-1.92E+00	1.44E-05
490059210	NADH dehydrogenase subunit F	1.43E+01	-2.99E+00	2.69E-06	-5.54E-01	1.18E-02	2.43E+00	6.85E-06
497681738	esterase	1.04E+01	9.57E-02	5.37E-01	-5.52E-01	1.01E-02	-6.48E-01	4.37E-03
490054158	elongation factor Tu	1.07E+01	1.14E+00	5.01E-05	-5.49E-01	3.19E-03	-1.69E+00	9.39E-06
490053474	von Willebrand factor A	1.46E+01	-1.27E+00	9.55E-05	-5.48E-01	9.51E-03	7.24E-01	2.23E-03
490051650	anti-sigma regulatory factor	1.33E+01	-6.78E-01	2.13E-03	-5.45E-01	8.94E-03	1.33E-01	4.04E-01
490058988	GntR family transcriptional regulator	1.13E+01	1.10E-01	4.34E-01	-5.43E-01	7.22E-03	-6.53E-01	2.62E-03
490054057	lauroyl acyltransferase	1.33E+01	2.11E+00	4.79E-06	-5.42E-01	6.27E-03	-2.65E+00	2.94E-06
490051811	hypothetical protein	1.27E+01	-6.68E-01	1.71E-03	-5.41E-01	7.05E-03	1.27E-01	4.01E-01
490056611	membrane protein	1.81E+01	-5.07E-01	2.35E-03	-5.40E-01	2.56E-03	-3.29E-02	7.84E-01
490053037	peptidyl-prolyl cis-trans isomerase	1.32E+01	-3.14E-01	7.45E-02	-5.40E-01	1.35E-02	-2.25E-01	2.05E-01
490059514	hypothetical protein	1.35E+01	1.49E+00	1.02E-05	-5.38E-01	2.58E-03	-2.03E+00	3.80E-06

490054035	molybdenum metabolism regulator	1.36E+01	-6.41E-01	2.45E-03	-5.37E-01	8.41E-03	1.04E-01	5.00E-01
490057834	ATP-dependent helicase	1.37E+01	7.93E-01	4.07E-04	-5.31E-01	4.65E-03	-1.32E+00	3.69E-05
497683969	electron transfer flavoprotein subunit alpha	1.01E+01	9.96E-01	3.67E-04	-5.30E-01	1.21E-02	-1.53E+00	5.03E-05
497682483	hypothetical protein	1.00E+01	5.81E-01	1.93E-03	-5.25E-01	4.75E-03	-1.11E+00	8.83E-05
490059100	hypothetical protein	1.58E+01	-1.32E+00	2.88E-05	-5.20E-01	4.99E-03	7.99E-01	4.90E-04
490054923	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1.32E+01	-5.54E-01	2.97E-03	-5.17E-01	6.16E-03	3.67E-02	7.90E-01
490054229	phosphotransferase	1.29E+01	-2.62E-01	1.02E-01	-5.16E-01	1.18E-02	-2.54E-01	1.32E-01
490051635	sugar hydrolase	1.27E+01	8.38E-01	2.84E-04	-5.15E-01	5.08E-03	-1.35E+00	3.13E-05
490061076	NUDIX hydrolase	1.25E+01	1.82E+00	4.69E-06	-5.09E-01	4.10E-03	-2.33E+00	2.62E-06
490057578	RNA helicase	1.23E+01	1.33E-01	3.39E-01	-5.08E-01	9.05E-03	-6.42E-01	2.65E-03
490055968	secretion protein	1.31E+01	-2.27E+00	6.36E-06	-5.08E-01	1.49E-02	1.76E+00	2.61E-05
497681646	thioesterase	1.31E+01	2.36E-01	1.45E-01	-5.05E-01	1.48E-02	-7.40E-01	2.20E-03
490059039	aldehyde dehydrogenase	1.27E+01	-1.82E+00	1.71E-05	-5.00E-01	1.49E-02	1.32E+00	1.02E-04
490058132	deoxyguanosinetriphosphate triphosphohydrolase	1.34E+01	6.90E-01	4.04E-04	-4.98E-01	3.22E-03	-1.19E+00	3.15E-05
490055449	metallo-beta-lactamase	1.07E+01	1.01E+00	1.27E-04	-4.96E-01	6.90E-03	-1.51E+00	2.12E-05
490058809	membrane protein	1.26E+01	3.23E-01	3.17E-02	-4.94E-01	7.59E-03	-8.17E-01	5.41E-04
490050021	6-phosphofructokinase	1.38E+01	8.57E-01	3.17E-04	-4.93E-01	7.57E-03	-1.35E+00	3.89E-05
490053318	cytochrome C oxidase subunit I	1.35E+01	-1.62E-01	2.10E-01	-4.89E-01	6.99E-03	-3.27E-01	3.49E-02
497681729	oxidoreductase	1.50E+01	3.88E-01	2.61E-02	-4.89E-01	1.45E-02	-8.77E-01	7.62E-04
490058811	prephenate dehydratase	1.32E+01	-2.75E-01	8.06E-02	-4.83E-01	1.37E-02	-2.08E-01	1.94E-01
497684083	hypothetical protein	1.65E+01	-3.40E-01	1.90E-02	-4.77E-01	6.27E-03	-1.37E-01	2.92E-01
490053799	NUDIX hydrolase	1.52E+01	-2.12E-01	8.05E-02	-4.74E-01	4.57E-03	-2.62E-01	4.95E-02
497683249	hypothetical protein	1.44E+01	4.09E-01	1.20E-02	-4.73E-01	9.24E-03	-8.83E-01	3.61E-04
490058978	phosphate ABC transporter ATP-binding protein	1.25E+01	-2.38E+00	2.71E-06	-4.70E-01	9.27E-03	1.91E+00	7.63E-06
497681123	secretion protein EccC	1.55E+01	1.78E-01	1.86E-01	-4.70E-01	9.64E-03	-6.48E-01	1.83E-03
490058118	acyl-CoA synthetase	1.41E+01	-1.10E+00	4.63E-05	-4.68E-01	5.29E-03	6.30E-01	1.06E-03
490053310	anthranilate phosphoribosyltransferase	1.42E+01	3.01E-02	8.44E-01	-4.67E-01	1.48E-02	-4.97E-01	1.03E-02
490057416	histidine kinase	1.30E+01	-2.72E+00	1.87E-06	-4.57E-01	1.16E-02	2.26E+00	4.39E-06
490059669	DNA ligase	1.29E+01	3.62E-01	1.59E-02	-4.53E-01	8.67E-03	-8.16E-01	4.05E-04
497682188	phosphoribosylaminoimidazole carboxylase	1.39E+01	1.07E+00	5.63E-05	-4.50E-01	6.87E-03	-1.52E+00	1.28E-05
497682649	chromosomal replication initiation protein	1.23E+01	-8.29E-02	4.55E-01	-4.48E-01	5.93E-03	-3.65E-01	1.36E-02

490051261	inorganic pyrophosphatase	1.18E+01	2.53E-03	9.87E-01	-4.43E-01	1.26E-02	-4.45E-01	1.13E-02
497682249	tetrapyrrole methylase	1.32E+01	3.74E-01	1.43E-02	-4.42E-01	1.00E-02	-8.16E-01	4.21E-04
490054741	transcriptional regulator	1.33E+01	1.80E+00	4.34E-06	-4.35E-01	7.05E-03	-2.24E+00	2.62E-06
490050489	transcriptional regulator	1.31E+01	1.42E-01	1.91E-01	-4.34E-01	5.31E-03	-5.76E-01	1.14E-03
497681264	phosphoenolpyruvate-protein phosphotransferase	1.15E+01	2.54E+00	1.87E-06	-4.26E-01	1.19E-02	-2.97E+00	1.68E-06
490050511	ATPase	1.36E+01	-6.14E-01	1.45E-03	-4.25E-01	1.23E-02	1.89E-01	1.72E-01
497682197	imidazolonepropionase	1.43E+01	-1.13E+00	4.04E-05	-4.12E-01	9.41E-03	7.13E-01	5.43E-04
497682392	hypothetical protein	1.37E+01	-2.40E+00	1.90E-06	-4.05E-01	1.23E-02	2.00E+00	4.72E-06
490060423	acetyl-CoA acetyltransferase	9.78E+00	1.76E-01	1.32E-01	-3.97E-01	9.83E-03	-5.72E-01	1.49E-03
490057691	cytochrome C peroxidase	1.35E+01	4.58E-01	2.82E-03	-3.87E-01	9.12E-03	-8.44E-01	1.53E-04
490054159	elongation factor G	1.22E+01	8.12E-01	1.88E-04	-3.82E-01	1.17E-02	-1.19E+00	3.29E-05
490056579	UDP-glucose 4-epimerase	1.32E+01	7.66E-01	2.16E-04	-3.75E-01	1.11E-02	-1.14E+00	3.56E-05
497681245	50S rRNA methyltransferase	1.41E+01	8.24E-01	1.88E-04	4.50E-01	6.03E-03	-3.74E-01	1.27E-02
497683636	DNA polymerase III subunit epsilon	1.20E+01	1.22E+00	4.52E-05	4.71E-01	8.29E-03	-7.54E-01	7.10E-04
497685165	DNA-binding protein	9.49E+00	-1.39E-01	2.86E-01	5.02E-01	6.90E-03	6.41E-01	1.83E-03
490056334	2-hydroxyacid dehydrogenase	1.50E+01	-1.27E-01	2.45E-01	5.07E-01	2.76E-03	6.34E-01	7.69E-04
497681010	dihydroxyacetone kinase subunit K	1.31E+01	-2.46E+00	1.87E-06	5.22E-01	4.17E-03	2.98E+00	1.58E-06
490059511	hypothetical protein	1.39E+01	1.10E+00	2.55E-04	5.24E-01	1.45E-02	-5.78E-01	8.57E-03
490051186	TetR family transcriptional regulator	1.20E+01	1.51E-01	2.78E-01	5.32E-01	6.87E-03	3.82E-01	2.63E-02
497681151	hypothetical protein	1.13E+01	-2.26E+00	4.34E-06	5.46E-01	7.13E-03	2.81E+00	2.62E-06
490051269	hypothetical protein	1.03E+01	-2.22E+00	3.93E-06	5.59E-01	4.75E-03	2.78E+00	2.49E-06
490054251	cytochrome BD ubiquinol oxidase subunit I	1.28E+01	1.45E+00	7.98E-05	5.62E-01	1.29E-02	-8.84E-01	1.31E-03
490050037	hypothetical protein	9.80E+00	3.73E+00	1.29E-06	5.67E-01	6.96E-03	-3.16E+00	2.23E-06
490054607	glutamate-binding protein	1.15E+01	-3.22E-02	8.39E-01	5.73E-01	7.18E-03	6.05E-01	5.01E-03
490053057	aminopeptidase	1.30E+01	6.85E-01	3.39E-03	5.75E-01	1.12E-02	-1.10E-01	5.32E-01
490060503	ABC transporter	1.25E+01	-9.91E-02	4.72E-01	5.91E-01	4.46E-03	6.90E-01	1.80E-03
490052653	hypothetical protein	1.42E+01	1.14E+00	1.63E-04	5.92E-01	6.51E-03	-5.43E-01	8.74E-03
490059071	hypothetical protein	1.33E+01	6.75E-01	2.19E-03	5.96E-01	5.96E-03	-7.92E-02	6.16E-01
497683410	hypothetical protein	1.33E+01	-1.33E+00	7.73E-05	6.12E-01	5.99E-03	1.95E+00	1.48E-05
490055478	DNA-binding protein	1.26E+01	-1.23E+00	5.29E-05	6.14E-01	2.77E-03	1.84E+00	9.37E-06
490055736	ribosomal subunit interface protein	1.55E+01	4.09E-01	4.69E-03	6.16E-01	9.06E-04	2.07E-01	8.78E-02

497681389	hypothetical protein	1.52E+01	-3.46E-01	1.91E-02	6.19E-01	1.92E-03	9.65E-01	1.64E-04
490053510	serine dehydratase	1.44E+01	1.08E+00	5.43E-04	6.47E-01	1.01E-02	-4.35E-01	4.62E-02
497682739	hypothetical protein	1.41E+01	-1.02E+00	9.92E-05	6.50E-01	1.48E-03	1.67E+00	1.10E-05
490055906	bacterioferritin	1.42E+01	5.29E-01	8.99E-03	6.63E-01	4.67E-03	1.33E-01	4.29E-01
490053994	Pirin	1.43E+01	-3.74E-03	9.79E-01	6.75E-01	1.18E-03	6.79E-01	1.02E-03
490054410	histidinol dehydrogenase	1.16E+01	2.14E+00	2.29E-05	6.79E-01	1.06E-02	-1.46E+00	2.00E-04
490052153	exodeoxyribonuclease III	1.42E+01	5.24E-01	1.56E-02	7.07E-01	6.03E-03	1.83E-01	3.37E-01
497683414	ABC transporter	1.31E+01	1.35E+00	1.37E-04	7.09E-01	5.32E-03	-6.37E-01	7.87E-03
490061352	UDP-glucose 4-epimerase	1.22E+01	-1.69E+00	7.81E-06	7.37E-01	7.35E-04	2.43E+00	2.57E-06
490057668	hypothetical protein	1.11E+01	-2.34E-01	2.52E-01	7.44E-01	8.63E-03	9.77E-01	2.05E-03
490058740	XRE family transcriptional regulator	1.32E+01	-3.29E-02	8.65E-01	7.49E-01	4.70E-03	7.82E-01	3.36E-03
490051472	exodeoxyribonuclease III	1.57E+01	7.02E-01	4.27E-03	7.50E-01	4.64E-03	4.80E-02	7.98E-01
490052924	fructose 1,6-bisphosphatase	1.42E+01	2.35E+00	2.21E-05	7.52E-01	9.99E-03	-1.60E+00	1.96E-04
490057575	MerR family transcriptional regulator	1.28E+01	3.50E-02	7.91E-01	7.80E-01	6.52E-04	7.45E-01	7.27E-04
490055741	initiation factor 2B subunit alpha	1.25E+01	2.16E+00	5.31E-05	7.86E-01	1.23E-02	-1.38E+00	7.13E-04
497683554	hypothetical protein	1.05E+01	-1.20E+00	1.43E-03	7.87E-01	1.50E-02	1.98E+00	1.31E-04
497681029	alpha-mannosidase	1.44E+01	-1.10E+00	6.21E-05	8.30E-01	3.99E-04	1.93E+00	5.70E-06
490050798	tellurium resistance protein	1.31E+01	-3.62E+00	1.48E-06	8.52E-01	1.09E-03	4.47E+00	8.19E-07
490057335	biotin synthase	1.33E+01	7.11E-01	6.43E-03	8.60E-01	3.88E-03	1.49E-01	4.78E-01
490051738	acyl carrier protein	1.46E+01	6.35E-01	1.09E-02	8.61E-01	4.03E-03	2.25E-01	2.92E-01
490051257	tRNA(Ile)-lysidine synthetase	1.27E+01	5.68E-01	2.07E-02	8.72E-01	4.54E-03	3.05E-01	1.80E-01
490051281	maltose O-acetyltransferase	1.39E+01	-1.92E+00	2.32E-05	8.89E-01	1.77E-03	2.81E+00	5.46E-06
497683507	ATP-binding protein	1.10E+01	4.63E-01	9.65E-03	9.27E-01	4.67E-04	4.63E-01	1.28E-02
490058342	membrane protein	1.33E+01	-1.08E+00	2.12E-04	9.30E-01	6.72E-04	2.01E+00	1.20E-05
490054724	cysteine desulfurase	1.14E+01	4.32E-01	5.40E-02	9.33E-01	2.99E-03	5.01E-01	4.05E-02
490059976	glyoxalase	1.20E+01	-9.10E-01	2.00E-03	9.40E-01	2.55E-03	1.85E+00	6.45E-05
490055235	L-asparagine permease	1.48E+01	5.84E-01	6.18E-03	9.55E-01	7.96E-04	3.72E-01	5.04E-02
490057267	transcriptional activator	1.45E+01	-1.07E+00	3.96E-03	9.80E-01	8.66E-03	2.05E+00	1.82E-04
497685228	hypothetical protein	1.41E+01	5.08E-01	4.48E-02	9.90E-01	3.84E-03	4.82E-01	6.73E-02
490054541	DNA-binding protein	1.52E+01	-8.79E-01	3.19E-04	1.02E+00	2.20E-04	1.90E+00	8.76E-06
497681054	sporulation protein	1.24E+01	-4.68E-01	6.20E-03	1.03E+00	1.74E-04	1.50E+00	2.18E-05

490055325	DNA-binding protein	1.43E+01	4.66E+00	5.43E-06	1.08E+00	1.10E-02	-3.58E+00	2.27E-05
490057583	peptidylprolyl isomerase	1.29E+01	3.21E-01	2.96E-01	1.08E+00	1.01E-02	7.61E-01	3.94E-02
490050602	hypothetical protein	1.45E+01	1.29E+00	3.02E-03	1.10E+00	9.51E-03	-1.93E-01	5.50E-01
497681283	amidohydrolase	1.18E+01	1.90E+00	1.43E-04	1.17E+00	2.66E-03	-7.36E-01	1.99E-02
490051786	HAD family hydrolase	1.15E+01	-1.07E+00	8.28E-03	1.17E+00	7.86E-03	2.24E+00	2.61E-04
490051769	membrane protein	1.41E+01	5.03E-01	3.52E-02	1.18E+00	1.07E-03	6.75E-01	1.42E-02
497681703	DNA-binding protein	1.09E+01	-9.07E-01	1.41E-02	1.19E+00	6.14E-03	2.10E+00	3.02E-04
497682770	hypothetical protein	1.13E+01	-1.93E+00	1.92E-05	1.19E+00	3.22E-04	3.12E+00	3.24E-06
490061463	calcium-binding protein	1.37E+01	-1.07E+00	1.20E-04	1.20E+00	9.84E-05	2.27E+00	4.52E-06
490051030	hypothetical protein	1.47E+01	6.22E-01	2.41E-03	1.25E+00	1.01E-04	6.26E-01	3.04E-03

[a] Identification is based on annotation by NCBI. **[b]** Description is based on NCBI annotation of protein similarity by BLAST. **[c]** Average normalized expression in the WT strain. **[d]** Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. **[e]** Adjusted P-value in *ΔbldG* as compared to the WT strain. **[f]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. **[g]** Adjusted P-value in *ΔbldA* as compared to the WT strain. **[h]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and **[i]** Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Table A.1.9: Proteins determined to be similarly expressed (P = 0.01) between the *ΔbldA* and the *ΔbldG* strains of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G -WT[e]	logFC A -WT[f]	adj.P.Val A-WT[g]	logFC A -G[h]	adj.P.Val A -G[i]
490055158	serine/threonine protein kinase	1.31E+01	4.61E-02	7.03E-01	-7.01E-01	8.52E-04	-7.48E-01	5.30E-04
490050127	GntR family transcriptional regulator	1.54E+01	8.57E-01	4.72E-04	1.10E-01	4.66E-01	-7.47E-01	1.27E-03
490055583	sporulation protein	1.42E+01	-7.20E-01	5.02E-03	-1.46E+00	2.07E-04	-7.43E-01	5.74E-03
490052572	methylmalonyl-CoA carboxyltransferase	1.10E+01	1.17E-01	4.84E-01	-6.24E-01	8.42E-03	-7.41E-01	3.31E-03
497681646	thioesterase	1.31E+01	2.36E-01	1.45E-01	-5.05E-01	1.48E-02	-7.40E-01	2.20E-03
497683621	uroporphyrinogen decarboxylase	1.35E+01	6.46E-01	1.08E-02	-9.33E-02	6.64E-01	-7.40E-01	7.88E-03
497684912	aminotransferase	1.30E+01	-2.30E+00	6.14E-06	-3.04E+00	4.11E-06	-7.39E-01	2.35E-03
490053985	aminoglycoside phosphotransferase	1.26E+01	-1.40E+00	1.82E-04	-2.13E+00	3.32E-05	-7.36E-01	6.16E-03
497681339	HIT family hydrolase	1.54E+01	7.63E-01	9.54E-04	2.74E-02	8.60E-01	-7.36E-01	1.51E-03
497683258	ABC transporter permease	1.31E+01	-1.34E-01	3.27E-01	-8.69E-01	5.55E-04	-7.36E-01	1.16E-03
490059369	regulatory protein	1.25E+01	-1.28E-01	3.06E-01	-8.60E-01	3.76E-04	-7.32E-01	7.65E-04
490057947	hypothetical protein	1.76E+01	3.31E-01	2.44E-02	-4.01E-01	1.58E-02	-7.31E-01	7.75E-04
490055607	modulator of DNA gyrase	1.30E+01	-1.21E-01	4.10E-01	-8.46E-01	9.91E-04	-7.26E-01	1.91E-03
490053350	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1.26E+01	7.47E-01	1.10E-03	3.17E-02	8.40E-01	-7.15E-01	1.79E-03
497683267	hypothetical protein	1.23E+01	1.21E-01	4.03E-01	-5.90E-01	5.58E-03	-7.12E-01	1.96E-03
497683180	hypothetical protein	1.52E+01	-7.34E-02	5.81E-01	-7.85E-01	8.43E-04	-7.11E-01	1.23E-03
490059001	folate-binding protein	1.08E+01	2.14E-01	2.37E-01	-4.96E-01	2.83E-02	-7.10E-01	5.47E-03
490057393	PadR family transcriptional regulator	1.28E+01	2.52E-02	8.75E-01	-6.83E-01	3.10E-03	-7.08E-01	2.25E-03
490059725	glycerol-3-phosphate dehydrogenase	1.33E+01	4.08E-01	4.60E-02	-2.92E-01	1.54E-01	-7.00E-01	6.51E-03
497681613	excinuclease ABC subunit C	1.15E+01	5.41E-02	7.66E-01	-6.36E-01	9.02E-03	-6.90E-01	5.59E-03
497681682	membrane protein	1.53E+01	5.71E-01	2.74E-03	-1.18E-01	4.03E-01	-6.90E-01	1.39E-03
490056250	glycerophosphoryl diester phosphodiesterase	8.63E+00	1.08E+00	4.94E-04	3.94E-01	6.42E-02	-6.87E-01	6.46E-03
490054133	preprotein translocase subunit SecY	1.60E+01	3.02E-01	8.13E-02	-3.83E-01	4.92E-02	-6.85E-01	3.86E-03
497682289	glutaredoxin	1.37E+01	3.08E-01	5.36E-02	-3.74E-01	3.67E-02	-6.82E-01	2.29E-03
490057896	Peptidase S16	1.04E+01	-4.61E-02	7.97E-01	-7.24E-01	4.53E-03	-6.78E-01	5.53E-03
490058051	ribonuclease	1.50E+01	6.78E-01	2.82E-03	9.25E-03	9.57E-01	-6.69E-01	3.98E-03

490054839	mannose-6-phosphate isomerase	1.38E+01	5.88E-01	8.26E-03	-7.76E-02	6.72E-01	-6.65E-01	6.15E-03
490055756	6,7-dimethyl-8-ribityllumazine synthase	1.38E+01	4.27E-01	4.14E-02	-2.37E-01	2.44E-01	-6.63E-01	8.95E-03
490056565	ATP-dependent Clp protease ATP-binding protein	1.20E+01	-6.46E-01	9.95E-04	-1.30E+00	4.20E-05	-6.56E-01	1.21E-03
497682319	diguanylate cyclase	1.26E+01	1.02E+00	4.30E-04	3.69E-01	6.05E-02	-6.53E-01	5.50E-03
490058988	GntR family transcriptional regulator	1.13E+01	1.10E-01	4.34E-01	-5.43E-01	7.22E-03	-6.53E-01	2.62E-03
490053438	adenine phosphoribosyltransferase	1.22E+01	-2.53E+00	3.86E-06	-3.19E+00	3.04E-06	-6.53E-01	3.70E-03
490055160	cell division protein FtsW	1.28E+01	6.00E-01	1.36E-02	-4.96E-02	8.15E-01	-6.50E-01	1.28E-02
490053856	membrane protein	1.50E+01	7.28E-01	3.87E-03	7.84E-02	6.85E-01	-6.49E-01	8.78E-03
497681123	secretion protein EccC	1.55E+01	1.78E-01	1.86E-01	-4.70E-01	9.64E-03	-6.48E-01	1.83E-03
497681738	esterase	1.04E+01	9.57E-02	5.37E-01	-5.52E-01	1.01E-02	-6.48E-01	4.37E-03
497683260	hypothetical protein	1.42E+01	1.56E-01	3.44E-01	-4.90E-01	2.15E-02	-6.45E-01	5.84E-03
490055279	ATP-dependent protease	1.30E+01	-8.66E-01	1.56E-03	-1.51E+00	1.32E-04	-6.44E-01	8.65E-03
490057594	peptidase M50	1.35E+01	-1.29E-01	4.53E-01	-7.73E-01	3.50E-03	-6.44E-01	7.46E-03
490054086	3-dehydroquinate synthase	1.31E+01	-2.75E-01	1.45E-01	-9.18E-01	1.82E-03	-6.43E-01	9.12E-03
490057578	RNA helicase	1.23E+01	1.33E-01	3.39E-01	-5.08E-01	9.05E-03	-6.42E-01	2.65E-03
490054887	uridylate kinase	1.57E+01	4.04E-01	5.81E-02	-2.34E-01	2.67E-01	-6.38E-01	1.29E-02
497683414	ABC transporter	1.31E+01	1.35E+00	1.37E-04	7.09E-01	5.32E-03	-6.37E-01	7.87E-03
490050051	ABC transporter	1.37E+01	2.59E-01	1.91E-01	-3.78E-01	9.11E-02	-6.37E-01	1.29E-02
490057512	nuclease PIN	1.22E+01	1.02E+00	9.40E-05	3.87E-01	1.63E-02	-6.34E-01	1.41E-03
490051363	hypothetical protein	1.27E+01	3.58E-01	2.06E-02	-2.73E-01	7.36E-02	-6.31E-01	1.99E-03
490053043	Ser/Thr protein kinase	1.40E+01	2.35E-01	2.26E-01	-3.96E-01	7.77E-02	-6.31E-01	1.28E-02
490058385	helicase	1.42E+01	-1.62E-01	2.88E-01	-7.91E-01	1.55E-03	-6.29E-01	4.34E-03
497683076	D-alanyl-D-alanine carboxypeptidase	1.34E+01	9.36E-01	6.60E-04	3.11E-01	9.92E-02	-6.25E-01	6.61E-03
497683691	hypothetical protein	1.55E+01	-1.06E+00	7.07E-04	-1.68E+00	9.75E-05	-6.23E-01	1.23E-02
497681154	hypothetical protein	1.11E+01	-4.65E-01	3.29E-02	-1.08E+00	9.98E-04	-6.20E-01	1.35E-02
490053926	preprotein translocase SecA	1.48E+01	-1.10E+00	1.87E-04	-1.72E+00	3.07E-05	-6.19E-01	4.59E-03
490054811	inosine-5`-monophosphate dehydrogenase	1.32E+01	4.17E-01	9.60E-03	-1.91E-01	1.75E-01	-6.08E-01	2.09E-03
497683472	phosphopantetheine adenylyltransferase	1.27E+01	6.16E-01	6.86E-03	8.04E-03	9.66E-01	-6.08E-01	9.63E-03
490061042	glycosyl transferase	1.57E+01	5.38E-01	4.20E-03	-6.82E-02	6.38E-01	-6.06E-01	3.08E-03
497681690	hypothetical protein	1.24E+01	6.93E-01	2.36E-03	9.11E-02	5.84E-01	-6.01E-01	6.22E-03

497683548	recombinase RecA	1.28E+01	2.98E-01	9.44E-02	-3.01E-01	1.13E-01	-5.99E-01	8.66E-03
490056017	UDP-N-acetylmuramate--alanine ligase	1.30E+01	-8.05E-02	6.16E-01	-6.77E-01	4.36E-03	-5.97E-01	7.08E-03
490051727	NADP-dependent oxidoreductase	1.23E+01	-1.44E+00	1.30E-05	-2.03E+00	5.40E-06	-5.96E-01	1.44E-03
490053332	LuxR family transcriptional regulator	1.58E+01	-4.13E-01	1.74E-02	-1.01E+00	3.45E-04	-5.95E-01	4.54E-03
497682435	esterase	1.10E+01	-5.12E-01	9.62E-03	-1.10E+00	3.18E-04	-5.91E-01	6.63E-03
490053804	hypothetical protein	1.34E+01	-4.18E-01	2.72E-02	-1.01E+00	6.60E-04	-5.88E-01	8.56E-03
497683444	3-phosphoglycerate dehydrogenase	1.18E+01	-6.07E-03	9.68E-01	-5.92E-01	1.78E-03	-5.86E-01	1.64E-03
490060420	penicillin-binding protein	1.24E+01	-3.45E-01	3.98E-02	-9.31E-01	6.10E-04	-5.86E-01	5.66E-03
490051267	transcriptional regulator	1.19E+01	3.74E-01	4.06E-02	-2.08E-01	2.41E-01	-5.82E-01	8.69E-03
490059294	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	1.44E+01	-2.26E-01	1.77E-01	-8.08E-01	2.03E-03	-5.82E-01	8.86E-03
497683188	dienelactone hydrolase	1.20E+01	-4.49E-01	1.04E-02	-1.03E+00	2.54E-04	-5.80E-01	4.24E-03
490059511	hypothetical protein	1.39E+01	1.10E+00	2.55E-04	5.24E-01	1.45E-02	-5.78E-01	8.57E-03
490050489	transcriptional regulator	1.31E+01	1.42E-01	1.91E-01	-4.34E-01	5.31E-03	-5.76E-01	1.14E-03
497682629	16S rRNA methyltransferase	1.38E+01	3.65E-01	2.59E-02	-2.09E-01	1.79E-01	-5.74E-01	4.73E-03
490060423	acetyl-CoA acetyltransferase	9.78E+00	1.76E-01	1.32E-01	-3.97E-01	9.83E-03	-5.72E-01	1.49E-03
490061374	beta-lactamase	1.28E+01	-1.04E+00	4.62E-04	-1.62E+00	7.30E-05	-5.72E-01	1.19E-02
490051696	ABC transporter permease	1.14E+01	-2.33E+00	6.15E-06	-2.90E+00	5.07E-06	-5.72E-01	8.66E-03
497683726	hypothetical protein	1.52E+01	9.05E-01	2.69E-04	3.47E-01	3.61E-02	-5.58E-01	4.26E-03
490054993	glutamate-1-semialdehyde 2,1-aminomutase	1.18E+01	-1.11E+00	1.55E-04	-1.66E+00	3.15E-05	-5.51E-01	7.11E-03
490052653	hypothetical protein	1.42E+01	1.14E+00	1.63E-04	5.92E-01	6.51E-03	-5.43E-01	8.74E-03
497681263	signal peptide protein	1.38E+01	-5.57E-01	2.79E-03	-1.10E+00	1.27E-04	-5.42E-01	4.20E-03
497682796	phosphoribosylformylglycinamidine synthase	1.21E+01	-5.32E-02	7.16E-01	-5.82E-01	5.54E-03	-5.28E-01	7.80E-03
490054938	peptidase C45	1.32E+01	-1.79E+00	6.95E-06	-2.32E+00	5.07E-06	-5.28E-01	4.29E-03
497684087	helicase	1.41E+01	-1.20E-01	4.08E-01	-6.46E-01	3.73E-03	-5.26E-01	8.79E-03
490058555	membrane protein	1.36E+01	1.02E-01	4.31E-01	-4.23E-01	1.53E-02	-5.25E-01	5.28E-03
497683323	hypothetical protein	1.36E+01	3.19E-01	3.17E-02	-1.96E-01	1.73E-01	-5.15E-01	5.38E-03
490053310	anthranilate phosphoribosyltransferase	1.42E+01	3.01E-02	8.44E-01	-4.67E-01	1.48E-02	-4.97E-01	1.03E-02
490061010	monooxygenase	1.47E+01	-1.19E+00	7.78E-05	-1.69E+00	2.27E-05	-4.96E-01	8.46E-03
490055743	acyl-CoA dehydrogenase	1.45E+01	7.27E-01	1.76E-03	2.32E-01	1.76E-01	-4.95E-01	1.43E-02
497683903	transcriptional regulator	9.62E+00	2.62E-01	3.88E-02	-2.31E-01	7.84E-02	-4.92E-01	3.27E-03

497681945	hypothetical protein	1.55E+01	-9.61E-02	4.11E-01	-5.86E-01	2.03E-03	-4.90E-01	4.41E-03
497685222	DNA-binding protein	1.24E+01	-2.80E+00	1.67E-06	-3.28E+00	1.68E-06	-4.73E-01	7.42E-03
490052832	PadR family transcriptional regulator	1.26E+01	1.35E-01	3.03E-01	-3.33E-01	3.85E-02	-4.67E-01	8.72E-03
490056048	transcriptional regulator	1.56E+01	2.16E-01	9.96E-02	-2.42E-01	9.04E-02	-4.59E-01	7.46E-03
497683535	histidine kinase	1.27E+01	-1.31E-01	2.80E-01	-5.88E-01	2.21E-03	-4.57E-01	6.76E-03
490052756	molecular chaperone DnaK	1.26E+01	1.03E-01	4.55E-01	-3.47E-01	4.16E-02	-4.49E-01	1.38E-02
490051261	inorganic pyrophosphatase	1.18E+01	2.53E-03	9.87E-01	-4.43E-01	1.26E-02	-4.45E-01	1.13E-02
490059338	hypothetical protein	1.36E+01	4.22E-02	7.55E-01	-3.97E-01	1.92E-02	-4.39E-01	1.15E-02
497681405	glutamate--ammonia ligase	1.65E+01	-5.85E-01	1.23E-03	-1.02E+00	1.03E-04	-4.37E-01	6.80E-03
497683303	GntR family transcriptional regulator	1.26E+01	-3.74E-01	6.74E-03	-7.66E-01	2.72E-04	-3.92E-01	7.15E-03
497681245	50S rRNA methyltransferase	1.41E+01	8.24E-01	1.88E-04	4.50E-01	6.03E-03	-3.74E-01	1.27E-02
497682649	chromosomal replication initiation protein	1.23E+01	-8.29E-02	4.55E-01	-4.48E-01	5.93E-03	-3.65E-01	1.36E-02
497683465	histidine kinase	1.39E+01	-1.34E+00	1.30E-05	-9.06E-01	1.29E-04	4.34E-01	4.97E-03
497682315	hypothetical protein	1.39E+01	-1.01E+00	1.41E-04	-5.69E-01	3.94E-03	4.40E-01	1.17E-02
490057935	LuxR family transcriptional regulator	1.51E+01	-1.05E+00	6.12E-05	-6.00E-01	1.61E-03	4.47E-01	6.15E-03
490055436	heat-shock protein	1.39E+01	-3.33E-01	2.02E-02	1.14E-01	3.77E-01	4.47E-01	7.46E-03
497683507	ATP-binding protein	1.10E+01	4.63E-01	9.65E-03	9.27E-01	4.67E-04	4.63E-01	1.28E-02
490058652	beta-lactamase	1.21E+01	-4.83E-01	9.46E-03	-2.55E-03	9.87E-01	4.80E-01	1.28E-02
497683013	hypothetical protein	1.30E+01	-1.92E-01	1.64E-01	3.04E-01	5.75E-02	4.97E-01	7.46E-03
490053886	NADH dehydrogenase subunit G	1.30E+01	-2.71E+00	2.35E-06	-2.20E+00	8.24E-06	5.16E-01	8.32E-03
490057132	membrane protein	1.32E+01	7.47E-01	8.49E-04	1.27E+00	8.25E-05	5.24E-01	6.63E-03
490057617	ATP-dependent exoDNAse Exonuclease V , alpha subunit/helicase superfamily I member	1.13E+01	-6.70E-01	4.04E-04	-1.43E-01	2.23E-01	5.27E-01	1.81E-03
490059695	short-chain dehydrogenase	1.26E+01	-2.24E+00	4.21E-06	-1.71E+00	2.28E-05	5.27E-01	7.01E-03
497685044	hypothetical protein	1.30E+01	-3.05E+00	1.87E-06	-2.51E+00	6.07E-06	5.39E-01	8.46E-03
497683280	hypothetical protein	1.12E+01	-3.76E-01	4.72E-02	1.66E-01	3.63E-01	5.42E-01	1.48E-02
497684722	translation initiation factor 2	1.33E+01	-2.91E+00	3.40E-06	-2.37E+00	1.34E-05	5.42E-01	1.46E-02
490060147	xylose isomerase	1.30E+01	-5.78E-01	6.89E-03	-2.95E-02	8.67E-01	5.49E-01	1.16E-02
490050318	cytochrome P450	9.47E+00	-1.30E+00	2.33E-05	-7.54E-01	5.69E-04	5.51E-01	2.51E-03
490057811	sugar kinase	1.46E+01	-4.71E-01	1.37E-02	8.25E-02	6.18E-01	5.53E-01	8.95E-03
490055263	metal-binding protein	1.34E+01	-1.02E+00	2.42E-04	-4.55E-01	1.79E-02	5.62E-01	6.44E-03
490054069	hypothetical protein	1.49E+01	-2.13E-01	1.09E-01	3.62E-01	2.43E-02	5.75E-01	2.67E-03

490051187	hypothetical protein	1.34E+01	-9.94E-01	2.81E-04	-4.14E-01	2.71E-02	5.80E-01	5.74E-03
497683434	hypothetical protein	1.37E+01	-1.03E+00	3.06E-04	-4.37E-01	2.65E-02	5.89E-01	6.70E-03
490060251	ATP-binding protein	1.21E+01	-1.70E+00	6.12E-05	-1.10E+00	8.55E-04	5.96E-01	1.48E-02
490054607	glutamate-binding protein	1.15E+01	-3.22E-02	8.39E-01	5.73E-01	7.18E-03	6.05E-01	5.01E-03
490056442	amino acid ABC transporter permease	1.44E+01	1.42E+00	3.13E-05	2.02E+00	1.00E-05	6.06E-01	3.21E-03
497684462	DSBA oxidoreductase	1.26E+01	-3.70E+00	1.15E-06	-3.09E+00	2.70E-06	6.15E-01	3.03E-03
497681415	ATPase AAA	1.42E+01	-1.36E+00	1.77E-04	-7.41E-01	5.72E-03	6.20E-01	1.17E-02
497684135	hypothetical protein	1.32E+01	-2.41E+00	8.11E-06	-1.79E+00	5.11E-05	6.22E-01	9.10E-03
490051030	hypothetical protein	1.47E+01	6.22E-01	2.41E-03	1.25E+00	1.01E-04	6.26E-01	3.04E-03
497683124	Fis family transcriptional regulator	1.30E+01	-2.11E+00	1.70E-05	-1.48E+00	1.42E-04	6.27E-01	9.53E-03
490058118	acyl-CoA synthetase	1.41E+01	-1.10E+00	4.63E-05	-4.68E-01	5.29E-03	6.30E-01	1.06E-03
490056334	2-hydroxyacid dehydrogenase	1.50E+01	-1.27E-01	2.45E-01	5.07E-01	2.76E-03	6.34E-01	7.69E-04
490061238	3-ketoacyl-ACP reductase	1.34E+01	-1.79E+00	5.02E-05	-1.16E+00	7.08E-04	6.35E-01	1.21E-02
497685165	DNA-binding protein	9.49E+00	-1.39E-01	2.86E-01	5.02E-01	6.90E-03	6.41E-01	1.83E-03
490054276	pterin-4-alpha-carbinolamine dehydratase	1.26E+01	-7.91E-01	3.50E-04	-1.50E-01	2.62E-01	6.42E-01	1.36E-03
490057052	Arginase/agmatinase/formiminoglutamase	1.33E+01	-2.32E+00	3.33E-06	-1.67E+00	2.13E-05	6.45E-01	2.12E-03
490055587	hypothetical protein	1.40E+01	-8.28E-01	3.55E-04	-1.76E-01	2.13E-01	6.52E-01	1.60E-03
490054320	branched-chain amino acid ABC transporter substrate-binding protein	1.19E+01	-2.18E+00	2.56E-05	-1.51E+00	2.46E-04	6.71E-01	1.25E-02
490061373	hypothetical protein	1.22E+01	-1.07E+00	8.28E-04	-3.98E-01	8.19E-02	6.73E-01	1.06E-02
490051769	membrane protein	1.41E+01	5.03E-01	3.52E-02	1.18E+00	1.07E-03	6.75E-01	1.42E-02
490056851	hypothetical protein	1.36E+01	-2.59E+00	1.67E-06	-1.92E+00	7.21E-06	6.77E-01	8.95E-04
490053994	pirin	1.43E+01	-3.74E-03	9.79E-01	6.75E-01	1.18E-03	6.79E-01	1.02E-03
490059556	ABC-type dipeptide transport system, solute-binding protein	1.28E+01	-3.03E+00	4.04E-06	-2.35E+00	2.02E-05	6.82E-01	8.05E-03
490058131	ferredoxin	1.31E+01	-1.40E+00	9.97E-05	-7.14E-01	4.56E-03	6.83E-01	5.03E-03
490051385	anti-sigma regulatory factor	1.36E+01	-6.92E-01	1.57E-03	-7.06E-03	9.64E-01	6.85E-01	2.17E-03
490050756	flavodoxin	1.26E+01	-2.63E+00	4.09E-06	-1.95E+00	2.49E-05	6.86E-01	4.04E-03
490058782	magnesium transporter CorA	1.30E+01	-1.33E+00	1.79E-04	-6.38E-01	1.01E-02	6.88E-01	6.54E-03
490060503	ABC transporter	1.25E+01	-9.91E-02	4.72E-01	5.91E-01	4.46E-03	6.90E-01	1.80E-03
497683549	arginine ABC transporter ATP-binding protein	1.35E+01	-1.01E+00	4.76E-04	-3.04E-01	1.09E-01	7.03E-01	3.95E-03
490051113	fructose-bisphosphate aldolase	1.32E+01	-1.46E+00	9.24E-05	-7.59E-01	3.94E-03	7.05E-01	5.02E-03

490051891	hypothetical protein	1.47E+01	-1.98E+00	6.92E-06	-1.28E+00	8.61E-05	7.06E-01	1.60E-03
497682197	imidazolonepropionase	1.43E+01	-1.13E+00	4.04E-05	-4.12E-01	9.41E-03	7.13E-01	5.43E-04
497685208	hypothetical protein	1.18E+01	-1.48E+00	1.96E-04	-7.61E-01	8.29E-03	7.20E-01	9.65E-03
490053474	von Willebrand factor A	1.46E+01	-1.27E+00	9.55E-05	-5.48E-01	9.51E-03	7.24E-01	2.23E-03
490050064	cob(I)yrinic acid a,c-diamide adenosyltransferase	1.25E+01	-2.01E-01	2.59E-01	5.26E-01	2.11E-02	7.26E-01	4.57E-03
490052906	alkyl hydroperoxide reductase	1.42E+01	-2.95E+00	2.79E-06	-2.22E+00	1.49E-05	7.31E-01	3.03E-03
497685168	hypothetical protein	1.35E+01	-3.28E+00	1.68E-06	-2.55E+00	6.07E-06	7.36E-01	2.00E-03
490057575	MerR family transcriptional regulator	1.28E+01	3.50E-02	7.91E-01	7.80E-01	6.52E-04	7.45E-01	7.27E-04
497681258	GntR family transcriptional regulator	1.40E+01	-3.29E-01	4.11E-02	4.28E-01	2.07E-02	7.57E-01	1.29E-03
497682482	aminotransferase	1.49E+01	-1.43E+00	1.80E-05	-6.71E-01	1.23E-03	7.58E-01	5.75E-04
490053425	saicar synthetase	1.38E+01	-4.20E+00	1.67E-06	-3.44E+00	5.07E-06	7.61E-01	5.44E-03
490061267	beta-lactamase	1.29E+01	-1.01E+00	7.98E-05	-2.36E-01	8.29E-02	7.73E-01	4.03E-04
490058353	hypothetical protein	1.39E+01	-9.86E-01	1.38E-03	-2.05E-01	3.40E-01	7.81E-01	5.75E-03
490058740	XRE family transcriptional regulator	1.32E+01	-3.29E-02	8.65E-01	7.49E-01	4.70E-03	7.82E-01	3.36E-03
490057042	Ser/Thr protein kinase	1.28E+01	-7.53E-01	3.01E-03	3.26E-02	8.66E-01	7.86E-01	3.23E-03
490058396	hypothetical protein	1.50E+01	-1.89E+00	2.32E-05	-1.10E+00	5.38E-04	7.88E-01	2.67E-03
497681509	ABC transporter ATPase	1.39E+01	-9.81E-01	8.76E-04	-1.92E-01	3.25E-01	7.89E-01	3.47E-03
490051916	hypothetical protein	1.23E+01	-1.84E+00	5.02E-05	-1.05E+00	1.33E-03	7.89E-01	5.03E-03
490051090	carbonate dehydratase	1.14E+01	-3.16E-01	1.27E-01	4.75E-01	4.75E-02	7.91E-01	5.22E-03
497683313	hypothetical protein	1.34E+01	-1.16E+00	9.54E-04	-3.64E-01	1.38E-01	7.93E-01	8.10E-03
490051214	phosphate ABC transporter substrate-binding protein	1.38E+01	-1.43E+00	5.40E-05	-6.32E-01	5.20E-03	7.97E-01	1.43E-03
490059100	hypothetical protein	1.58E+01	-1.32E+00	2.88E-05	-5.20E-01	4.99E-03	7.99E-01	4.90E-04
490059102	glycosyl transferase	1.32E+01	-1.96E+00	1.23E-04	-1.16E+00	2.72E-03	8.02E-01	1.38E-02
497683561	hypothetical protein	1.31E+01	-8.74E-01	5.37E-03	-7.01E-02	7.80E-01	8.04E-01	1.04E-02
490059876	integral membrane protein	1.52E+01	-1.57E+00	4.69E-06	-7.58E-01	2.50E-04	8.11E-01	1.48E-04
490050156	N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase	1.25E+01	-2.94E+00	1.32E-06	-2.12E+00	5.07E-06	8.18E-01	3.09E-04
490050168	cytochrome P450	1.35E+01	-2.90E+00	2.71E-06	-2.08E+00	1.73E-05	8.24E-01	1.40E-03
490054314	pyruvate kinase	1.24E+01	-1.21E+00	2.37E-04	-3.80E-01	6.52E-02	8.31E-01	2.16E-03
490060987	hypothetical protein	1.44E+01	-1.01E+00	1.16E-04	-1.54E-01	2.60E-01	8.54E-01	3.44E-04
490050047	cellulose-binding protein	1.39E+01	-1.60E+00	1.55E-05	-7.45E-01	1.10E-03	8.58E-01	4.61E-04

490054018	2-hydroxyacid dehydrogenase	1.62E+01	-1.29E+00	1.30E-04	-4.25E-01	3.73E-02	8.66E-01	1.33E-03
490056177	cytochrome C	1.21E+01	-1.05E+00	1.70E-04	-1.83E-01	2.39E-01	8.70E-01	5.90E-04
490053060	butyryl-CoA dehydrogenase	1.38E+01	-5.48E-01	8.68E-03	3.23E-01	8.66E-02	8.72E-01	1.20E-03
490057610	phosphoglycerate mutase	1.59E+01	-1.03E+00	1.53E-04	-1.51E-01	3.04E-01	8.80E-01	4.46E-04
490060245	TetR family transcriptional regulator	1.54E+01	-1.26E+00	6.86E-05	-3.74E-01	3.43E-02	8.84E-01	5.42E-04
490058755	CRISPR-associated protein Cse4	1.46E+01	-1.78E+00	1.56E-04	-8.91E-01	7.49E-03	8.85E-01	6.99E-03
497682206	cystathionine beta-synthase	1.24E+01	-1.31E+00	2.17E-04	-4.18E-01	5.88E-02	8.90E-01	2.08E-03
490060320	hypothetical protein	1.21E+01	-2.92E+00	4.44E-06	-2.03E+00	3.73E-05	8.94E-01	2.05E-03
490061480	hypothetical protein	1.35E+01	-9.28E-01	1.12E-04	-2.65E-02	8.31E-01	9.02E-01	1.60E-04
497684393	CRISPR-associated Cse1 family protein	1.34E+01	-3.81E+00	6.08E-06	-2.91E+00	3.30E-05	9.05E-01	9.88E-03
490056077	acetyltransferase	1.21E+01	-3.33E+00	1.11E-05	-2.42E+00	7.59E-05	9.05E-01	9.64E-03
490058296	hypothetical protein	1.44E+01	-7.31E-01	3.04E-03	1.75E-01	3.47E-01	9.06E-01	1.37E-03
490052722	ornithine cyclodeaminase	1.33E+01	-2.52E+00	2.04E-05	-1.62E+00	2.85E-04	9.07E-01	4.84E-03
490057278	histidine kinase	1.24E+01	-1.48E+00	3.69E-05	-5.77E-01	6.63E-03	9.08E-01	5.97E-04
497682603	short-chain dehydrogenase	1.53E+01	-1.27E+00	1.09E-04	-3.62E-01	5.42E-02	9.08E-01	7.92E-04
490057028	Germacradienol/germacrene D synthase	1.24E+01	-2.87E+00	2.11E-05	-1.96E+00	2.13E-04	9.11E-01	8.95E-03
497683965	phosphohydrolase	1.38E+01	-1.15E+00	6.76E-05	-2.36E-01	1.10E-01	9.12E-01	2.79E-04
490058291	beta-N-acetylhexosaminidase	1.18E+01	-1.16E+00	4.71E-04	-2.47E-01	2.37E-01	9.12E-01	2.12E-03
490060513	terpene synthase	1.25E+01	-2.57E+00	4.16E-06	-1.65E+00	4.76E-05	9.13E-01	8.62E-04
490056340	DSBA oxidoreductase	1.52E+01	-1.76E+00	5.08E-05	-8.45E-01	3.30E-03	9.18E-01	1.92E-03
497685041	calcium-binding protein	1.18E+01	-3.32E+00	2.41E-06	-2.39E+00	1.46E-05	9.29E-01	1.26E-03
490057127	regulator	1.05E+01	-7.29E-01	4.47E-04	2.15E-01	1.13E-01	9.44E-01	1.48E-04
497681741	cholesterol oxidase	1.35E+01	-1.36E+00	4.23E-04	-4.11E-01	1.02E-01	9.50E-01	3.48E-03
490058163	16S rRNA methyltransferase	1.44E+01	-3.67E-01	1.85E-01	5.84E-01	6.71E-02	9.50E-01	9.41E-03
490050677	short-chain dehydrogenase	1.16E+01	-2.77E+00	6.10E-06	-1.81E+00	6.86E-05	9.59E-01	1.58E-03
490059562	Clavaminate synthase 2	1.25E+01	-3.70E+00	1.02E-05	-2.74E+00	6.44E-05	9.61E-01	1.10E-02
497681389	hypothetical protein	1.52E+01	-3.46E-01	1.91E-02	6.19E-01	1.92E-03	9.65E-01	1.64E-04
490055176	sulfurtransferase	1.51E+01	-1.10E+00	4.28E-03	-1.29E-01	6.64E-01	9.66E-01	1.02E-02
490057668	hypothetical protein	1.11E+01	-2.34E-01	2.52E-01	7.44E-01	8.63E-03	9.77E-01	2.05E-03
490057118	N-acetyltransferase GCN5	1.45E+01	-2.45E+00	9.38E-06	-1.43E+00	2.00E-04	1.02E+00	9.85E-04
490050165	conserved hypothetical protein	1.30E+01	-3.14E+00	1.15E-06	-2.11E+00	4.11E-06	1.03E+00	6.22E-05

490059602	GCN5 family acetyltransferase	8.99E+00	-8.18E-01	3.49E-03	2.15E-01	3.18E-01	1.03E+00	1.44E-03
490054110	30S ribosomal protein S9	1.51E+01	-1.52E+00	5.63E-04	-4.80E-01	1.05E-01	1.04E+00	5.10E-03
497685139	peptidoglycan-binding protein	1.34E+01	-2.36E+00	2.83E-06	-1.32E+00	5.57E-05	1.05E+00	1.48E-04
490053554	flavoprotein	1.21E+01	-4.27E+00	3.03E-06	-3.22E+00	1.64E-05	1.05E+00	3.51E-03
497681630	hypothetical protein	1.36E+01	-1.18E+00	5.76E-05	-1.28E-01	3.55E-01	1.05E+00	1.29E-04
497685451	hydrolase	1.47E+01	-2.90E+00	6.56E-06	-1.85E+00	8.76E-05	1.05E+00	1.38E-03
490057622	phenoxazinone synthase	1.16E+01	-2.82E+00	2.70E-05	-1.77E+00	4.41E-04	1.06E+00	5.39E-03
497682714	3-hydroxyacyl-CoA dehydrogenase	1.37E+01	-1.18E+00	4.04E-04	-1.22E-01	5.40E-01	1.06E+00	9.36E-04
490055030	methyltransferase	1.38E+01	-1.67E+00	1.40E-05	-6.03E-01	3.51E-03	1.06E+00	1.61E-04
497681663	hypothetical protein	1.49E+01	-1.29E+00	7.88E-04	-2.17E-01	3.84E-01	1.07E+00	2.66E-03
490050095	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	1.43E+01	-8.02E-01	5.46E-03	2.68E-01	2.52E-01	1.07E+00	1.74E-03
490056065	N-acetyl-gamma-glutamyl-phosphate reductase	1.22E+01	-1.56E+00	1.40E-03	-4.83E-01	1.70E-01	1.08E+00	1.10E-02
490054396	dienelactone hydrolase	1.15E+01	1.68E+00	2.04E-05	2.75E+00	5.01E-06	1.08E+00	2.39E-04
490059108	cytochrome P450	1.34E+01	-3.79E+00	1.15E-06	-2.71E+00	2.89E-06	1.08E+00	1.02E-04
497682964	chorismate mutase	1.25E+01	-2.72E+00	1.14E-05	-1.62E+00	2.19E-04	1.10E+00	1.41E-03
490060086	peptide ABC transporter substrate-binding protein	1.39E+01	-1.41E+00	1.70E-03	-2.92E-01	3.59E-01	1.12E+00	7.03E-03
490054981	aldehyde dehydrogenase	1.17E+01	-2.46E+00	7.43E-06	-1.33E+00	2.26E-04	1.13E+00	4.76E-04
490054313	hypothetical protein	1.45E+01	-1.47E+00	2.00E-05	-3.30E-01	3.82E-02	1.14E+00	8.65E-05
490060449	cyclic diguanylate phosphodiesterase	1.34E+01	-1.23E-01	7.15E-01	1.02E+00	1.78E-02	1.15E+00	1.00E-02

[a]Identification is based on annotation by NCBI. [b] Description is based on NCBI annotation of protein similarity by BLAST. [c] Average normalized expression in the WT strain. [d] Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. [e]Adjusted P-value in *ΔbldG* as compared to the WT strain. [f] Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. [g] Adjusted P-value in *ΔbldA* as compared to the WT strain. [h] Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and [i] Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Table A.1.10: Transcriptional regulators determined to be significantly (P = 0.01) over or under-expressed in the *ΔbldA* compared to the WT strain of *S. clavuligerus*.

ID[a]	Description[b]	AveExpr-WT[c]	logFC G-WT[d]	adj.P.Val G-WT[e]	logFC A-WT[f]	adj.P.Val A-WT[g]	logFC A-G[h]	adj.P.Val A-G[i]
497681972	Fur family transcriptional regulator	1.37E+01	-1.38E+00	2.36E-03	-4.25E+00	1.46E-05	-2.87E+00	6.96E-05
490051238	MarR family transcriptional regulator	1.17E+01	6.92E-01	1.12E-03	-4.10E+00	1.11E-06	-4.79E+00	4.00E-07
497685222	DNA-binding protein	1.24E+01	-2.80E+00	1.67E-06	-3.28E+00	1.68E-06	-4.73E-01	7.42E-03
490056384	LuxR family transcriptional regulator	1.50E+01	-1.79E+00	5.87E-03	-3.24E+00	4.38E-04	-1.45E+00	1.94E-02
490056694	GntR family transcriptional regulator	1.35E+01	-2.01E+00	1.28E-03	-3.04E+00	2.22E-04	-1.03E+00	3.40E-02
497682165	XRE family transcriptional regulator	1.04E+01	1.38E+00	5.22E-03	-2.96E+00	1.61E-04	-4.34E+00	2.01E-05
490051193	LacI family transcriptional regulator	1.35E+01	-9.46E-01	2.79E-03	-2.84E+00	1.84E-05	-1.89E+00	1.00E-04
490051417	MarR family transcriptional regulator	1.43E+01	-5.68E-01	1.79E-02	-2.83E+00	1.23E-05	-2.26E+00	2.46E-05
490051912	GntR family transcriptional regulator	1.33E+01	2.78E-01	4.90E-02	-2.81E+00	2.74E-06	-3.09E+00	1.61E-06
497683061	NmrA family protein	1.21E+01	-9.51E-01	1.66E-03	-2.76E+00	1.39E-05	-1.81E+00	7.54E-05
497682848	TetR family transcriptional regulator	1.27E+01	-2.37E+00	1.13E-03	-2.72E+00	8.42E-04	-3.44E-01	4.81E-01
497685265	LuxR family transcriptional regulator	1.04E+01	-1.61E+00	2.70E-05	-2.69E+00	5.34E-06	-1.08E+00	2.72E-04
497684806	GntR family transcriptional regulator	1.16E+01	3.93E-01	1.33E-01	-2.68E+00	4.05E-05	-3.07E+00	1.72E-05
490056872	AsnC family transcriptional regulator	1.32E+01	-7.50E-01	1.10E-02	-2.67E+00	3.10E-05	-1.92E+00	1.29E-04
490055448	HrcA family transcriptional regulator	1.07E+01	3.86E-01	3.54E-01	-2.66E+00	5.65E-04	-3.04E+00	2.40E-04
490057306	TetR family transcriptional regulator	1.15E+01	-8.32E-01	1.18E-03	-2.64E+00	7.11E-06	-1.81E+00	2.78E-05
490058107	LuxR family transcriptional regulator	1.25E+01	-8.07E-01	6.02E-02	-2.61E+00	4.37E-04	-1.81E+00	2.57E-03
490055493	MarR family transcriptional regulator	1.44E+01	-3.44E-01	3.60E-02	-2.61E+00	5.07E-06	-2.27E+00	5.80E-06
497683347	putative regulatory protein (AfsR-like protein)	1.52E+01	-2.64E+00	8.11E-06	-2.57E+00	1.59E-05	7.25E-02	7.22E-01
497682579	transcriptional regulator	1.15E+01	3.14E-01	2.33E-01	-2.56E+00	6.05E-05	-2.87E+00	2.82E-05
490051829	LysR family transcriptional regulator	1.42E+01	-7.73E-01	1.06E-02	-2.54E+00	4.30E-05	-1.76E+00	2.31E-04
490051029	DtxR family transcriptional regulator	1.42E+01	-1.25E+00	4.95E-04	-2.53E+00	2.28E-05	-1.29E+00	5.52E-04
490055879	AraC family transcriptional regulator	1.36E+01	-1.26E+00	8.85E-05	-2.52E+00	5.93E-06	-1.26E+00	1.09E-04
490058723	LuxR family transcriptional regulator	1.36E+01	-9.05E-01	1.27E-01	-2.52E+00	3.49E-03	-1.61E+00	2.34E-02
490047179	MerR-family transcriptional regulator	1.03E+01	-3.17E-02	9.63E-01	-2.45E+00	3.27E-03	-2.42E+00	3.06E-03
490050159	PbsX family transcriptional regulator	1.38E+01	-2.52E+00	3.03E-06	-2.45E+00	5.79E-06	7.16E-02	6.35E-01

490050038	MarR family transcriptional regulator	1.08E+01	4.89E-01	1.09E-02	-2.43E+00	7.49E-06	-2.92E+00	2.96E-06
497681386	GntR family transcriptional regulator	1.18E+01	-2.82E-01	6.71E-01	-2.35E+00	9.48E-03	-2.07E+00	1.53E-02
490050197	DNA-binding protein	9.67E+00	-1.17E+00	9.20E-04	-2.34E+00	4.11E-05	-1.17E+00	1.24E-03
490060004	regulatory protein	1.09E+01	3.90E-01	2.38E-02	-2.32E+00	7.67E-06	-2.71E+00	3.34E-06
490057927	transcriptional regulator	1.51E+01	-1.74E+00	1.66E-04	-2.32E+00	5.72E-05	-5.80E-01	3.91E-02
497681275	GntR family transcriptional regulator	9.47E+00	1.08E+00	2.23E-04	-2.31E+00	9.05E-06	-3.39E+00	2.03E-06
497683951	LysR family transcriptional regulator	1.13E+01	2.81E+00	1.45E-05	-2.30E+00	5.62E-05	-5.11E+00	2.03E-06
497685129	ArsR family transcriptional regulator	1.09E+01	-2.57E-01	6.16E-02	-2.27E+00	5.07E-06	-2.02E+00	5.57E-06
490058041	XRE family transcriptional regulator	1.05E+01	-1.32E+00	1.75E-04	-2.26E+00	1.96E-05	-9.43E-01	1.30E-03
490053914	LuxR family transcriptional regulator	1.37E+01	-1.33E+00	1.36E-04	-2.22E+00	1.81E-05	-8.91E-01	1.40E-03
497683559	TerD-family protein	1.39E+01	-2.67E+00	1.17E-05	-2.17E+00	4.81E-05	5.04E-01	4.50E-02
497683714	GntR family transcriptional regulator	1.31E+01	2.23E-01	1.18E-01	-2.12E+00	7.83E-06	-2.34E+00	4.06E-06
490056617	transcriptional regulator	1.15E+01	-1.14E-01	7.77E-01	-2.12E+00	1.24E-03	-2.00E+00	1.46E-03
490052578	DeoR family transcripitonal regulator	8.23E+00	-9.72E-01	1.87E-03	-2.11E+00	5.35E-05	-1.14E+00	1.11E-03
490058573	LuxR family transcriptional regulator	1.28E+01	-8.38E-01	4.13E-02	-2.10E+00	9.46E-04	-1.26E+00	1.02E-02
490057572	regulatory protein	1.34E+01	3.88E-01	4.78E-02	-2.09E+00	2.58E-05	-2.47E+00	9.23E-06
490059040	RpiR family transcriptional regulator	1.34E+01	-4.70E-01	9.60E-02	-1.97E+00	2.50E-04	-1.50E+00	9.01E-04
490051647	DeoR family transcriptional regulator	1.14E+01	1.41E+00	4.00E-05	-1.96E+00	1.46E-05	-3.37E+00	1.73E-06
490053558	XRE family transcriptional regulator	9.14E+00	-7.75E-04	9.97E-01	-1.90E+00	1.11E-04	-1.90E+00	9.26E-05
497683509	PucR family transcriptional regulator	1.36E+01	8.44E-01	4.39E-04	-1.89E+00	1.39E-05	-2.74E+00	2.57E-06
490052791	transcriptional regulator	1.40E+01	-2.16E+00	1.90E-05	-1.87E+00	5.82E-05	2.97E-01	1.54E-01
497682129	IclR family transcriptional regulator	1.52E+01	-1.93E+00	3.86E-05	-1.86E+00	6.86E-05	6.58E-02	7.49E-01
490051556	TetR family transcriptional regulator	1.23E+01	2.83E-02	9.42E-01	-1.86E+00	1.02E-03	-1.89E+00	8.35E-04
490055137	transcriptional regulator	1.37E+01	-2.42E-01	3.25E-01	-1.84E+00	2.43E-04	-1.60E+00	4.39E-04
490058790	IclR family transcriptional regulator	1.23E+01	-1.97E+00	1.35E-03	-1.82E+00	2.95E-03	1.43E-01	7.33E-01
490060648	LuxR family transcriptional regulator	9.47E+00	1.80E+00	9.31E-03	-1.80E+00	1.33E-02	-3.61E+00	3.88E-04
490054063	transcriptional regulator	1.41E+01	-2.86E-01	4.34E-02	-1.76E+00	1.34E-05	-1.48E+00	2.15E-05
490051741	PucR family transcriptional regulator	1.12E+01	-5.67E-01	2.83E-02	-1.74E+00	1.97E-04	-1.18E+00	1.32E-03
497682584	XRE family transcriptional regulator	1.16E+01	2.11E+00	1.14E-05	-1.74E+00	4.30E-05	-3.86E+00	1.73E-06
490051191	transcriptional regulator	1.30E+01	-3.64E-01	3.28E-01	-1.72E+00	2.89E-03	-1.36E+00	8.09E-03
497681422	LuxR family transcriptional regulator	1.18E+01	4.68E-01	3.73E-02	-1.70E+00	1.22E-04	-2.16E+00	3.01E-05

490057142	regulatory protein	1.14E+01	-8.91E-03	9.61E-01	-1.69E+00	2.60E-05	-1.68E+00	2.10E-05
497681429	GntR family transcriptional regulator	1.44E+01	-4.61E-01	1.73E-01	-1.69E+00	1.70E-03	-1.23E+00	7.27E-03
497683533	regulatory protein	1.47E+01	-7.38E-01	3.23E-03	-1.67E+00	7.51E-05	-9.31E-01	1.34E-03
490056868	RpiR family transcriptional regulator	1.24E+01	2.35E-01	1.33E-01	-1.66E+00	3.44E-05	-1.89E+00	1.48E-05
490057686	transcriptional regulator	1.31E+01	5.10E-01	9.20E-03	-1.65E+00	3.92E-05	-2.16E+00	8.94E-06
490057423	GntR family transcriptional regulator	1.54E+01	-1.45E+00	2.39E-04	-1.61E+00	2.10E-04	-1.59E-01	4.75E-01
490055173	LuxR family transcriptional regulator	1.36E+01	-1.77E+00	9.21E-05	-1.59E+00	2.32E-04	1.79E-01	4.27E-01
490051157	PhoU family transcriptional regulator	1.38E+01	-7.23E-01	1.23E-03	-1.56E+00	3.74E-05	-8.35E-01	7.69E-04
497683124	Fis family transcriptional regulator	1.30E+01	-2.11E+00	1.70E-05	-1.48E+00	1.42E-04	6.27E-01	9.53E-03
490055317	AsnC family transcriptional regulator	1.37E+01	-1.94E+00	1.49E-05	-1.48E+00	8.36E-05	4.68E-01	2.14E-02
490054231	MarR family transcriptional regulator	1.37E+01	-1.06E+00	3.31E-03	-1.42E+00	1.12E-03	-3.65E-01	1.92E-01
490053695	transcriptional regulator	1.32E+01	-3.07E-03	9.87E-01	-1.41E+00	1.09E-04	-1.41E+00	9.22E-05
490055141	DNA-binding protein	1.45E+01	-3.10E+00	1.30E-05	-1.41E+00	1.02E-03	1.69E+00	3.37E-04
490060107	XRE family transcriptional regulator	1.33E+01	3.99E-01	4.45E-02	-1.41E+00	1.82E-04	-1.81E+00	4.19E-05
490058894	LuxR family transcriptional regulator	1.50E+01	9.10E-01	2.18E-04	-1.37E+00	4.24E-05	-2.28E+00	3.85E-06
497681813	LacI family transcriptional regulator	1.68E+01	-2.29E-01	1.76E-01	-1.36E+00	1.46E-04	-1.13E+00	3.27E-04
490056421	DNA-binding protein	1.10E+01	-2.97E-01	1.40E-01	-1.33E+00	3.69E-04	-1.04E+00	1.20E-03
490054315	transcriptional regulator	1.28E+01	5.07E-01	5.32E-02	-1.32E+00	1.14E-03	-1.82E+00	1.79E-04
490050132	DNA-binding protein	1.34E+01	-4.75E-01	1.96E-02	-1.27E+00	2.44E-04	-8.00E-01	2.35E-03
497685154	regulatory protein	1.58E+01	3.41E-01	3.10E-01	-1.27E+00	7.49E-03	-1.61E+00	2.09E-03
490059720	IclR family transcriptional regulator	1.49E+01	8.09E-01	1.51E-02	-1.11E+00	5.43E-03	-1.91E+00	2.88E-04
490055876	response regulator	1.44E+01	-1.24E+00	2.76E-05	-1.10E+00	7.59E-05	1.40E-01	2.68E-01
497685379	DNA-binding protein	1.54E+01	1.18E-01	6.46E-01	-1.09E+00	4.16E-03	-1.21E+00	2.19E-03
497683997	MarR family transcriptional regulator	1.38E+01	-8.66E-02	4.23E-01	-1.07E+00	6.29E-05	-9.80E-01	7.95E-05
497681565	IclR family transcriptional regulator	1.34E+01	-1.07E+00	1.77E-04	-1.06E+00	2.75E-04	1.05E-02	9.45E-01
497682175	LytR family transcriptional regulator	1.01E+01	-2.28E-01	1.58E-01	-1.06E+00	4.04E-04	-8.30E-01	1.26E-03
490054828	LuxR family transcriptional regulator	1.57E+01	-5.52E-01	7.05E-03	-1.04E+00	4.41E-04	-4.87E-01	1.62E-02
490052594	transcriptional regulator	1.52E+01	-9.31E-01	1.57E-04	-1.04E+00	1.34E-04	-1.05E-01	4.26E-01
497681563	MarR family transcriptional regulator	1.47E+01	4.56E-01	1.46E-02	-1.03E+00	4.01E-04	-1.49E+00	5.06E-05
490058915	TetR family transcriptional regulator	1.27E+01	-1.99E-01	4.54E-01	-1.03E+00	7.20E-03	-8.27E-01	1.71E-02
497683030	regulator	1.37E+01	-6.56E-01	2.58E-03	-1.01E+00	4.12E-04	-3.58E-01	4.62E-02

490053332	LuxR family transcriptional regulator	1.58E+01	-4.13E-01	1.74E-02	-1.01E+00	3.45E-04	-5.95E-01	4.54E-03
497682597	XRE family transcriptional regulator	1.22E+01	-2.70E+00	2.76E-05	-1.00E+00	6.34E-03	1.70E+00	3.87E-04
490052695	XRE family transcriptional regulator	1.24E+01	-2.17E-01	3.07E-01	-9.99E-01	2.61E-03	-7.83E-01	7.55E-03
490055603	GntR family transcriptional regulator	1.33E+01	9.18E-01	1.12E-03	-9.84E-01	1.17E-03	-1.90E+00	3.33E-05
490053058	DNA-binding protein	1.48E+01	5.15E-01	1.69E-02	-9.51E-01	1.40E-03	-1.47E+00	1.25E-04
497681284	AsnC family transcriptional regulator	1.29E+01	4.10E-01	1.30E-01	-9.35E-01	9.10E-03	-1.35E+00	1.38E-03
490059687	transcriptional regulator	1.33E+01	2.13E+00	1.16E-05	-9.34E-01	1.10E-03	-3.06E+00	3.40E-06
497683911	transcriptional regulator	1.27E+01	-5.29E-01	5.87E-03	-8.89E-01	6.52E-04	-3.60E-01	3.87E-02
497683062	TetR family transcriptional regulator	1.45E+01	1.75E+00	6.19E-05	-8.82E-01	3.13E-03	-2.63E+00	1.08E-05
490058535	REX family transcriptional regulator	1.26E+01	1.38E+00	4.17E-04	-8.76E-01	6.13E-03	-2.26E+00	4.11E-05
490060366	TetR family transcriptional regulator	1.56E+01	3.13E-01	2.35E-02	-8.64E-01	2.68E-04	-1.18E+00	4.52E-05
490059369	regulatory protein	1.25E+01	-1.28E-01	3.06E-01	-8.60E-01	3.76E-04	-7.32E-01	7.65E-04
490057346	transcriptional regulator	1.01E+01	1.20E-01	6.24E-01	-8.47E-01	1.09E-02	-9.67E-01	5.43E-03
490053302	AsnC family transcriptional regulator	1.56E+01	-4.72E-01	4.97E-03	-8.42E-01	3.99E-04	-3.70E-01	1.94E-02
497683782	DNA-binding protein	1.25E+01	3.06E-01	7.30E-02	-8.08E-01	1.73E-03	-1.11E+00	2.82E-04
497682488	regulatory protein	1.40E+01	-6.82E-01	7.17E-03	-7.82E-01	5.58E-03	-1.00E-01	6.23E-01
497683303	GntR family transcriptional regulator	1.26E+01	-3.74E-01	6.74E-03	-7.66E-01	2.72E-04	-3.92E-01	7.15E-03
490057455	transcriptional regulator	1.00E+01	8.74E-02	5.61E-01	-7.64E-01	1.80E-03	-8.52E-01	9.12E-04
497681294	DeoR family transcriptional regulator	1.34E+01	3.79E-01	9.13E-02	-7.62E-01	9.04E-03	-1.14E+00	1.12E-03
497681703	DNA-binding protein	1.09E+01	-9.07E-01	1.41E-02	1.19E+00	6.14E-03	2.10E+00	3.02E-04
490054440	DNA-binding protein	1.21E+01	1.93E-01	7.22E-01	1.77E+00	1.34E-02	1.57E+00	2.01E-02
490059845	GntR family transcriptional regulator	1.37E+01	-2.52E-01	7.66E-01	3.85E+00	2.66E-03	4.10E+00	1.68E-03

[a] Identification is based on annotation by NCBI. **[b]** Description is based on NCBI annotation of protein similarity by BLAST. **[c]** Average normalized expression in the WT strain. **[d]** Normalized $\log_2$ fold change in *ΔbldG* as compared to the WT strain. **[e]** Adjusted P-value in *ΔbldG* as compared to the WT strain. **[f]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the WT strain. **[g]** Adjusted P-value in *ΔbldA* as compared to the WT strain. **[h]** Normalized $\log_2$ fold change in *ΔbldA* as compared to the *ΔbldG* strain and **[i]** Adjusted P-value in *ΔbldA* as compared to the *ΔbldG* strain.

Appendix B: R code used for data analysis

```
##### July 2013
##### Author: Lourdes Pena-Castillo

#######
####### Analysis of protein intensity data S. clavuligerus

#Set the working directory to where the files are
dir = "Documents/Memorial/Proyectos/streptomyces_clavuligerus/"

setwd(dir)


## Read intensity matrix

int_raw <- read.table("intensityMatrix_S.clav_text.csv", sep =
"\t", header = TRUE)

#Let's verify the data was read correctly
colnames(int_raw)
str(int_raw)

#Read design matrix
design <- read.table("Designmatrix_prot_text.csv")

#Read ID and Description of proteins
ID_Description <- read.table("ID_Description.csv", sep = "\t",
header = FALSE, row.names = 1)
dim(ID_Description)
head(ID_Description)

####
# Aggregate intensity values per peptide using median

int_perProtein <-  apply(int_raw[,-1], 2, function(c, f) {
     tapply(c,f,median, na.rm = TRUE)
}, int_raw[,1] )

dim(int_perProtein)


int_perProtein_NZ <-  apply(int_perProtein, 2, function(c) {
      ifelse(is.na(c), 1, ifelse(c < 1, 1, c))
} )

#How many proteins - 2442
dim(int_perProtein_NZ)
```

```
#Let's get the log2 of the data

int_perProtein_NZ <- log2(int_perProtein_NZ)

#Let's look at the data

colors <- c(rep("orange", 3), rep("green",3), rep("magenta",2))

createPlots <- function(m, title, colors) {
     pdf(file = paste(title, "pdf", sep =".."), onefile = TRUE)
     plot(density(m[,1]), xlab = "Intensity", col = colors[1],
main = "Log2 Intensity", ylim = c(0, 0.3))
     sapply(2:ncol(m), function(i){
          lines(density(m[,i]), col = colors[i])
     })
     legend(5, 0.20, legend = colnames(design), fill =
colors[c(1,4,7)] )
     boxplot(m, col= colors, ylab = "Log2 Intensity")
     dev.off()
}

createPlots(int_perProtein_NZ, "Raw_Intensity", colors)

### Let's normalize using quantile normalization each strain
separately
### Remove technical variation between replicates

library(limma)
targets <- c(rep("WT",3), rep("bldG",3), rep("bldA",2) )
int_perProtein_norm <-
cbind(normalizeBetweenArrays(int_perProtein_NZ[,1:3], method =
"quantile"), normalizeBetweenArrays(int_perProtein_NZ[,4:6],
method = "quantile"),
normalizeBetweenArrays(int_perProtein_NZ[,7:8], method =
"quantile") )

createPlots(int_perProtein_norm, "Normalized_Intensity", colors)

### Identify DE proteins
### See Limma Manual Section 8.3

fit <- lmFit(int_perProtein_norm, design)

#Specify the comparison we want to make
contrast.matrix <- makeContrasts(bldG-WT,bldA-WT, bldA-bldG,
levels = design)

fit2 <- contrasts.fit(fit, contrast.matrix)
fit2 <- eBayes(fit2)
```

```
#which proteins are DE on each comparison
results <- decideTests(fit2, method = "separate", adjust.method =
"fdr", p.value = 0.05)
vennCounts(results)

#Let's look at the intersection between the conditions
pdf(file = "VennDiagram.pdf")
par(mfrow=c(2,1))
#This diagram also includes genes that were up in one sample and
down in the other, which is a less restrictive criterion.
vennDiagram(results, include = "both")
#This diagram shows only those genes that were either up in both
samples or down in both samples.
vennDiagram(results,include=c("up","down"),counts.col=c("red","gr
een"))
dev.off()


#Write the tables with the results
#First one file for each comparison
sapply(1:3, function(i){
     tmp <- topTable(fit2, coef = i, number = Inf, adjust.method
= "fdr", sort.by = "p")
     tmp <- cbind(tmp, ID_Description[tmp$ID,])
     colnames(tmp) <- c(colnames(tmp)[-ncol(tmp)],
"Description")
     filename <-  paste( gsub(" ", "",
colnames(contrast.matrix)[i]), "_results", ".csv", sep = "")
     write.table(tmp, file = filename, sep = "\t", row.names =
FALSE, col.names = TRUE)
})

#Ranked based on three comparisons
#The statistic fit2$F and the corresponding fit2$F.p.value
combine the three pair-wise comparisons into one F-test. This is
equivalent to a one-way ANOVA for each gene except that the
residual mean squares have been moderated between genes. To find
genes which vary between the three strains  in any way, look for
genes with small p-values
tmp <- topTableF(fit2, number=Inf, adjust.method = "fdr", sort.by
= "F")
tmp <- cbind(tmp, results[tmp$ID,], ID_Description[tmp$ID,])
write.table(tmp, file = "ANOVA_3Comparisons.csv", sep = "\t",
row.names = FALSE, col.names = TRUE)

########################
########################
#### Read Annotations
```

```
dirA <- "Annotations"
files <- list.files(dirA, pattern = "*_ID*", include.dirs = TRUE,
recursive = TRUE, full.names = TRUE)

files_des <- list.files(dirA, pattern = "*_description",
include.dirs = TRUE, recursive = TRUE, full.names = TRUE)

annotations <- sapply(files, read.table, sep = "\t",
stringsAsFactors = FALSE)
names(annotations) <- c("DC", "DcGO", "Pfam")

descriptions <- list()
descriptions$DC <- read.table(files_des[[1]], sep = "\t",
row.names = 1, stringsAsFactors = FALSE)
descriptions$DcGO <- read.table(files_des[[2]], sep = "\t",
row.names = 1, stringsAsFactors = FALSE)
descriptions$Pfam <- read.table(files_des[[3]], sep = "\t",
row.names = 1, stringsAsFactors = FALSE)

lapply(annotations, dim)
lapply(descriptions, dim)


#Select score to filter dcGO predictions
plot(density(as.numeric(annotations[[2]][,3, drop = TRUE])), main
= "dcGO Predictions", xlab = "Score")

#Filter dcGO to those predictions with a score > 0.85
annotations$DcGO <- annotations$DcGO[annotations$DcGO[,3] >
0.85,-3]


## Functional Enrichment DE Proteins

#Annot is a matrix with the proteinID on the first column and the
annotation ID
# in the second column
#DE is a vector with the list of DE proteins
#allproteins is a vector with the list of proteins in the
experiment
getEnrichmentDE <- function(Annot, DE, allproteins){
     require(GSEABase)
     require(GOstats)
     Annot <- as.matrix(Annot)
     #Separate protein ID based on the annotations
     gs <- split(Annot[,1], factor(Annot[,2], levels =
unique(Annot[,2])))
     # Create a gene set collection
```

```
      gsc <- GeneSetCollection( mapply(function(geneIds,
AnnotId){
        GeneSet(geneIds, setName= AnnotId)
       },gs, names(gs)))

      #Call the hypergeometric test
      params <- GSEAKEGGHyperGParams(name="My Custom GSEA based
annot Params",

      geneSetCollection=gsc,
                                              geneIds = DE,
                                              universeGeneIds =
allproteins,
                                              pvalueCutoff = 0.05,
                                              testDirection =
"over")
       over <- hyperGTest(params)
       return(over)
}


### Function to format results
### resOver is hyperG results
### gs is a list of gene sets
### descTerm is a matrix with the annotation ID as row name and
the annotation description
getTableResults <- function(resOver, Annot, DE, descTerm = NA){
      #get significant results - uncorrected pvalue 0.05
      SigResults <- summary(resOver)
       ###correct pvalues for multiple testing
      pvaluesFDR <- p.adjust(pvalues(resOver), method = "fdr")
      Annot <- as.matrix(Annot)
      #Separate protein ID based on the annotations
      gs <- split(Annot[,1], factor(Annot[,2], levels =
unique(Annot[,2])))

      ### Get DE genes in gene set
      DE_inGeneSets <- sapply(summary(resOver)[,1],  function(x,
geneSets) {
       paste(intersect(geneSets[[x]], DE), collapse =", ")}, gs)

      if (! is.na(descTerm)) {
            #descTerm has names == ID in SigResults
             SigResults[,"Term"] <- descTerm[SigResults[,1], ,
drop = TRUE]
      }

      tmp <- cbind(SigResults[,c("Term","KEGGID","Size","Count",
"Pvalue")] ,  pvaluesFDR[SigResults[,1]],
```

```
SigResults[,c("OddsRatio","ExpCount")],
DE_inGeneSets[SigResults[,1]] )

     colnames(tmp) <- c("Term", "ID", "Size", "Count", "Pvalue",
"Pvalue_FDR", "OddsRatio", "ExpCount","DE_Genes")
     return(tmp)
 }

#Get overenrichment for each comparison - annotation pair. Keep
in lists by annotation

Pfam_OE <- lapply(colnames(contrast.matrix), function(i){
     getEnrichmentDE(annotations$Pfam, topTable(fit2, coef = i,
number = Inf, adjust.method = "fdr", sort.by = "p", p.value =
10^-5)$ID, row.names(int_perProtein_norm))
})

DC_OE <- sapply(colnames(contrast.matrix), function(i){
     getEnrichmentDE(annotations$DC, topTable(fit2, coef = i,
number = Inf, adjust.method = "fdr", sort.by = "p", p.value =
10^-5)$ID, row.names(int_perProtein_norm))
})

GO_OE <- sapply(colnames(contrast.matrix), function(i){
     getEnrichmentDE(annotations$DcGO, topTable(fit2, coef = i,
number = Inf, adjust.method = "fdr", sort.by = "p", p.value =
10^-5)$ID, row.names(int_perProtein_norm))
})

names(Pfam_OE) <- names(DC_OE) <- names(GO_OE) <-
colnames(contrast.matrix)


#For each comparison and annotation pair get the table of
overenriched annotations
sapply(colnames(contrast.matrix), function(i, filename){
write.table(x = cbind(i, getTableResults(Pfam_OE[[i]],
annotations$Pfam, topTable(fit2, coef = i, number = Inf,
adjust.method = "fdr", sort.by = "p", p.value = 0.0001)$ID,
descriptions$Pfam)), file = filename, append = TRUE, sep = "\t",
row.names = FALSE)
}, "Pfam_OE_results_10-5.csv")


sapply(colnames(contrast.matrix), function(i, filename){
write.table(x = cbind(i, getTableResults(DC_OE[[i]],
annotations$DC, topTable(fit2, coef = i, number = Inf,
adjust.method = "fdr", sort.by = "p", p.value = 0.0001)$ID,
```

```
descriptions$DC)), file = filename, append = TRUE, sep = "\t",
row.names = FALSE)
}, "DC_OE_results_10-5.csv")


sapply(colnames(contrast.matrix), function(i, filename){
write.table(x = cbind(i, getTableResults(GO_OE[[i]],
annotations$DcGO, topTable(fit2, coef = i, number = Inf,
adjust.method = "fdr", sort.by = "p", p.value = 0.0001)$ID,
descriptions$DcGO)), file = filename, append = TRUE, sep = "\t",
row.names = FALSE)
}, "GO_OE_results_10-5.csv")



########################################
########################################
## Functional Class-scoring Analysis
library(gage)

#bldG - WT
bldG_WT_FCS <- lapply(annotations, function(Annot, expMatrix){
sigGeneSet(gage(expMatrix, ref =1:3, samp = 4:6, gsets =
split(Annot[,1], factor(Annot[,2], levels = unique(Annot[,2])))),
same.dir = TRUE, compare = "unpaired"))
}, int_perProtein_norm)

#bldA- WT
bldA_WT_FCS <- lapply(annotations, function(Annot, expMatrix){
sigGeneSet(gage(expMatrix, ref =1:3, samp = 7:8, gsets =
split(Annot[,1], factor(Annot[,2], levels = unique(Annot[,2])))),
same.dir = TRUE, compare = "unpaired"))
}, int_perProtein_norm)

#bldA- bldG
bldA_bldG_FCS <- lapply(annotations, function(Annot, expMatrix){
sigGeneSet(gage(expMatrix, ref =4:6, samp = 7:8, gsets =
split(Annot[,1], factor(Annot[,2], levels = unique(Annot[,2])))),
same.dir = TRUE, compare = "unpaired"))
}, int_perProtein_norm)

FCS_res <- do.call('rbind', lapply(names(bldG_WT_FCS),
function(i, FCS){
 rbind(
 cbind(FCS[[i]]$greater[,1:5, drop = FALSE],
descriptions[[i]][row.names(FCS[[i]]$greater),]),
 cbind(FCS[[i]]$less[,1:5, drop = FALSE],
descriptions[[i]][row.names(FCS[[i]]$less),]))
}, bldG_WT_FCS))
```

```
write.table(x = FCS_res, file = "FCS_results.csv", sep = "\t",
row.names = TRUE)

########################################
########################################



> sessionInfo()

# R version 3.0.0 (2013-04-03)
# Platform: x86_64-apple-darwin10.8.0 (64-bit)

# locale:
# [1] en_CA.UTF-8/en_CA.UTF-8/en_CA.UTF-8/C/en_CA.UTF-
8/en_CA.UTF-8

# attached base packages:
# [1] parallel  stats     graphics  grDevices utils     datasets
methods   base

# other attached packages:
 # [1] gage_2.10.0          GSEABase_1.22.0      annotate_1.38.0
KEGG.db_2.9.1        limma_3.16.5
 # [6] RSQLite_0.11.4       DBI_0.2-7            graph_1.38.2
Category_2.26.0      AnnotationDbi_1.22.6
# [11] Biobase_2.20.1       BiocGenerics_0.6.0

# loaded via a namespace (and not attached):
 # [1] AnnotationForge_1.2.2 genefilter_1.42.0     IRanges_1.18.1
RBGL_1.36.2           splines_3.0.0
 # [6] stats4_3.0.0          survival_2.37-4       tools_3.0.0
XML_3.95-0.2          xtable_1.7-1
```